Package ‘loon’

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License GPL-2

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as.graph

Convert a loongraph object to an object of class graph

Description

Loon’s native graph class is fairly basic. The graph package (on bioconductor) provides a more
powerful alternative to create and work with graphs. Also, many other graph theoretic algorithms
such as the complement function and some graph layout and visualization methods are implemented
for the graph objects in the RBGL and Rgraphviz R packages. For more information on packages
that are useful to work with graphs see the gRaphical Models in R CRAN Task View at https://
cran.r-project.org/web/views/.

Usage

as.graph(loongraph)

Arguments

loongraph object of class loongraph

Details

See https://www.bioconductor.org/packages/release/bioc/html/graph.html for more in-
formation about the graph R package.

Value

graph object of class loongraph

Examples

if (requireNamespace("graph", quietly = TRUE)) {
  g <- loongraph(letters[1:4], letters[1:3], letters[2:4], FALSE)
  g1 <- as.graph(g)
}
as.loongraph

Convert a graph object to a loongraph object

Description

Sometimes it is simpler to work with objects of class loongraph than to work with object of class graph.

Usage

as.loongraph(graph)

Arguments

graph object of class graph (defined in the graph library)

Details


For more information run: `l_help("learn_R_display_graph.html.html#graph-utilities")`

Value

graph object of class loongraph

Examples

```r
if (requireNamespace("graph", quietly = TRUE)) {
  graph_graph = graph::randomEGraph(LETTERS[1:15], edges=100)
  loon_graph <- as.loongraph(graph_graph)
}
```

as_grid_size

Turn a loon size to a grid size

Description

The size of loon is determined by pixel (px), while, in grid graphics, the size is determined by pointsize (pt)
as_grid_size(
  size,
  type = c("points", "texts", "images", "radial", "parallel", "polygon", "lines"),
  adjust = 1,
  ...
)

Arguments

size input loon size

type glyph type; one of "points", "texts", "images", "radial", "parallel", "polygon", "lines".

adjust a pixel (px) at 960PI (dots per inch) is equal to 0.75 point. However, for different machines, the DPI is slightly different. Argument adjust is used to twist the size. IT IS A HACK and should be removed in the later version.

... some arguments used to specify the size, e.g. pch for "points", ratio for "image" and p for "parallel".

as_hex6color  

Return a 6 hexadecimal digit color representations

Description

Return a 6 hexadecimal digit color representations

Usage

as_hex6color(color)

Arguments

color input color

Details

Compared with hex12tohex6(), it could accommodate 6 digit code, 12 digit code or real color names.

See Also

l_hexcolor, hex12tohex6, l_colorName
Examples

color <- c("#FF00FF", "#999999999999", "red")
# return 12 hexadecimal digit color
loon:::l_hexcolor(color)
# return 6 hexadecimal digit color
as_hex6color(color)
# return color names
l_colorName(color)

## Not run: # WRONG COLORS
hex12tohex6(color)
## End(Not run)

char2num.data.frame A Character Data Frame to a Numerical Data Frame

Description

Turn a data frame of characters to a data frame of numerical values. If the character cannot be
converted to numerical in direct, it will be turned to factor first, then to numerical data

Usage

char2num.data.frame(chardataframe)

Arguments

chardataframe A char data frame

Examples

data <- data.frame(x = c("1", "2", "3"),
y = c("foo", "bar", "foo"),
z = 4:6)
# ERROR
# data + 1
numData <- char2num.data.frame(data)
numData + 1

if(interactive()) {
  s <- l_serialaxes(iris)
data <- s["data"]
  # it is a character data frame
data[1,1]
numData <- char2num.data.frame(data)
numData[1,1]
}
Create a palette with loon’s color mapping

Description

Used to map nominal data to colors. By default these colors are chosen so that the categories can be well differentiated visually (e.g. to highlight the different groups)

Usage

color_loon()

Details

This is the function that loon uses by default to map values to colors. Loon’s mapping algorithm is as follows:

1. if all values already represent valid Tk colors (see tkcolors) then those colors are taken
2. if the number of distinct values is less than the number of values in loon’s color mapping list then they get mapped according to the color list, see l_setColorList and l_getColorList.
3. if there are more distinct values than there are colors in loon’s color mapping list then loon’s own color mapping algorithm is used. See loon_palette and the details section in the documentation of l_setColorList.

For other mappings see the col_numeric and col_factor functions from the scales package.

Value

A function that takes a vector with values and maps them to a vector of 6 digit hexadecimal encoded color representation (strings). Note that loon uses internally 12 digit hexadecimal encoded color values. If all the values that get passed to the function are valid color names in Tcl then those colors get returned hexencoded. Otherwise, if there is one or more elements that is not a valid color name it uses the loons default color mapping algorithm.

See Also

l_setColorList, l_getColorList, loon_palette, l_hexcolor, l_colorName, as_hex6color

Examples

```r
pal <- color_loon()
pal(letters[1:4])
pal(c('a','a','b','c'))
pal(c('green', 'yellow'))
```

# show color choices for different n's
if (requireNamespace("grid", quietly = TRUE)) {

```r
```

```r
```
Create the Complement Graph of a Graph

Description

Creates a complement graph of a graph

Usage

complement(x)

Arguments

x  

Value

graph object
completegraph

Create the Complement Graph of a loong Graph

Description

Creates a complement graph of a graph

Usage

```r
## S3 method for class 'loongraph'
complement(x)
```

Arguments

- `x`: loongraph object

Details

This method is currently only implemented for undirected graphs.

Value

graph object of class loongraph

completegraph

Create a complete graph or digraph with a set of nodes

Description

From Wikipedia: "a complete graph is a simple undirected graph in which every pair of distinct vertices is connected by a unique edge. A complete digraph is a directed graph in which every pair of distinct vertices is connected by a pair of unique edges (one in each direction)

Usage

```r
completegraph(nodes, isDirected = FALSE)
```

Arguments

- `nodes`: a character vector with node names, each element defines a node hence the elements need to be unique
- `isDirected`: a boolean scalar to indicate whether the returned object is a complete graph (undirected) or a complete digraph (directed).
condGrob

Details
Note that this function masks the completegraph function of the graph package. Hence it is a good
idea to specify the package namespace with ::, i.e. loon::completegraph and graph::completegraph.
For more information run: l_help("learn_R_display_graph.html.html#graph-utilities")

Value
graph object of class loongraph

Examples

```r
g <- loon::completegraph(letters[1:5])
```

condGrob

Create a named grob or a template grob depending on a test

Description
Creates and returns a grid object using the function given by ‘grobFun’ when ‘test’ is ‘TRUE’
Otherwise a simple ‘grob()’ is produced with the same parameters. All grob parameters are given
in ‘...’.

Usage

```r
condGrob(test = TRUE, grobFun = grid::grob, name = "grob name", ...)
```

Arguments
test Either ‘TRUE’ or ‘FALSE’ to indicate whether ‘grobFun’ is to be used (default
‘TRUE’) or not.
grobFun The function to be used to create the grob when ‘test = TRUE’ (e.g. ‘textGrob’,
‘polygonGrob’, etc.).
name The name to be used for the returned grob.
... The arguments to be given to the ‘grobFun’ (or to ‘grob()’ when ‘test = FALSE’).

Value
A grob as produced by either the ‘grobFun’ given or by ‘grob()’ using the remaining arguments. If
‘test = FALSE’ then the name is suffixed by ": ‘grobFun name’ arguments”.

Examples

```r
myGrob <- condGrob(test = (runif(1) > 0.5),
                  grobFun = textGrob,
                  name = "my label",
                  label = "Some random text")
```

myGrob
facet_grid_layout  Layout as a grid

Description

Layout as a grid

Usage

```r
facet_grid_layout(
  plots,
  subtitles,
  by = NULL,
  prop = 10,
  parent = NULL,
  title = "",
  xlabel = "",
  ylabel = "",
  labelLocation = c("top", "right"),
  byrow = FALSE,
  swapAxes = FALSE,
  labelBackground = l_getOption("facetLabelBackground"),
  labelForeground = l_getOption("foreground"),
  labelBorderwidth = 2,
  labelRelief = "ridge",
  plotWidth = 200,
  plotHeight = 200,
  sep = "*",
  maxCharInOneRow = 10,
  new.toplevel = TRUE,

  ...
)
```

Arguments

- **plots**: A list of loon plots
- **subtitles**: The subtitles of the layout. It is a list and the length is equal to the number of by variables. Each element in a list is the unique values of such by variable.
- **by**: an object of class "formula" (or one that can be coerced to that class): a symbolic description of the plots separated by
- **prop**: The proportion of the label height and widget height
- **parent**: a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like `tkpack` or `tkplace` in order to be displayed. See the examples below.
- **title**: The title of the widget
facet_separate_layout

Description

layout separately

Usage

```r
facet_separate_layout(
  plots,
  subtitles,
  title = "",
  xlabel = "",
  ylabel = "",
  sep = "*",
  maxCharInOneRow = 10,
  ...
)
```
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facet_wrap_layout

Arguments

plots A list of loon plots
subtitles The subtitles of the layout. It is a list and the length is equal to the number of by
variables. Each element in a list is the unique values of such by variable.
title The title of the widget
xlabel The xlabel of the widget
ylabel The ylabel of the widget
sep The character string to separate or combine a vector
maxCharInOneRow

... named arguments to modify plot states. See l_info_states of any instantiated
l_plot for examples of names and values.

Description

Layout as a wrap

Usage

facet_wrap_layout(
  plots,
  subtitles,
  prop = 10,
  parent = NULL,
  title = "",
  xlabel = "",
  ylabel = "",
  nrow = NULL,
  ncol = NULL,
  labelLocation = "top",
  byrow = TRUE,
  swapAxes = FALSE,
  labelBackground = l_getOption("facetLabelBackground"),
  labelForeground = l_getOption("foreground"),
  labelBorderwidth = 2,
  labelRelief = "ridge",
  plotWidth = 200,
  plotHeight = 200,
  sep = ",",
  maxCharInOneRow = 10,
  new.toplevel = TRUE,
  ...
)
**Arguments**

- **plots**: A list of loon plots
- **subtitles**: The subtitles of the layout. It is a list and the length is equal to the number of by variables. Each element in a list is the unique values of such by variable.
- **prop**: The proportion of the label height and widget height
- **parent**: a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like `tkpack` or `tkplace` in order to be displayed. See the examples below.
- **title**: The title of the widget
- **xlabel**: The xlabel of the widget
- **ylabel**: The ylabel of the widget
- **nrow**: The number of layout rows
- **ncol**: The number of layout columns
- **labelLocation**: Labels location.
  - Length two vector for layout grid. The first one is used to determine the position of column labels ('top' or 'bottom'). The second one is used to determine the position of row labels ('right' or 'left').
  - Length one vector for layout wrap, 'top' or 'bottom'.
- **byrow**: Place widget by row or by column
- **swapAxes**: swap axes, TRUE or FALSE
- **labelBackground**: Label background color
- **labelForeground**: Label foreground color
- **labelBorderwidth**: Label border width
- **labelRelief**: Label relief
- **plotWidth**: default plot width (in pixel)
- **plotHeight**: default plot height (in pixel)
- **sep**: The character string to separate or combine a vector
- **maxCharInOneRow**: deprecated
- **new.toplevel**: determine whether the parent is a new top level. If it is not a new window, the widgets will not be packed
- **...**: named arguments to modify plot states. See `l_info_states` of any instantiated `l_plot` for examples of names and values.
get_display_color  Return the Displayed Color

Description
Always reflect the current displayed color.

Usage
get_display_color(color, selected)

Arguments
- color: the loon widget color
- selected: the selected states

Details
In loon, each element (i.e. point, bin, line) has a "temporary" color and a "permanent" color. If one element is selected, the color is switched to the "temporary" color to highlight it. If the selection state is eliminated, the "permanent" color of this element will be displayed. Our function always gives the "temporary" displayed color.

Value
The color shown on the plot

Examples
if(interactive()) {
  p <- l_plot(1:10)
  p['selected'][c(1,3,5)] <- TRUE

  displayedColor <- get_display_color(p['color'], p['selected'])
  plot(1:10, bg = as_hex6color(displayedColor), pch = 21)
}

get_font_info_from_tk  Return Font Information

Description
Return Font Information

Usage
get_font_info_from_tk(tkFont)
get_layer_states

**Arguments**

- **tkFont**: A specified tk font character, one of `l_getOption("font-scales")`, `l_getOption("font-title")`, `l_getOption("font-xlabel")`, `l_getOption("font-ylabel")`

**Value**

A list of font information, containing font "family", font "face" and font "size"

**Examples**

```r
fontscales <- l_getOption("font-scales")
get_font_info_from_tk(fontscales)
```

---

**Description**

Return the input widget states

**Usage**

```r
get_layer_states(target, native_unit = TRUE, omit = NULL)
```

**Arguments**

- **target**: either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. `.l0.plot`), the remaining objects by their ids.
- **native_unit**: return numerical vectors or unit objects
- **omit**: deprecated

**Details**

get layer states

**Examples**

```r
if(interactive()){
p <- l_plot(x = c(0,1), y = c(0,1))
l <- l_layer_rectangle(p, x = c(0,0.5), y = c(0, 0.5))
# the coordinates are in 'unit'
get_layer_states(p)
# the coordinates are numerical
get_layer_states(p, native_unit = FALSE)
# get 'l_layer' state
get_layer_states(l)
}
```
get_model_display_order

*Get the Order of the Display*

### Description

In *loon*, if points (in scatter plot) or lines (in parallel or radial coordinate) are highlighted, the displayed order will be changed. This function always reflects the current displayed order.

### Usage

```r
get_model_display_order(widget)
```

### Arguments

- **widget**
  - An *l_plot* or *l_serialaxes* widget

### Examples

```r
if(interactive()) {
  p <- l_plot(rnorm(10))
  get_model_display_order(p)
  p$selected[c(1,3,5,7)] <- TRUE
  # The 1st, 3rd, 5th, 7th points will be drawn afterwards
  # to make sure that they are displayed on top
  get_model_display_order(p)
}
```

glyph_to_pch

*Glyph to Pch*

### Description

turn a *loon* point glyph to an R graphics plotting 'character' (pch)

### Usage

```r
glyph_to_pch(glyph)
```

### Arguments

- **glyph**
  - glyph type in *loon*, must be "circle", "ocircle", "ccircle", "square", "osquare", "csquare", "triangle", "otriangle", "ctriangle", "diamond", "cdiamond", "odiamond". If the input glyph is not valid, NA is returned.
Value

A `pch` type

Examples

glyph_to_pch(c("circle", "ocircle", "ccircle", "square", "osquare", "csquare", "triangle", "otriangle", "ctriangle", "diamond", "cdiamond", "odiamond", "foo"))

Description

Reduce a graph to have unique node names

Usage

graphreduce(graph, separator)

Arguments

- `graph`: graph of class loongraph
- `separator`: one character that separates the spaces in node names

Details

Note this is a string based operation. Node names must not contain the separator character!

Value

Graph object of class loongraph

Examples

```r
G <- completegraph(nodes=LETTERS[1:4])
LG <- linegraph(G)
LLG <- linegraph(LG)
R_LLG <- graphreduce(LLG)
```
grid.loon

Create and optionally draw a grid grob from a loon widget handle

Description

Create and optionally draw a grid grob from a loon widget handle

Usage

grid.loon(target, name = NULL, gp = gpar(), draw = TRUE, vp = NULL)

Arguments

target
  either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. '/quotesingle.Var\l_0.plot'), the remaining objects by their ids.

name
  a character identifier for the grob, or NULL. Used to find the grob on the display list and/or as a child of another grob.

gp
  a gpar object, or NULL, typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.

draw
  a logical value indicating whether graphics output should be produced.

vp
  a grid viewport object (or NULL).

Value

a grid grob of the loon plot

See Also

loonGrob, plot.loon

Examples

## Not run:
library(grid)
widget <- with(iris, l_plot(Sepal.Length, Sepal.Width))
grid.loon(widget)

## End(Not run)
**hex12tohex6**

Convert 12 hexadecimal digit color representations to 6 hexadecimal digit color representations

**Description**

Tk colors must be in 6 hexadecimal format with two hexadecimal digits for each of the red, green, and blue components. Twelve hexadecimal digit colors have 4 hexadecimal digits for each. This function converts the 12 digit format to the 6 provided the color is preserved.

**Usage**

hex12tohex6(x)

**Arguments**

- **x**: a vector with 12 digit hexcolors

**Details**

Function throws a warning if the conversion loses information. The `l_hexcolor` function converts any Tcl color specification to a 12 digit hexadecimal color representation.

**Examples**

```r
x <- l_hexcolor(c("red", "green", "blue", "orange"))
x
hex12tohex6(x)
```

---

**L2_distance**

Euclidean distance between two vectors, or between column vectors of two matrices.

**Description**

Quickly calculates and returns the Euclidean distances between m vectors in one set and n vectors in another. Each set of vectors is given as the columns of a matrix.

**Usage**

L2_distance(a, b, df = 0)
Arguments

a  A d by m numeric matrix giving the first set of m vectors of dimension d as the columns of a.
b  A d by n numeric matrix giving the second set of n vectors of dimension d as the columns of b.
df Indicator whether to force the diagonals of the returned matrix to be zero (df = 1) or not (the default df = 0).

Details

This fully vectorized (VERY FAST!) function computes the Euclidean distance between two vectors by:
\[ \|A-B\| = \sqrt{\|A\|^2 + \|B\|^2 - 2*A.B} \]
Originally written as L2_distance.m for Matlab by Roland Bunschoten of the University of Amsterdam, Netherlands.

Value

An m by n matrix containing the Euclidean distances between the column vectors of the matrix a and the column vectors of the matrix b.

Author(s)

Roland Bunschoten (original), Adrian Waddell, Wayne Oldford

See Also

dist

Examples

```r
A <- matrix(rnorm(400), nrow = 10)
B <- matrix(rnorm(800), nrow = 10)
L2_distance(A[,1, drop = FALSE], B[,1, drop = FALSE])
d_AB <- L2_distance(A,B)
d_BB <- L2_distance(B,B, df = 1) # force diagonal to be zero
```

Description

The line graph of G, here denoted L(G), is the graph whose nodes correspond to the edges of G and whose edges correspond to nodes of G such that nodes of L(G) are joined if and only if the corresponding edges of G are adjacent in G.
Usage

\texttt{linegraph(x, \ldots)}

Arguments

\begin{itemize}
  \item \texttt{x} \quad \text{graph of class graph or loongraph}
  \item \texttt{\ldots} \quad \text{arguments passed on to method}
\end{itemize}

Value

graph object

\hline

\texttt{linegraph.loongraph} \quad \textit{Create a linegraph of a graph}

\hline

Description

Create a lingraph of a loongraph

Usage

\begin{verbatim}
## S3 method for class 'loongraph'
linegraph(x, separator = ":", \ldots)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{x} \quad \text{loongraph object}
  \item \texttt{separator} \quad \text{one character - node names in x get concatenated with this character}
  \item \texttt{\ldots} \quad \text{additional arguments are not used for this method}
\end{itemize}

Details

\texttt{linegraph.loongraph} needs the code part for directed graphs (i.e. isDirected=TRUE)

Value

graph object of class loongraph

Examples

\begin{verbatim}
g <- loongraph(letters[1:4], letters[1:3], letters[2:4], FALSE)
linegraph(g)
\end{verbatim}
Description

Loon is a toolkit for highly interactive data visualization. Interactions with plots are provided with mouse and keyboard gestures as well as via command line control and with inspectors that provide graphical user interfaces (GUIs) for modifying and overseeing plots.

Details

Currently, loon implements the following statistical graphs: histogram, scatterplot, serialaxes plot (star glyphs, parallel coordinates) and a graph display for creating navigation graphs.

Some of the implemented scatterplot features, for example, are zooming, panning, selection and moving of points, dynamic linking of plots, layering of visual information such as maps and regression lines, custom point glyphs (images, text, star glyphs), and event bindings. Event bindings provide hooks to evaluate custom code at specific plot state changes or mouse and keyboard interactions. Hence, event bindings can be used to add to or modify the default behavior of the plot widgets.

Loon’s capabilities are very useful for statistical analysis tasks such as interactive exploratory data analysis, sensitivity analysis, animation, teaching, and creating new graphical user interfaces.

To get started using loon read the package vignettes or visit the loon website at https://great-northern-diver.github.io/loon/.

Author(s)

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• Zehao Xu <z267xu@uwaterloo.ca> [contributor]
• Martin Gauch <martin.gauch@student.kit.edu> [contributor]

See Also

Useful links:

• https://great-northern-diver.github.io/loon/
• Report bugs at https://github.com/great-northern-diver/loon/issues
Create a graph object of class loongraph

Description

The loongraph class provides a simple alternative to the graph class to create common graphs that are useful for use as navigation graphs.

Usage

loongraph(nodes, from = character(0), to = character(0), isDirected = FALSE)

Arguments

- **nodes**: a character vector with node names, each element defines a node hence the elements need to be unique
- **from**: a character vector with node names, each element defines an edge
- **to**: a character vector with node names, each element defines an edge
- **isDirected**: boolean scalar, defines whether from and to define directed edges

Details

loongraph objects can be converted to graph objects (i.e. objects of class graph which is defined in the graph package) with the as.graph function.

For more information run: l_help("learn_R_display_graph.html.html#graph-utilities")

Value

graph object of class loongraph

See Also

completegraph, linegraph, complement, as.graph

Examples

```r
  g <- loongraph(
    nodes = c("A", "B", "C", "D"),
    from = c("A", "A", "B", "B", "C"),
    to = c("B", "C", "C", "D", "D")
  )

  # Not run:
  # create a loon graph plot
  p <- l_graph(g)

  # End(Not run)

  lg <- linegraph(g)
```
Create a grid grob from a loon widget handle

Description

Grid grobs are useful to create publication quality graphics.

Usage

loonGrob(target, name = NULL, gp = NULL, vp = NULL)

## S3 method for class 'l_compound'
loonGrob(target, name = NULL, gp = NULL, vp = NULL)

## S3 method for class 'l_layer_graph'
loonGrob(target, name = NULL, gp = NULL, vp = NULL)

## S3 method for class 'l_layer_histogram'
loonGrob(target, name = NULL, gp = NULL, vp = NULL)

## S3 method for class 'l_layer_scatterplot'
loonGrob(target, name = NULL, gp = NULL, vp = NULL)

## S3 method for class 'l_navgraph'
loonGrob(target, name = NULL, gp = NULL, vp = NULL)

## S3 method for class 'l_navigator'
loonGrob(target, name = NULL, gp = NULL, vp = NULL)

## S3 method for class 'l_serialaxes'
loonGrob(target, name = NULL, gp = NULL, vp = NULL)

## S3 method for class 'l_ts'
loonGrob(target, name = NULL, gp = NULL, vp = NULL)

Arguments

target

either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. `.l0.plot`), the remaining objects by their ids.

name

a character identifier for the grob, or NULL. Used to find the grob on the display list and/or as a child of another grob.

gp

a gpar object, or NULL, typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.

vp

a grid viewport object (or NULL).
loonGrob

Value

a grid grob

See Also

grid.loon

Examples

## Not run:

```r
widget <- with(iris, l_plot(Sepal.Length, Sepal.Width))
lgrob <- loonGrob(widget)
library(grid)
grid.ls(lgrob, viewports=TRUE, fullNames=TRUE)
grid.newpage(); grid.draw(lgrob)
p <- demo("l_layers", ask = FALSE)$value
lgrob <- loonGrob(p)
grid.newpage(); grid.draw(lgrob)
p <- demo("l_glyph_sizes", ask = FALSE)$value
lgrob <- loonGrob(p)
grid.newpage()
grid.draw(lgrob)
## End(Not run)
```

## Not run:

```r
library(grid)
## l_pairs (scatterplot matrix) examples
p <- l_pairs(iris[-5], color=iris$Species)
lgrob <- loonGrob(p)
grid.newpage()
grid.draw(lgrob)
## Time series decomposition examples

decompose <- decompose(co2)
# or decompose <- stl(co2, "per")
p <- l_plot(decompose, title = "Atmospheric carbon dioxide over Mauna Loa")
# To print directly use either
plot(p)
```
# or grid.loon(p)
# or to save structure
lgrob <- loonGrob(p)
grid.newpage()
grid.draw(lgrob)

## End(Not run)

## Not run:
## graph examples

G <- completeGraph(names(iris[, -5]))
LG <- lineGraph(G)
g <- l_graph(LG)

nav0 <- l_navigator_add(g)
l_configure(nav0, label = 0)
con0 <- l_context_add_geodesic2d(navigator=nav0, data=iris[, -5])

nav1 <- l_navigator_add(g, from = "Sepal.Length\:Petal.Width",
                         to = "Petal.Length\:Petal.Width", proportion = 0.6)
l_configure(nav1, label = 1)
con1 <- l_context_add_geodesic2d(navigator=nav1, data=iris[, -5])

nav2 <- l_navigator_add(g, from = "Sepal.Length\:Sepal.Width",
                         to = "Petal.Length\:Petal.Length", proportion = 0.5)
l_configure(nav2, label = 2)
con2 <- l_context_add_geodesic2d(navigator=nav2, data=iris[, -5])

# To print directly use either
plot(g)
# or
grid.loon(g)
# or to save structure
library(grid)
lgrub <- loonGrob(g)
grid.newpage(); grid.draw(lgrob)

## End(Not run)

## Not run:
## histogram examples

h <- l_hist(iris$Sepal.Length, color=iris$Species)
g <- loonGrob(h)
library(grid)
grid.newpage(); grid.draw(g)
h['showStackedColors'] <- TRUE

g <- loonGrob(h)

grid.newpage(); grid.draw(g)

h['colorStackingOrder'] <- c("selected", unique(h['color']))

g <- loonGrob(h)
grid.newpage(); grid.draw(g)

h['colorStackingOrder'] <- rev(h['colorStackingOrder'])

# To print directly use either
plot(h)
# or
grid.loon(h)

## End(Not run)

if(interactive()) {

## l_plot scatterplot examples

p <- l_plot(x = c(0,1), y = c(0,1))
l_layer_rectangle(p, x = c(0,1), y = c(0,1))

g <- loonGrob(p)

library(grid)
grid.newpage(); grid.draw(g)

p['glyph'] <- "ctriangle"
p['color'] <- "blue"
p['size'] <- c(10, 20)
p['selected'] <- c(TRUE, FALSE)

g <- loonGrob(p)
grid.newpage(); grid.draw(g)

}

## Not run:
## navgraph examples

ng <- l_navgraph(oliveAcids, separator='- ', color=olive$Area)

# To print directly use either
plot(ng)
# or
grid.loon(ng)
# or to save structure
lgrob <- loonGrob(ng)
library(grid)
grid.newpage()
grid.draw(lgrob)

## End(Not run)

## Serial axes (radial and parallel coordinate) examples
if(interactive()) {
  s <- l_serialaxes(data = oliveAcids, color = olive$Area, title = "olive data")
  sGrob_radial <- loonGrob(s)
  library(grid)
  grid.newpage(); grid.draw(sGrob_radial)
  s['axesLayout'] <- 'parallel'
  sGrob_parallel <- loonGrob(s)
  grid.newpage(); grid.draw(sGrob_parallel)
}

## Not run:

## Time series decomposition examples
decompose <- decompose(co2)
# or decompose <- stl(co2, "per")
p <- l_plot(decompose, title = "Atmospheric carbon dioxide over Mauna Loa")

# To print directly use either
plot(p)
# or
grid.loon(p)
# or to save structure
lgrob <- loonGrob(p)
grid.newpage()
grid.draw(lgrob)

## End(Not run)

### loonGrobInstantiation

**Instantiate a Grob**

**Description**

Functions used to instantiate grob descriptions appearing in the gTree produced by loonGrob().

**Usage**

```r
l_updateGrob(grobDesc, grobFun, ...)

l_instantiateGrob(loonGrob, gPath, grobFun, ...)

l_setGrobPlotView(loonGrob, margins)
```
loonGrobInstantiation

Arguments

- **grobDesc**: A grob description. Generally, it is created by the function `grob()`.  
- **grobFun**: A new grob function. If missing, a best guess (based on `gPath`) will be tried.  
- **...**: arguments used to set in the new grob function  
- **loonGrob**: A loonGrob (a gTree object)  
- **gPath**: A grob path object specifying a descendant of the specified gTree  
- **margins**: plot view margins. If missing, a loon default margin will be used.

Details

- **l_updateGrob**: query arguments from a grob description and assign these arguments to a new grob function.  
- **l_instantiateGrob**: query a descendant from a loonGrob, update it via a new grob function, then return the new edited loonGrob

See Also

loonGrob

Examples

```r
library(grid)
grobDesc <- grob(label = "loon",
                  gp = gpar(col = "red"))
grid.newpage()
# Nothing is displayed
grid.draw(grobDesc)
textDesc <- l_updateGrob(grobDesc, grid::textGrob)
grid.newpage()
# label "loon" is shown
grid.draw(textDesc)

if(interactive()) {
  # a loon plot with hidden labels
  p <- l_plot(iris, showLabels = FALSE)
  lg <- loonGrob(p)
  # x label and y label are invisible
  grid.newpage()
  grid.draw(lg)

  # show x label
  lg <- l_instantiateGrob(lg, "x label: textGrob arguments")
  # show y label
  lg <- l_instantiateGrob(lg, "y label: textGrob arguments")
  # reset margins
  lg <- l_setGrobPlotView(lg)
  grid.newpage()
  grid.draw(lg)
}  
```
# show axes
if(packageVersion("loon") < '1.3.8') {
  lg <- l_instantiateGrob(lg, "x axis: .xaxisGrob arguments")
  lg <- l_instantiateGrob(lg, "y axis: .yaxisGrob arguments")
} else {
  lg <- l_instantiateGrob(lg, "x axis: .xaxisGrob arguments")
  lg <- l_instantiateGrob(lg, "y axis: .yaxisGrob arguments")
}

lg <- l_setGrobPlotView(lg)
grid.newpage()
# the labels are too close to the plot
grid.draw(lg)

# reset the labels’ positions
lg <- l_instantiateGrob(lg, "x label: textGrob arguments",
  y = unit(-3.5, "lines"))
lg <- l_instantiateGrob(lg, "y label: textGrob arguments",
  x = unit(-6.5, "lines"))
grid.newpage()
ggrid.draw(lg)

loonGrob_layoutType

loonGrob_layoutType A generic function used to distinguish whether only the locations of plots will be used to arrange them in a grob, or whether all arguments to ‘gridExtra::arrangeGrob()’ will be used.

Description
A generic function used to distinguish whether only the locations of plots will be used to arrange them in a grob, or whether all arguments to ‘gridExtra::arrangeGrob()’ will be used.

Usage
loonGrob_layoutType(target)

Arguments

  target the (compound) loon plot to be laid out.

Value
either the string "locations" (the default) or the string "arrangeGrobArgs". If "locations", then the generic function ‘l_getLocations()’ will be called and only the location arguments of ‘gridExtra::arrangeGrob()’ used (i.e. a subset of c("ncol", "nrow", "layout_matrix", "heights", "widths")). The grobs to be laid out are constructed using the generic function ‘l_getPlots()’. 
loon_palette

Description

Loon has a color sequence generator implemented that creates a color palette where the first $m$ colors of a color palette of size $m+1$ are the same as the colors in a color palette of size $m$, for all positive natural numbers $m$. See the details in the `l_setColorList` documentation.

Usage

loon_palette(n)

Arguments

n number of different colors in the palette

Value

vector with hex-encoded color values

See Also

`l_setColorList`

Examples

loon_palette(12)

l_after_idle

Evaluate a function once the processor is idle

Description

It is possible for an observer to call the configure method of that plot while the plot is still in the configuration pipeline. In this case, a warning is thrown as unwanted side effects can happen if the next observer in line gets an outdated notification. In this case, it is recommended to use the `l_after_idle` function that evaluates some code once the processor is idle.

Usage

l_after_idle(fun)

Arguments

fun function to be evaluated once tcl interpreter is idle
l_aspect<- Query the aspect ratio of a plot

Description
The aspect ratio is defined by the ratio of the number of pixels for one data unit on the y axis and
the number of pixels for one data unit on the x axes.

Usage
l_aspect(widget)

Arguments
widget widget path as a string or as an object handle

Value
aspect ratio

Examples
## Not run:
p <- with(iris, l_plot(Sepal.Length ~ Sepal.Width, color=Species))
l_aspect(p)
l_aspect(p) <- 1
## End(Not run)

l_aspect<- Set the aspect ratio of a plot

Description
The aspect ratio is defined by the ratio of the number of pixels for one data unit on the y axis and
the number of pixels for one data unit on the x axes.

Usage
l_aspect(widget) <- value

Arguments
widget widget path as a string or as an object handle
value aspect ratio
Changing the aspect ratio with `l_aspect<-` changes effectively the `zoomY` state to obtain the desired aspect ratio. Note that the aspect ratio in loon depends on the plot width, plot height and the states `zoomX`, `zoomY`, `deltaX`, `deltaY` and `swapAxes`. Hence, the aspect aspect ratio can not be set permanently for a loon plot.

Examples

```r
## Not run:
p <- with(iris, l_plot(Sepal.Length ~ Sepal.Width, color=Species))

l_aspect(p)
l_aspect(p) <- 1

## End(Not run)
```

---

**Description**

Loon’s plots are constructed in TCL and identified with a path string appearing in the window containing the plot. The path string begins with a unique identifier for the plot and ends with a suffix describing the type of loon plot being displayed.

The path identifying the plot is the string concatenation of both the identifier and the type.

This function returns the set of the base (non-compound) loon path types.

**Usage**

```r
l_basePaths()
```

**Value**

character vector of the base path types.

**See Also**

`l_compoundPaths` `l_getFromPath` `l_loonWidgets`
Description

`l_binCut` divides `l_hist` widget `x` into current histogram intervals and codes values `x` according to which interval they fall (if active). It is modelled on `cut` in base package.

Usage

```r
l_binCut(widget, labels, digits = 2, inactive)
```

Arguments

- **widget**: A loon histogram widget.
- **labels**: Labels to identify which bin observations are in. By default, labels are constructed using 
  `[a,b]` interval notation. If `labels = FALSE`, simple integer codes given by the histogram’s bin number are returned instead of a factor. The labels can also be any vector of length equal to the number of bins; these will be used to construct a vector identifying the bins.
- **digits**: The number of digits used in formatting the breaks for default labels.
- **inactive**: The value to use for inactive observations when labels is a vector. Default depends on `labels`.

Value

A vector of bin identifiers having length equal to the total number of observations in the histogram. The type of vector depends on the `labels` argument. For default labels = `NULL`, a factor is returned, for `labels = FALSE`, a vector of bin numbers, and for arbitrary vector labels a vector of bins labelled in order of labels will be returned. Inactive cases appear in no bin and so are assigned the value of active when given. The default active value also depends on `labels`: when `labels = NULL`, the default active is `"(-Inf,Inf)"`; when `codelabels = FALSE`, the default active is `-1`; and when `labels` is a vector of length equal to the number of bins, the default active is `NA`. The value of active denotes the bin name for the inactive cases.

See Also

`l_getBinData, l_getBinIds, l_breaks`

Examples

```r
if(interactive()) {
  h <- l_hist(iris)
  h["active"] <- iris$Species != "setosa"
  binCut <- l_binCut(h)
  h["color"] <- binCut
  ## number of bins
```
nBins <- length(l_getBinIds(h))
## ggplot color hue
gg_color_hue <- function(n) {
    hues <- seq(15, 375, length = n + 1)
    hcl(h = hues, l = 65, c = 100)[1:n]
}
h['color'] <- l_binCut(h, labels = gg_color_hue(nBins), inactive = "firebrick")
h['active'] <- TRUE
}
Examples

```r
# binding for when plot is resized
if(interactive()){
  p <- l_plot(iris[,1:2], color=iris$Species)

  printSize <- function(p) {
    size <- l_size(p)
    cat(paste('Size of widget ', p, ' is: ',
             size[1], 'x', size[2], ' pixels\n', sep=''))
  }

  l_bind_canvas(p, event='<Configure>', function(W) {printSize(W)})

  id <- l_bind_canvas_ids(p)
  id

  l_bind_canvas_get(p, id)
}
```

---

**l_bind_canvas_delete**  
*Delete a canvas binding*

**Description**

Remove a canvas binding

**Usage**

```r
l_bind_canvas_delete(widget, id)
```

**Arguments**

- `widget`  
  widget path as a string or as an object handle
- `id`  
  canvas binding id

**Details**

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

**See Also**

`l_bind_canvas, l_bind_canvas_ids, l_bind_canvas_get, l_bind_canvas_reorder`
\texttt{l_bind_canvas_get} \hspace{1cm} \textit{Get the event pattern and callback Tcl code of a canvas binding}

\textbf{Description}

This function returns the registered event pattern and the Tcl callback code that the Tcl interpreter evaluates after a event occurs that matches the event pattern.

\textbf{Usage}

\texttt{l_bind_canvas_get(widget, id)}

\textbf{Arguments}

- \texttt{widget} \hspace{1cm} widget path as a string or as an object handle
- \texttt{id} \hspace{1cm} canvas binding id

\textbf{Details}

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run \texttt{l_help("learn_R_bind")}

\textbf{Value}

Character vector of length two. First element is the event pattern, the second element is the Tcl callback code.

\textbf{See Also}

\texttt{l_bind_canvas, l_bind_canvas_ids, l_bind_canvas_delete, l_bind_canvas_reorder}

\textbf{Examples}

\begin{verbatim}
# binding for when plot is resized
if(interactive()){
  p <- \texttt{l_plot(iris[,1:2], color=iris$Species)}

  printSize <- \texttt{function(p) {}
    size <- \texttt{l_size(p)}
    \texttt{cat(paste('Size of widget ', p, ' is: ',
                     size[1], ' x ', size[2], ' pixels\n', sep=''))}
  }

  \texttt{l_bind_canvas(p, event='<Configure>', function(W) {printSize(W)})}

  id <- \texttt{l_bind_canvas_ids(p)}

  \texttt{l_bind_canvas_get(p, id)}
\end{verbatim}
### 1_bind_canvas_ids

**List canvas binding ids**

**Description**
List all user added canvas binding ids

**Usage**

```r
1_bind_canvas_ids(widget)
```

**Arguments**

- `widget` widget path as a string or as an object handle

**Details**

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

**Value**

vector with canvas binding ids

**See Also**

- `1_bind_canvas`, `1_bind_canvas_get`, `1_bind_canvas_delete`, `1_bind_canvas_reorder`

**Examples**

```r
# binding for when plot is resized
if(interactive()){
  p <- l_plot(iris[,1:2], color=iris$Species)

  printSize <- function(p) {
    size <- l_size(p)
    cat(paste('Size of widget ', p, ' is: ',
              size[1], 'x', size[2], ' pixels
n', sep=''))
  }

  l_bind_canvas(p, event='<Configure>', function(W) {printSize(W)})

  id <- l_bind_canvas_ids(p)
  id

  l_bind_canvas_get(p, id)
}
```
**l_bind_canvas_reorder**  
*Reorder the canvas binding evaluation sequence*

**Description**

The order the canvas bindings defines how they get evaluated once an event matches event patterns of multiple canvas bindings.

**Usage**

```r
l_bind_canvas_reorder(widget, ids)
```

**Arguments**

- `widget` widget path as a string or as an object handle
- `ids` new canvas binding id evaluation order, this must be a rearrangement of the elements returned by the `l_bind_canvas_ids` function.

**Details**

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

**Value**

vector with binding id evaluation order (same as the `id` argument)

**See Also**

- `l_bind_canvas`, `l_bind_canvas_ids`, `l_bind_canvas_get`, `l_bind_canvas_delete`

---

**l_bind_context**  
*Add a context binding*

**Description**

Creates a binding that evaluates a callback for particular changes in the collection of contexts of a display.

**Usage**

```r
l_bind_context(widget, event, callback)
```
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>widget</td>
<td>widget path as a string or as an object handle</td>
</tr>
<tr>
<td>event</td>
<td>a vector with one or more of the following events: 'add', 'delete', 'relabel'</td>
</tr>
<tr>
<td>callback</td>
<td>callback function is an R function which is called by the Tcl interpreter if the event of interest happens. Note that in loon the callback functions support different optional arguments depending on the binding type, read the details for more information</td>
</tr>
</tbody>
</table>

Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

Value

context binding id

See Also

`l_bind_context_ids, l_bind_context_get, l_bind_context_delete, l_bind_context_reorder`

---

**Description**

Remove a context binding

**Usage**

`l_bind_context_delete(widget, id)`

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>widget</td>
<td>widget path as a string or as an object handle</td>
</tr>
<tr>
<td>id</td>
<td>context binding id</td>
</tr>
</tbody>
</table>

**Details**

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

**See Also**

`l_bind_context, l_bind_context_ids, l_bind_context_get, l_bind_context_reorder`
l_bind_context_get

Get the event pattern and callback Tcl code of a context binding

Description
This function returns the registered event pattern and the Tcl callback code that the Tcl interpreter evaluates after a event occurs that matches the event pattern.

Usage
l_bind_context_get(widget, id)

Arguments
- widget: widget path as a string or as an object handle
- id: context binding id

Details
Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run l_help("learn_R_bind")

Value
Character vector of length two. First element is the event pattern, the second element is the Tcl callback code.

See Also
l_bind_context, l_bind_context_ids, l_bind_context_delete, l_bind_context_reorder

l_bind_context_ids
List context binding ids

Description
List all user added context binding ids

Usage
l_bind_context_ids(widget)

Arguments
- widget: widget path as a string or as an object handle
Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

Value

vector with context binding ids

See Also

`l_bind_context`, `l_bind_context_get`, `l_bind_context_delete`, `l_bind_context_reorder`

---

**l_bind_context_reorder**

*Reorder the context binding evaluation sequence*

---

Description

The order the context bindings defines how they get evaluated once an event matches event patterns of multiple context bindings.

Usage

`l_bind_context_reorder(widget, ids)`

Arguments

- `widget` widget path as a string or as an object handle
- `ids` new context binding id evaluation order, this must be a rearrangement of the elements returned by the `l_bind_context_ids` function.

Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

Value

vector with binding id evaluation order (same as the id argument)

See Also

`l_bind_context`, `l_bind_context_ids`, `l_bind_context_get`, `l_bind_context_delete`
Add a glyph binding

Description

Creates a binding that evaluates a callback for particular changes in the collection of glyphs of a display.

Usage

l_bind_glyph(widget, event, callback)

Arguments

- **widget**: widget path as a string or an object handle
- **event**: a vector with one or more of the following events: 'add', 'delete', 'relabel'
- **callback**: callback function is an R function which is called by the Tcl interpreter if the event of interest happens. Note that in loon the callback functions support different optional arguments depending on the binding type, read the details for more information

Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run l_help("learn_R_bind")

Value

glyph binding id

See Also

l_bind_glyph_ids, l_bind_glyph_get, l_bind_glyph_delete, l_bind_glyph_reorder

Delete a glyph binding

Description

Remove a glyph binding

Usage

l_bind_glyph_delete(widget, id)
Arguments

  widget    widget path as a string or as an object handle
  id        glyph binding id

Details

  Bindings, callbacks, and binding substitutions are described in detail in loon's documentation webpage, i.e. run l_help("learn_R_bind")

See Also

  l_bind_glyph, l_bind_glyph_ids, l_bind_glyph_get, l_bind_glyph_reorder

Value

  Character vector of length two. First element is the event pattern, the second element is the Tcl callback code.

See Also

  l_bind_glyph, l_bind_glyph_ids, l_bind_glyph_delete, l_bind_glyph_reorder
**l_bind_glyph_ids**

*List glyph binding ids*

**Description**

List all user added glyph binding ids

**Usage**

```r
l_bind_glyph_ids(widget)
```

**Arguments**

- **widget**: widget path as a string or as an object handle

**Details**

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

**Value**

vector with glyph binding ids

**See Also**

`l_bind_glyph, l_bind_glyph_get, l_bind_glyph_delete, l_bind_glyph_reorder`

---

**l_bind_glyph_reorder**

*Reorder the glyph binding evaluation sequence*

**Description**

The order the glyph bindings defines how they get evaluated once an event matches event patterns of multiple glyph bindings.

**Usage**

```r
l_bind_glyph_reorder(widget, ids)
```

**Arguments**

- **widget**: widget path as a string or as an object handle
- **ids**: new glyph binding id evaluation order, this must be a rearrangement of the elements returned by the `l_bind_glyph_ids` function.
Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run \texttt{l\_help("learn\_R\_bind")}

Value

vector with binding id evaluation order (same as the \texttt{id} argument)

See Also

\texttt{l\_bind\_glyph}, \texttt{l\_bind\_glyph\_ids}, \texttt{l\_bind\_glyph\_get}, \texttt{l\_bind\_glyph\_delete}

\begin{knitrout}
\begin{longtable}{ll}
\texttt{l\_bind\_item} & \textit{Create a Canvas Binding} \\
\end{longtable}
\end{knitrout}

Description

Canvas bindings are triggered by a mouse/keyboard gesture over the plot as a whole.

Usage

\begin{verbatim}
l_bind_item(widget, tags, event, callback)
\end{verbatim}

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>widget</td>
<td>widget path as a string or as an object handle</td>
</tr>
<tr>
<td>tags</td>
<td>item tags as explained in \texttt{l_help(&quot;learn_R_bind.html#item-bindings&quot;)}</td>
</tr>
<tr>
<td>event</td>
<td>event patterns as defined for Tk canvas widget <a href="https://www.tcl.tk/man/tcl8.6/TkCmd/bind.htm#M5">https://www.tcl.tk/man/tcl8.6/TkCmd/bind.htm#M5</a>.</td>
</tr>
<tr>
<td>callback</td>
<td>callback function is an R function which is called by the Tcl interpreter if the event of interest happens. Note that in loon the callback functions support different optional arguments depending on the binding type, read the details for more information</td>
</tr>
</tbody>
</table>

Details

Item bindings are used for evaluating callbacks at certain mouse and/or keyboard gestures events (i.e. X events) on visual items on the canvas. Items on the canvas can have tags and item bindings are specified to be evaluated at certain X events for items with specific tags. Note that item bindings get currently evaluated in the order that they are added.

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run \texttt{l\_help("learn\_R\_bind")}

Value

item binding id
l_bind_item_delete

Delete a item binding

Description

Remove an item binding

Usage

l_bind_item_delete(widget, id)

Arguments

widget     widget path as a string or as an object handle
id         item binding id

Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run l_help("learn_R_bind")

See Also

l_bind_item, l_bind_item_ids, l_bind_item_get, l_bind_item_reorder

l_bind_item_get

Get the event pattern and callback Tcl code of a item binding

Description

This function returns the registered event pattern and the Tcl callback code that the Tcl interpreter evaluates after a event occurs that matches the event pattern.

Usage

l_bind_item_get(widget, id)

Arguments

widget     widget path as a string or as an object handle
id         item binding id
Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run l_help("learn_R_bind")

Value

Character vector of length two. First element is the event pattern, the second element is the Tcl callback code.

See Also

l_bind_item, l_bind_item_ids, l_bind_item_delete, l_bind_item_reorder
l_bind_item_reorder  Reorder the item binding evaluation sequence

Description

The order the item bindings defines how they get evaluated once an event matches event patterns of multiple item bindings.

Reordering item bindings has currently no effect. Item bindings are evaluated in the order in which they have been added.

Usage

l_bind_item_reorder(widget, ids)

Arguments

widget  widget path as a string or as an object handle
ids  new item binding id evaluation order, this must be a rearrangement of the elements returned by the l_bind_item_ids function.

Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run l_help("learn_R_bind")

Value

vector with binding id evaluation order (same as the id argument)

See Also

l_bind_item, l_bind_item_ids, l_bind_item_get, l_bind_item_delete

l_bind_layer  Add a layer binding

Description

Creates a binding that evaluates a callback for particular changes in the collection of layers of a display.

Usage

l_bind_layer(widget, event, callback)
**Arguments**

- **widget**: widget path as a string or as an object handle
- **event**: a vector with one or more of the following events: 'add', 'delete', 'move', 'hide', 'show', 'relabel'
- **callback**: callback function is an R function which is called by the Tcl interpreter if the event of interest happens. Note that in loon the callback functions support different optional arguments depending on the binding type, read the details for more information

**Details**

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_RBind")`

**Value**

layer binding id

**See Also**

`l_bind_layer`, `l_bind_layer_ids`, `l_bind_layer_get`, `l_bind_layer_delete`, `l_bind_layer_reorder`

---

**Description**

Remove a layer binding

**Usage**

```r
l_bind_layer_delete(widget, id)
```

**Arguments**

- **widget**: widget path as a string or as an object handle
- **id**: layer binding id

**Details**

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_RBind")`

**See Also**

`l_bind_layer`, `l_bind_layer_ids`, `l_bind_layer_get`, `l_bind_layer_delete`, `l_bind_layer_reorder`
l_bind_layer_get

Get the event pattern and callback Tcl code of a layer binding

Description
This function returns the registered event pattern and the Tcl callback code that the Tcl interpreter evaluates after an event occurs that matches the event pattern.

Usage
l_bind_layer_get(widget, id)

Arguments
- widget: widget path as a string or as an object handle
- id: layer binding id

Details
Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run l_help("learn_R_bind")

Value
Character vector of length two. First element is the event pattern, the second element is the Tcl callback code.

See Also
l_bind_layer, l_bind_layer_ids, l_bind_layer_delete, l_bind_layer_reorder

l_bind_layer_ids

List layer binding ids

Description
List all user added layer binding ids

Usage
l_bind_layer_ids(widget)

Arguments
- widget: widget path as a string or as an object handle
Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

Value

vector with layer binding ids

See Also

`l_bind_layer`, `l_bind_layer_get`, `l_bind_layer_delete`, `l_bind_layer_reorder`

---

`l_bind_layer_reorder`  Reorder the layer binding evaluation sequence

Description

The order the layer bindings defines how they get evaluated once an event matches event patterns of multiple layer bindings.

Usage

`l_bind_layer_reorder(widget, ids)`

Arguments

- **widget**: widget path as a string or as an object handle
- **ids**: new layer binding id evaluation order, this must be a rearrangement of the elements returned by the `l_bind_layer_ids` function.

Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

Value

vector with binding id evaluation order (same as the `id` argument)

See Also

`l_bind_layer`, `l_bind_layer_ids`, `l_bind_layer_get`, `l_bind_layer_delete`
**l_bind_navigator**  
*Add a navigator binding*

**Description**

Creates a binding that evaluates a callback for particular changes in the collection of navigators of a display.

**Usage**

```r
l_bind_navigator(widget, event, callback)
```

**Arguments**

- `widget`: widget path as a string or as an object handle
- `event`: a vector with one or more of the following events: 'add', 'delete', 'relabel'
- `callback`: callback function is an R function which is called by the Tcl interpreter if the event of interest happens. Note that in loon the callback functions support different optional arguments depending on the binding type, read the details for more information

**Details**

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

**Value**

navigator binding id

**See Also**

- `l_bind_navigator_ids`, `l_bind_navigator_get`, `l_bind_navigator_delete`, `l_bind_navigator_reorder`

---

**l_bind_navigator_delete**  
*Delete a navigator binding*

**Description**

Remove a navigator binding

**Usage**

```r
l_bind_navigator_delete(widget, id)
```
Arguments

widget         widget path as a string or as an object handle
id             navigator binding id

Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

See Also

`l_bind_navigator`, `l_bind_navigator_ids`, `l_bind_navigator_get`, `l_bind_navigator_reorder`

---

`l_bind_navigator_get`   Get the event pattern and callback Tcl code of a navigator binding

Description

This function returns the registered event pattern and the Tcl callback code that the Tcl interpreter evaluates after a event occurs that matches the event pattern.

Usage

`l_bind_navigator_get(widget, id)`

Arguments

widget         widget path as a string or as an object handle
id             navigator binding id

Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

Value

Character vector of length two. First element is the event pattern, the second element is the Tcl callback code.

See Also

`l_bind_navigator`, `l_bind_navigator_ids`, `l_bind_navigator_delete`, `l_bind_navigator_reorder`
l_bind_navigator_ids

**List navigator binding ids**

**Description**

List all user added navigator binding ids

**Usage**

```
l_bind_navigator_ids(widget)
```

**Arguments**

- `widget`: widget path as a string or as an object handle

**Details**

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

**Value**

vector with navigator binding ids

**See Also**

- `l_bind_navigator`, `l_bind_navigator_get`, `l_bind_navigator_delete`, `l_bind_navigator_reorder`

---

l_bind_navigator_reorder

**Reorder the navigator binding evaluation sequence**

**Description**

The order the navigator bindings define how they get evaluated once an event matches event patterns of multiple navigator bindings.

**Usage**

```
l_bind_navigator_reorder(widget, ids)
```

**Arguments**

- `widget`: widget path as a string or as an object handle
- `ids`: new navigator binding id evaluation order, this must be a rearrangement of the elements returned by the `l_bind_navigator_ids` function.
Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

Value

vector with binding id evaluation order (same as the `id` argument)

See Also

`l_bind_state_ids`, `l_bind_state_get`, `l_bind_state_delete`

---

### l_bind_state

Add a state change binding

**Description**

The callback of a state change binding is evaluated when certain states change, as specified at binding creation.

**Usage**

```r
l_bind_state(target, event, callback)
```

**Arguments**

- **target**: either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. `.10.plot`), the remaining objects by their ids.
- **event**: vector with state names
- **callback**: callback function is an R function which is called by the Tcl interpreter if the event of interest happens. Note that in loon the callback functions support different optional arguments depending on the binding type, read the details for more information

**Details**

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

**Value**

state change binding id

**See Also**

`l_info_states`, `l_bind_state_ids`, `l_bind_state_get`, `l_bind_state_delete`, `l_bind_state_reorder`
l_bind_state_delete  Delete a state binding

Description
Remove a state binding

Usage
l_bind_state_delete(target, id)

Arguments
- target: either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. './Var/l0.plot/Var'), the remaining objects by their ids.
- id: state binding id

Details
Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run l_help("learn_R_bind")

See Also
l_bind_state, l_bind_state_ids, l_bind_state_get, l_bind_state_reorder

l_bind_state_get  Get the event pattern and callback Tcl code of a state binding

Description
This function returns the registered event pattern and the Tcl callback code that the Tcl interpreter evaluates after a event occurs that matches the event pattern.

Usage
l_bind_state_get(target, id)

Arguments
- target: either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. './Var/l0.plot/Var'), the remaining objects by their ids.
- id: state binding id
Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

Value

Character vector of length two. First element is the event pattern, the second element is the Tcl callback code.

See Also

`l_bind_state, l_bind_state_ids, l_bind_state_delete, l_bind_state_reorder`

---

```
1_bind_state_ids  List state binding ids
```

Description

List all user added state binding ids

Usage

```
l_bind_state_ids(target)
```

Arguments

target
either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. `".l0.plot"`), the remaining objects by their ids.

Details

Bindings, callbacks, and binding substitutions are described in detail in loon’s documentation webpage, i.e. run `l_help("learn_R_bind")`

Value

vector with state binding ids

See Also

`l_bind_state, l_bind_state_get, l_bind_state_delete, l_bind_state_reorder`
l_bind_state_reorder  Reorder the state binding evaluation sequence

Description

The order the state bindings defines how they get evaluated once an event matches event patterns of multiple state bindings.

Usage

l_bind_state_reorder(target, ids)

Arguments

target  either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. '/Var.l0.plot'), the remaining objects by their ids.

ids  new state binding id evaluation order, this must be a rearrangement of the elements returned by the l_bind_state_ids function.

Details

Bindings, callbacks, and binding substitutions are described in detail in loon's documentation webpage, i.e. run l_help("learn_R_bind")

Value

vector with binding id evaluation order (same as the id argument)

See Also

l_bind_state, l_bind_state_ids, l_bind_state_get, l_bind_state_delete

l_breaks  Gets the boundaries of the histogram bins containing active points.

Description

Queries the histogram and returns the ids of all active points in each bin that contains active points.

Usage

l_breaks(widget)

Arguments

widget  A loon histogram widget.
Value

A named list of the minimum and maximum values of the boundaries for each active bins in the histogram.

See Also

l_getBinData, l_getBinIds, l_binCut

Usage

l_cget(target, state)

Arguments

target either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. '/.var.l0.plot'), the remaining objects by their ids.

state state name

See Also

l_configure, l_info_states, l_create_handle

Examples

if(interactive()){
  p <- l_plot(iris, color = iris$Species)
  l_cget(p, "color")
  p['selected']
}
Get Color Names from the Hex Code

Description

Return the built-in color names by the given hex code.

Usage

`l_colorName(color, error = TRUE, precise = FALSE)`

Arguments

- `color`: A vector of 12 digit (tcl) or 6 (8 with transparency) digit color hex code, e.g. "#FFFFFF000000", "#FF0000"
- `error`: Suppose the input is not a valid color, if TRUE, an error will be returned; else the input vector will be returned.
- `precise`: Logical; When precise = FALSE, the name of the nearest built-in colour is returned. When precise = TRUE, the name is returned only if the minimum Euclidean distance is zero; otherwise the hex code of the colour is returned. See details.

Details

Function `colors` returns the built-in color names which R knows about. To convert a hex code to a real color name, we first convert these built-in colours and the hex code to RGB (red/green/blue) values (e.g., "black" -> [0, 0, 0]). Then, using this RGB vector value, the closest (Euclidean distance) built-in colour is determined.

Matching is "precise" whenever the minimum distance is zero; otherwise it is "approximate", locating the nearest R colour.

Value

A vector of built-in color names

See Also

`l_hexcolor, hex12tohex6, as_hex6color`

Examples

```r
l_colorName(c("#FFFFFF000000", "#FF00FF", "blue"))
if(require(grid)) {
  # redGradient is a matrix of 20 different colors
  redGradient <- matrix(hcl(0, 80, seq(49, 68, 1)), nrow=4, ncol=5, byrow = TRUE)
```
# a color plate
grid::grid.newpage()
grid::grid.raster(redGradient,
    interpolate = FALSE)

# a “rough matching”;
r <- l_colorName(redGradient)
# the color name of each row is identical...
r
grid::grid.newpage()
# very different from the first plate
grid::grid.raster(r, interpolate = FALSE)

# a "precise matching";
p <- l_colorName(redGradient, precise = TRUE)
# no built-in color names can be precisely matched...
p
}
## Not run:
# an error will be returned
l_colorName(c("foo", "bar", "red"))

# c("foo", "bar", "red") will be returned
l_colorName(c("foo", "bar", "#FFFF00000000"), error = FALSE)

## End(Not run)

l_colRemoveAlpha

Convert color representations having an alpha transparency level to 6
digit color representations

Description

Colors in the standard tk used by loon do not allow for alpha transparency. This function allows
loon to use color palettes (e.g. l_setColorList) that produce colors with alpha transparency by
simply using only the rgb.

Usage

l_colRemoveAlpha(col)

Arguments

col a vector of colors (potentially) containing an alpha level

Examples

x <- l_colRemoveAlpha(rainbow(6))
# Also works with ordinary color string representations
# since it just extracts the rgb values from the colors.
l_compoundPaths

x <- l_colRemoveAlpha(c("red", "blue", "green", "orange"))
x

l_compoundPaths

Get the set of basic path types for loon plots.

Description

Loon’s plots are constructed in TCL and identified with a path string appearing in the window containing the plot. The path string begins with a unique identifier for the plot and ends with a suffix describing the type of loon plot being displayed.

The path identifying the plot is the string concatenation of both the identifier and the type.

This function returns the set of the loon path types for compound loon plots.

Usage

l_compoundPaths()

Value

character vector of the compound path types.

See Also

l_basePaths l_loonWidgets l_getFromPath

l_configure

Modify one or multiple plot states

Description

All of loon’s displays have plot states. Plot states specify what is displayed, how it is displayed and if and how the plot is linked with other loon plots. Layers, glyphs, navigators and contexts have states too (also referred to as plot states). This function modifies one or multiple plot states.

Usage

l_configure(target, ...)

Arguments

target: either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. '.10.plot'), the remaining objects by their ids.

...: state=value pairs
See Also

l_cget, l_info_states, l_create_handle

Examples

if(interactive()){
  p <- l_plot(iris, color = iris$Species)
  l_configure(p, color='red')
  p['size'] <- ifelse(iris$Species == "versicolor", 2, 8)
}

---

l_context_add_context2d

Create a context2d navigator context

Description

A context2d maps every location on a 2d space graph to a list of xvars and a list of yvars such that, while moving the navigator along the graph, as few changes as possible take place in xvars and yvars.

Contexts are in more detail explained in the webmanual accessible with l\_help. Please read the section on context by running l\_help("learn\_R\_display\_graph.html#contexts").

Usage

l\_context\_add\_context2d(navigator, ...)

Arguments

- **navigator**: navigator handle object
- **...**: arguments passed on to modify context states

Value

context handle

See Also

l_info_states, l_context_ids, l_context_add_geodesic2d, l_context_add_slicing2d, l_context_getLabel, l_context_relabel
l_context_add_geodesic2d

Create a geodesic2d navigator context

Description

Geodesic2d maps every location on the graph as an orthogonal projection of the data onto a two-dimensional subspace. The nodes then represent the sub-space spanned by a pair of variates and the edges either a 3d- or 4d-transition of one scatterplot into another, depending on how many variates the two nodes connected by the edge share (see Hurley and Oldford 2011). The geodesic2d context inherits from the context2d context.

Contexts are in more detail explained in the webmanual accessible with l_help. Please read the section on context by running l_help("learn_R_display_graph.html#contexts").

Usage

l_context_add_geodesic2d(navigator, ...)

Arguments

navigator navigator handle object

... arguments passed on to modify context states

Value

context handle

See Also

l_info_states, l_context_ids, l_context_add_context2d, l_context_add_slicing2d, l_context_getLabel, l_context_relabel

l_context_add_slicing2d

Create a slicing2d navigator context

Description

The slicing2d context implements slicing using navigation graphs and a scatterplot to condition on one or two variables.

Contexts are in more detail explained in the webmanual accessible with l_help. Please read the section on context by running l_help("learn_R_display_graph.html#contexts").
Usage

l_context_add_slicing2d(navigator, ...)

Arguments

navigator   navigator handle object
...
... arguments passed on to modify context states

Value

context handle

Examples

if(interactive()){

names(oliveAcids) <- c('p','p1','s','o','l','l1','a','e')
nodes <- apply(combn(names(oliveAcids),2),2,
               function(x)paste(x, collapse=':'))
G <- completeGraph(nodes)
g <- l_graph(G)
nav <- l_navigator_add(g)
con <- l_context_add_slicing2d(nav, data=oliveAcids)

# symmetric range proportion around nav['proportion']
con['proportion'] <- 0.2

con['conditioning4d'] <- "union"
con['conditioning4d'] <- "intersection"
}

l_context_delete  Delete a context from a navigator

Description

Navigators can have multiple contexts. This function removes a context from a navigator.

Usage

l_context_delete(navigator, id)

Arguments

navigator   navigator handle
id            context id
l_context_getLabel

Details

For more information run: l_help("learn_R_display_graph.html#contexts")

See Also

l_context_ids, l_context_add_context2d, l_context_add_geodesic2d, l_context_add_slicing2d, l_context_getLabel, l_context_relabel

l_context_getLabel (navigator, id)

Arguments

navigator navigator handle
id context id

Details

For more information run: l_help("learn_R_display_graph.html#contexts")

See Also

l_context_getLabel, l_context_add_context2d, l_context_add_geodesic2d, l_context_add_slicing2d, l_context_delete
**l_context_ids**  
*List context ids of a navigator*

**Description**  
Navigators can have multiple contexts. This function list the context ids of a navigator.

**Usage**  
\[
l_{\text{context\_ids}}(\text{navigator})
\]

**Arguments**  
- **navigator**: navigator handle

**Details**  
For more information run: \texttt{l\_help("learn\_R\_display\_graph.html#contexts")}

**See Also**  
\texttt{l\_context\_delete}, \texttt{l\_context\_add\_context2d}, \texttt{l\_context\_add\_geodesic2d}, \texttt{l\_context\_add\_slicing2d}, \texttt{l\_context\_getLabel}, \texttt{l\_context\_relabel}

---

**l_context_relabel**  
*Change the label of a context*

**Description**  
Context labels are eventually used in the context inspector. This function relabels a context.

**Usage**  
\[
l_{\text{context\_relabel}}(\text{navigator}, \text{id}, \text{label})
\]

**Arguments**  
- **navigator**: navigator handle  
- **id**: context id  
- **label**: context label shown

**Details**  
For more information run: \texttt{l\_help("learn\_R\_display\_graph.html#contexts")}
See Also

l_context_getLabel, l_context_add_context2d, l_context_add_geodesic2d, l_context_add_slicing2d, l_context_delete

l_copyStates

A generic function to transfer the values of the states of one 'loon' structure to another.

Description

l_copyStates reads the values of the states of the 'source' and assigns them to the states of the same name on the 'target'.

Usage

l_copyStates(
  source,
  target,
  states = NULL,
  exclude = NULL,
  excludeBasicStates = TRUE,
  returnNames = FALSE
)

Arguments

source
  the 'loon' object providing the values of the states.

target
  the 'loon' object whose states are assigned the values of the 'source's states of the same name.

states
  a character vector of the states to be copied. If 'NULL' (the default), then all states in common (excluding those identified by exclusion parameters) are copied from the 'source' to the 'target'.

exclude
  a character vector naming those common states to be excluded from copying. Default is NULL.

excludeBasicStates
  a logical indicating whether certain basic states are to be excluded from the copy (if 'TRUE', the default). These states include those derived from data variables (like "x", "xTemp", "zoomX", "panX", "deltaX", "xlabel", and the "y" counterparts) since these values determine coordinates in the plot and so are typically not to be copied. Similarly "swapAxes" is one of these basic states because in l_compound plots such as l_pairs() swapping axes can wreak havoc if unintended. Finally, an important pair of basic states to exclude are "linkingKey" and "linkingGroup" since such changes require proper synchronization. Setting 'excludeBasicStates = TRUE' is a simple way to avoid copying the values of these basic states. Setting 'excludeBasicStates = FALSE' will allow these to be copied as well.
returnNames  a logical to indicate whether to return the names of all states successfully copied for all plots. Default is ‘FALSE’

Value

a character vector of the names of the states successfully copied (for each plot whose states were affected), or NULL if none were copied or ‘returnNames == FALSE’.

See Also

l_saveStates  l_info_states  saveRDS

Examples

if(interactive()){
  # Source and target are ‘l_plots’
  p <- with(iris,
    l_plot(x = Sepal.Width, y = Petal.Width,
        color = Species, glyph = "ccircle",
        size = 10, showGuides = TRUE,
        title = "Edgar Anderson’s Iris data"
    )
  )

  p2 <- with(iris,
    l_plot(x = Sepal.Length, y = Petal.Length,
        title = "Fisher’s Iris data"
    )
  )

  # Copy the states of p to p2
  # First just the size and title
  l_copyStates(source = p, target = p2,
               states = c("size", "title")
  )

  # Copy all but those associated with the variables
  l_copyStates(source = p, target = p2)

  # Suppose p had a linkingGroup, say "Edgar"
  l_configure(p, linkingGroup = "Edgar", sync = "push")

  # To force this linkingGroup to be copied to a new plot
  p3 <- with(iris,
    l_plot(x = Sepal.Length, y = Petal.Length,
        title = "Fisher’s Iris data"
    )
  )

  l_copyStates(source = p, target = p3,
               states = c("linkingGroup"),
               # To allow this to happen:
               excludeBasicStates = FALSE
  )}
```r
h <- with(iris,
  l_hist((Petal.Width * Petal.Length),
  showStackedColors = TRUE,
  yshows = "density")
)  
l_copyStates(source = p, target = h)

sa <- l_serialaxes(iris, axes = "parallel")
l_copyStates(p, sa)

pp <- l_pairs(iris, showHistograms = TRUE)
suppressWarnings(l_copyStates(p, pp))

pp2 <- l_pairs(iris,
  color = iris$Species,
  showGuides = TRUE,
  title = "Iris data",
  glyph = "ctriangle")
l_copyStates(pp2, pp)
l_copyStates(pp2, p)
)
```

---

**l_createCompoundGrob**

For the target compound loon plot, creates the final grob from the class of the 'target' and the 'arrangeGrob.args'

---

**Description**

For the target compound loon plot, creates the final grob from the class of the 'target' and the 'arrangeGrob.args'

**Usage**

```r
l_createCompoundGrob(target, arrangeGrob.args)
```

**Arguments**

- **target**: the (compound) loon plot
- **arrangeGrob.args**: arguments as described by `gridExtra::arrangeGrob()`

**Value**

A grob (or list of grobs) that can be handed to `gTree()` as `children = gList(returnedValue)` as the final grob constructed for the compound loon plot. Default for an `l_compound` is to simply execute `gridExtra::arrangeGrob(arrangeGrob.args)`.
l_create_handle

Create a loon object handle

Description

This function can be used to create the loon object handles from a vector of the widget path name and the object ids (in the order of the parent-child relationships).

Usage

l_create_handle(target)

Arguments

target 
loon object specification (e.g. ".10.plot")

Details

loon’s plot handles are useful to query and modify plot states via the command line.

For more information run: l_help("learn_R_intro.html#re-creating-object-handles")

See Also

l_getFromPath

Examples

if(interactive()){

    # plot handle
    p <- l_plot(x=1:3, y=1:3)
    p_new <- l_create_handle(unclass(p))
    p_new['showScales']

    # glyph handle
    gl <- l_glyph_add_text(p, text=LETTERS[1:3])
    gl_new <- l_create_handle(c(as.vector(p), as.vector(gl)))
    gl_new['text']

    # layer handle
    l <- l_layer_rectangle(p, x=c(1,3), y=c(1,3), color='yellow', index='end')
    l_new <- l_create_handle(c(as.vector(p), as.vector(l)))
    l_new['color']

    # navigator handle
    g <- l_graph(linegraph(completegraph(LETTERS[1:3])))
    nav <- l_navigator_add(g)
    nav_new <- l_create_handle(c(as.vector(g), as.vector(nav)))
}
\texttt{l_currentindex} \hspace{2em} \textit{Get layer-relative index of the item below the mouse cursor}

**Description**

Checks if there is a visual item below the mouse cursor and if there is, it returns the index of the visual item’s position in the corresponding variable dimension of its layer.

**Usage**

\texttt{l_currentindex(widget)}

**Arguments**

- \texttt{widget} \hspace{1em} widget path as a string or as an object handle

**Details**

For more details see \texttt{l\_help("learn\_R\_bind.html\#item-bindings")}

**Value**

index of the visual item’s position in the corresponding variable dimension of its layer

**See Also**

\texttt{l\_bind\_item, l\_currenttags}

**Examples**

\begin{verbatim}
if(interactive()){
  p <- l_plot(iris[,1:2], color=iris$Species)

  printEntered <- function(W) {
    cat(paste('Entered point ', l_currentindex(W), '\n'))
  }

  printLeave <- function(W) {
    cat(paste('Left point ', l_currentindex(W), '\n'))
  }

  # context handle
  con <- l_context_add_context2d(nav)
  con_new <- l_create_handle(c(as.vector(g), as.vector(nav), as.vector(con)))
  con_new['separator']
}\end{verbatim}
Get tags of the item below the mouse cursor

Description

Retrieves the tags of the visual item that at the time of the function evaluation is below the mouse cursor.

Usage

\[ l\_currenttags(widget) \]

Arguments

widget \hspace{1em} \text{widget path as a string or as an object handle}

Details

For more details see \l_{\text{help}}(\text{"learn_R\_bind.html\#item-bindings"})

Value

vector with item tags of visual

See Also

\l_{\text{bind\_item}}, \l_{\text{current\_index}}

Examples

\begin{verbatim}
if(interactive()){

printTags <- function(W) {
  print(l_currenttags(W))
}

p <- l_plot(x=1:3, y=1:3, title='Query Visual Item Tags')

l_bind_item(p, 'all', '<ButtonPress>', function(W)printTags(W))
}
\end{verbatim}
**l_data**

Convert an R data.frame to a Tcl dictionary

**Description**

This is a helper function to convert an R data.frame object to a Tcl data frame object. This function is useful when changing a data state with `l_configure`.

**Usage**

```r
l_data(data)
```

**Arguments**

- `data` a data.frame object

**Value**

a string that represents with data.frame with a Tcl dictionary data structure.

---

**l_export**

Export a loon plot as an image

**Description**

The supported image formats are dependent on the system environment. Plots can always be exported to the PostScript format. Exporting displays as .pdfs is only possible when the command line tool `epstopdf` is installed. Finally, exporting to either png, jpg, bmp, tiff or gif requires the Img Tcl extension. When choosing one of the formats that depend on the Img extension, it is possible to export any Tk widget as an image including inspectors.

**Usage**

```r
l_export(widget, filename, width, height)
```

**Arguments**

- `widget` widget path as a string or as an object handle
- `filename` path of output file
- `width` image width in pixels
- `height` image height in pixels
Details

Note that the CTRL-P key combination opens a dialog to export the graphic.

The native export format is to ps as this is what the Tk canvas offers. If the the l_export fails with other formats then please resort to a screen capture method for the moment.

Value

path to the exported file

See Also

l_export_valid_formats, plot.loon

---

l_export_valid_formats

    Return a list of the available image formats when exporting a loon plot

---

Description

The supported image formats are dependent on the system environment. Plots can always be exported to the Postscript format. Exporting displays as .pdfs is only possible when the command line tool epstopdf is installed. Finally, exporting to either png, jpg, bmp, tiff or gif requires the Img Tcl extension. When choosing one of the formats that depend on the Img extension, it is possible to export any Tk widget as an image including inspectors.

Usage

l_export_valid_formats()

Value

a vector with the image formats available for exporting a loon plot.

---

l_facet

    Layout Facets across multiple panels

---

Description

It takes a loon widget and forms a matrix of loon widget facets.
l_facet

Usage

l_facet(widget, by, on, layout = c("grid", "wrap", "separate"), ...)

## S3 method for class 'loon'

l_facet(
  widget,
  by,
  on,
  layout = c("grid", "wrap", "separate"),
  connectedScales = c("cross", "row", "column", "both", "x", "y", "none"),
  linkingGroup,
  nrow = NULL,
  ncol = NULL,
  inheritLayers = TRUE,
  labelLocation = c("top", "right"),
  labelBackground = "gray80",
  labelForeground = "black",
  labelBorderwidth = 2,
  labelRelief = c("groove", "flat", "raised", "sunken", "ridge", "solid"),
  plotWidth = 200,
  plotHeight = 200,
  parent = NULL,
  ...
)

## S3 method for class 'l_serialaxes'

l_facet(
  widget,
  by,
  on,
  layout = c("grid", "wrap", "separate"),
  linkingGroup,
  nrow = NULL,
  ncol = NULL,
  labelLocation = c("top", "right"),
  labelBackground = "gray80",
  labelForeground = "black",
  labelBorderwidth = 2,
  labelRelief = c("groove", "flat", "raised", "sunken", "ridge", "solid"),
  plotWidth = 200,
  plotHeight = 200,
  parent = NULL,
  ...
)

Arguments

widget A loon widget
by loon plot can be separated by some variables into multiple panels. This argument can take a vector, a list of same lengths or a data.frame as input.

on if the by is a formula, an optional data frame containing the variables in the by. If variables in by is not found in data, the variables are taken from environment(formula), typically the environment from which the function is called.

layout layout facets as 'grid', 'wrap' or 'separate'

... named arguments to modify the 'loon' widget states

connectedScales Determines how the scales of the facets are to be connected depending on which layout is used. For each value of layout, the scales are connected as follows:

- layout = "wrap": Across all facets, when connectedScales is
  - "x", then only the "x" scales are connected
  - "y", then only the "y" scales are connected
  - "both", both "x" and "y" scales are connected
  - "none", neither "x" nor "y" scales are connected. For any other value, only the "y" scale is connected.

- layout = "grid": Across all facets, when connectedScales is
  - "cross", then only the scales in the same row and the same column are connected
  - "row", then both "x" and "y" scales of facets in the same row are connected
  - "column", then both "x" and "y" scales of facets in the same column are connected
  - "x", then all of the "x" scales are connected (regardless of column)
  - "y", then all of the "y" scales are connected (regardless of row)
  - "both", both "x" and "y" scales are connected in all facets
  - "none", neither "x" nor "y" scales are connected in any facets.

linkingGroup A linkingGroup for widgets. If missing, default would be a paste of "layout" and the current tk path number.

nrow The number of layout rows

ncol The number of layout columns

inheritLayers Logical value. Should widget layers be inherited into layout panels?

labelLocation Labels location.
  - Length two vector for layout grid. The first one is used to determine the position of column labels ('top' or 'bottom'). The second one is used to determine the position of row labels ('right' or 'left').
  - Length one vector for layout wrap, 'top' or 'bottom'.

labelBackground Label background colour

labelForeground Label foreground colour

labelBorderwidth Label border width
`l_facet`  

<table>
<thead>
<tr>
<th>labelRelief</th>
<th>Label relief</th>
</tr>
</thead>
<tbody>
<tr>
<td>plotWidth</td>
<td>default plot width (in pixels)</td>
</tr>
<tr>
<td>plotHeight</td>
<td>default plot height (in pixels)</td>
</tr>
<tr>
<td>parent</td>
<td>a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like <code>tkpack</code> or <code>tkplace</code> in order to be displayed. See the examples below.</td>
</tr>
</tbody>
</table>

**Value**

an `l_facet` object (an `l_compound` object), being a list with named elements, each representing a separate interactive plot. The names of the plots should be self explanatory and a list of all plots can be accessed from the `l_facet` object via `l_getPlots()`.

**Examples**

```r
if(interactive()) {
  library(maps)
  p <- with(quakes, l_plot(long, lat, linkingGroup = "quakes"))
  p["color"][(quakes$mag < 5 & quakes$mag >= 4)] <- "lightgreen"
  p["color"][(quakes$mag < 6 & quakes$mag >= 5)] <- "lightblue"
  p["color"][(quakes$mag >= 6)] <- "firebrick"

  # A Fiji map
  NZFijiMap <- map("world2", regions = c("New Zealand", "Fiji"), plot = FALSE)
  l_layer(p, NZFijiMap,
    label = "New Zealand and Fiji",
    color = "forestgreen",
    index = "end")
  fp <- l_facet(p, by = "color", layout = "grid",
    linkingGroup = "quakes")

  size <- c(rep(50, 2), rep(25, 2), rep(50, 2))
  color <- c(rep("red", 3), rep("green", 3))
  p <- l_plot(x = 1:6, y = 1:6,
    size = size,
    color = color)
  g <- l_glyph_add_text(p, text = 1:6)
  p["glyph"] <- g
  on <- data.frame(Factor1 = c(rep("A", 3), rep("B", 3)),
    Factor2 = rep(c("C", "D"), 3))
  cbind(on, size = size, color = color)
  fp <- l_facet(p, by = Factor1 ~ Factor2, on = on)
}
if(interactive()) {
  # serialaxes facets
  s <- l_serialaxes(iris[, -5], color = iris$Species)
  fs <- l_facet(s, layout = "wrap", by = iris$Species)
  # The linkingGroup can be printed or accessed by
  l_configure(s, linkingGroup = fs[[1]]['linkingGroup'], sync = "pull")
}
```
l_getBinData  *Get information on current bins from a histogram*

**Description**

Queries the histogram and returns information about all active cases contained by the histogram’s bins.

**Usage**

```r
l_getBinData(widget)
```

**Arguments**

- `widget`  A loon histogram widget.

**Value**

A nested list of the bins in the histogram which contain active points. Each bin is a list of the counts, the point indices, and the minimum (x0) and maximum (x1) of that bin. Loon histogram bins are open on the left and closed on the right by default, namely "](x0, x1]". The counts and the points further identify the number and ids of all points, those which are selected, and those of each colour in that bin (identified by their hex12 colour from tcl).

**See Also**

`l_getBinIds`, `l_breaks`, `l_binCut`

---

l_getBinIds  *Gets the ids of the active points in each bin of a histogram*

**Description**

Queries the histogram and returns the ids of all active points in each bin that contains active points.

**Usage**

```r
l_getBinIds(widget)
```

**Arguments**

- `widget`  A loon histogram widget.

**Value**

A named list of the bins in the histogram and the ids of their active points.
See Also

l_getBinData, l_breaks, l_binCut

---

l_getColorList  
_Get loon’s color mapping list_

Description

The color mapping list is used by loon to convert nominal values to color values, see the documentation for l_setColorList.

Usage

l_getColorList()

Value

a vector with hex-encoded colors

See Also

l_setColorList

---

l_getFromPath  
_Create loon objects from path name_

Description

This function can be used to create the loon objects from a valid widget path name. The main difference from l_create_handle is that l_getFromPath can take a loon compound widget path but l_create_handle cannot.

Usage

l_getFromPath(target)

Arguments

target  
loon object specification (e.g. ".10.plot")

Details

For more information run: l_help("learn_R_intro.html#re-creating-object-handles")

See Also

l_create_handle l_loonWidgets
Examples

```r
## Not run:
l_pairs(iris, showHistogram = TRUE)
# The path can be found at the top of tk title
# Suppose it is the first loon widget, this path should be ".l0.pairs"
p <- l_create_handle(".l0.pairs") # error
p <- l_getFromPath(".l0.pairs")
## End(Not run)
```

### l_getGraph

Extract a loongraph or graph object from loon’s graph display

#### Description

The graph display represents a graph with the nodes, from, to, and isDirected plot states. This function creates a loongraph or a graph object using these states.

#### Usage

```r
l_getGraph(widget, asloongraph = TRUE)
```

#### Arguments

- `widget`: a graph widget handle
- `asloongraph`: boolean, if TRUE then the function returns a loongraph object, otherwise the function returns a graph object defined in the graph R package.

#### Value

a loongraph or a graph object

#### See Also

`l_graph`, `loongraph`
\texttt{l\_getLinkedStates} \hspace{1cm} \textit{Query the States that are Linked with Loon's Standard Linking Model}

\textbf{Description}

Loon's standard linking model is based on three levels, the \texttt{linkingGroup} and \texttt{linkingKey} states and the \textit{used linkable states}. See the details in the documentation for \texttt{l\_setLinkedStates}.

\textbf{Usage}

\texttt{l\_getLinkedStates(widget)}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{widget} \hspace{1cm} \text{widget path as a string or as an object handle}
\end{itemize}

\textbf{Value}

\begin{itemize}
  \item \text{vector with state names that are linked states}
\end{itemize}

\textbf{See Also}

\texttt{l\_setLinkedStates}

\texttt{l\_getLocations} \hspace{1cm} \textit{For the target compound loon plot, determines location (only and excluding the grobs) arguments to pass to \texttt{gridExtra::arrangeGrob}()}

\textbf{Description}

For the target compound loon plot, determines location (only and excluding the grobs) arguments to pass to \texttt{gridExtra::arrangeGrob}()

\textbf{Usage}

\texttt{l\_getLocations(target)}

## S3 method for class 'l\_facet'
l\_getLocations(target)

## S3 method for class 'l\_pairs'
l\_getLocations(target)

## S3 method for class 'l\_ts'
l\_getLocations(target)
l_getOption

Get the value of a loon display option

Description

All of loon’s displays access a set of common options. This function accesses and returns the current value of the named option.

Usage

l_getOption(option)

Arguments

option the name of the option being queried.

Value

the value of the named option.

See Also

l_getOptionNames, l_userOptions, l_userOptionDefault, l_setOption

Arguments

target the (compound) loon plot whose locations are needed lay it out.

Value

a list of an appropriate subset of the named location arguments ‘c("ncol", "nrow", "layout_matrix", "heights", "widths")’. There are as many heights and widths as there are plots returned by l_getPlots(); these specify the relative height and width of each plot in the display. layout_matrix is an nrow by ncol matrix whose entries identify the location of each plot in l_getPlots() by their index.

Examples

if(interactive()) {

  pp <- l_pairs(iris, showHistograms = TRUE)
  ll <- l_getLocations(pp)
  nplots <- length(l_getPlots(pp))
  # the plots returned by l_getPlots(pp) are positioned
  # in order by the layout_matrix
  ll$layout_matrix
}
l_getOptionNames

Examples

   l_getOption("background")

Description

All of loon’s displays access a set of common options. This function accesses and returns the names of all loon options.

Usage

   l_getOptionNames()

Value

   a vector of all loon display option names.

See Also

   l_getOption, l_userOptions, l_userOptionDefault, l_setOption

Examples

   l_getOptionNames()

l_getPlots

For the target compound loon plot, determines all the loon plots in that compound plot.

Description

For the target compound loon plot, determines all the loon plots in that compound plot.

Usage

   l_getPlots(target)

## S3 method for class 'l_facet'
   l_getPlots(target)

## S3 method for class 'l_pairs'
   l_getPlots(target)

## S3 method for class 'l_ts'
   l_getPlots(target)
getSavedStates

Arguments

target  the (compound) loon plot to be laid out.

Value

a list of the named arguments and their values to be passed to `gridExtra::arrangeGrob()`.

Description

getSavedStates reads a file created by saveStates() containing the saved info states of a loon plot returning a loon object of class "l_savedStates". This is helpful, for example, when using RMarkdown or some other notebooking facility to recreate an earlier saved loon plot so as to present it in the document.

Note that if the plot saved was an "l_compound" then getSavedStates will return a list of the plots with each list item being the saved states of the corresponding plots.

Usage

getSavedStates(file = stop("missing name of file"), ...)

Arguments

file  a connection or the name of the file where the "l_savedStates" R object is to be read from (as in readRDS()).

...  further arguments passed to readRDS().

Value

a list of class 'l_savedStates' containing the states and their values. Also has an attribute 'l_plot_class' which contains the class vector of the plot 'p'

See Also

getSavedStates copyStates info_states readRDS saveRDS

Examples

if(interactive()){
  # Suppose you have some plot that you created like
  p <- l_plot(iris, showGuides = TRUE)
  #
  # and coloured groups by hand (using the mouse and inspector)
  # so that you ended up with these colours:
p["color"] <- rep(c("lightgreen", "firebrick", "skyblue"),
    each = 50)
#
# Having determined the colours you could save them (and other states)
# in a file of your choice, here some tempfile:
myFileName <- tempfile("myPlot", fileext = ".rds")
#
# Save the named states of p
l_saveStates(p,
    states = c("color", "active", "selected"),
    file = myFileName)
#
# These can later be retrieved and used on a new plot
# (say in RMarkdown) to set the new plot's values to those
# previously determined interactively.
p_new <- l_plot(iris, showGuides = TRUE)
p_saved_info <- l_getSavedStates(myFileName)
#
# We can tell what kind of plot was saved
attr(p_saved_info, "l_plot_class")
#
# The result is a list of class "l_savedStates" which
# contains the names of the
p_new["color"] <- p_saved_info$color
#
# The result is that p_new looks like p did
# (after your interactive exploration)
# and can now be plotted as part of the document
plot(p_new)
#
# For compound plots, the info_states are saved for each plot
pp <- l_pairs(iris)
myPairsFile <- tempfile("myPairsPlot", fileext = ".rds")
#
# Save the names states of pp
l_saveStates(pp,
    states = c("color", "active", "selected"),
    file = myPairsFile)
pairs_info <- l_getSavedStates(myPairsFile)
#
# For compound plots, the info states for all constituent
# plots are saved. The result is a list of class "l_savedStates"
# whose elements are the named plots as "l_savedStates"
# themselves.
#
# The names of the plots which were saved
names(pairs_info)
#
# And the names of the info states whose values were saved for
# the first plot
names(pairs_info$x1y1)
#
# While it is generally recommended to access (or assign) saved
# state values using the $ sign accessor, paying attention to the
# nested list structure of an "l_savedStates" object (especially for
# l_compound plots). R’s square bracket notation [ ] has also been
# specialized to allow a syntactically simpler (but less precise)
# access to the contents of an l_savedStates object.
#
# For example,
p_saved_info["color"]
#
# returns the saved "color" as a vector of colours.
#
# In contrast,
pairs_info["x2y1"]
# returns the l_savedStates object of the states of the plot named "x2y1",
# but
pairs_info["color"]
# returns a LIST of colour vectors, by plot as they were named in pairs_info
#
# As a consequence, the following two are equivalent,
pairs_info["x2y1"]["color"]
# finds the value of "color" from an "l_savedStates" object
# whereas
pairs_info["color"][["x2y1"]]
# finds the value of "x2y1" from a "list" object
#
# Also, setting a state of an "l_savedStates" is possible
# (though not generally recommended; better to save the states again)
#
p_saved_info["color"] <- rep("red", 150)
# changes the saved state "color" on p_saved_info
# whereas
pairs_info["color"] <- rep("red", 150)
# will set the red color for any plot within pairs_info having "color" saved.
# In this way the assignment function via [ ] is trying to be clever
# for l_savedStates for compound plots and so may have unintentional
# consequences if the user is not careful.
#
# Generally, one does not want/need to change the value of saved states.
# Instead, the states would be saved again from the interactive plot
# if change is necessary.
# Alternatively, more nuanced and careful control is maintained using
# the $ selectors for lists.
}

l_getScaledData Data Scaling

Description

Scaling the data set
Usage

```r
l_getScaledData(
  data,
  sequence = NULL,
  scaling = c("variable", "observation", "data", "none"),
  displayOrder = NULL,
  reserve = FALSE,
  as.data.frame = FALSE
)
```

Arguments

- `data`: A data frame
- `sequence`: vector with variable names that are scaled. If NULL, it will be set as the whole column names (all data set will be scaled).
- `scaling`: one of 'variable', 'data', 'observation' or 'none' to specify how the data is scaled. See details
- `displayOrder`: the order of the display
- `reserve`: If TRUE, return the variables not shown in sequence as well; else only return the variables defined in sequence.
- `as.data.frame`: Return a matrix or a data.frame

Details

The `scaling` state defines how the data is scaled. The axes display 0 at one end and 1 at the other. For the following explanation assume that the data is in a nxp dimensional matrix. The scaling options are then:

- `variable`: per column scaling
- `observation`: per row scaling
- `data`: whole matrix scaling
- `none`: do not scale

See Also

- `l_serialaxes`

Description

For the target (compound) loon plot, determines all arguments (i.e. including the grobs) to be passed to `gridExtra::arrangeGrob()` so as to determine the layout in `grid` graphics.
Usage

l_get_arrangeGrobArgs(target)

Arguments

  target  the (compound) loon plot to be laid out.

Value

  a list of the named arguments and their values to be passed to `gridExtra::arrangeGrob()`.

l_glyphs_inspector
Create a Glyphs Inspector

Description

Inspectors provide graphical user interfaces to oversee and modify plot states

Usage

l_glyphs_inspector(parent = NULL, ...)

Arguments

  parent  parent widget path
  ...    state arguments

Value

  widget handle

See Also

  l_create_handle

Examples

  if(interactive()){
    i <- l_glyphs_inspector()
  }
Create an Image Glyph Inspector

Description
Inpectors provide graphical user interfaces to oversee and modify plot states

Usage
l_glyphs_inspector_image(parent = NULL, ...)

Arguments
parent
parent widget path
...
state arguments

Value
widget handle

See Also
l_create_handle

Examples
if(interactive()){
  i <- l_glyphs_inspector_image()
}

Create a Pointrange Glyph Inspector

Description
Inpectors provide graphical user interfaces to oversee and modify plot states

Usage
l_glyphs_inspector_pointrange(parent = NULL, ...)


Arguments

parent: parent widget path
...

state arguments

Value

widget handle

See Also

l_create_handle

Examples

if(interactive()){
  i <- l_glyphs_inspector_pointrange()
}

l_glyphs_inspector_serialaxes

Create a Serialaxes Glyph Inspector

Description

Inspectors provide graphical user interfaces to oversee and modify plot states

Usage

l_glyphs_inspector_serialaxes(parent = NULL, ...)

Arguments

parent: parent widget path
...

state arguments

Value

widget handle

See Also

l_create_handle
**Examples**

```r
if(interactive()){

  i <- l_glyphs_inspector_serialaxes()
}
```

---

**l_glyphs_inspector_text**

*Create a Text Glyph Inspector*

**Description**

Inspectors provide graphical user interfaces to oversee and modify plot states.

**Usage**

```r
l_glyphs_inspector_text(parent = NULL, ...)
```

**Arguments**

- `parent`: parent widget path
- `...`: state arguments

**Value**

widget handle

**See Also**

- `l_create_handle`

**Examples**

```r
if(interactive()){

  i <- l_glyphs_inspector_text()
}
```
l_glyph_add

Add non-primitive glyphs to a scatterplot or graph display

Description

Generic method for adding user-defined glyphs. See details for more information about non-primitive and primitive glyphs.

Usage

l_glyph_add(widget, type, ...)

Arguments

- widget: widget path as a string or as an object handle
- type: object used for method dispatch
- ...: arguments passed on to method

Details

The scatterplot and graph displays both have the n-dimensional state ‘glyph’ that assigns each data point or graph node a glyph (i.e. a visual representation).

Loon distinguishes between primitive and non-primitive glyphs: the primitive glyphs are always available for use whereas the non-primitive glyphs need to be first specified and added to a plot before they can be used.

The primitive glyphs are:

- 'circle', 'ocircle', 'ccircle'
- 'square', 'osquare', 'csquare'
- 'triangle', 'otriangle', 'ctriangle'
- 'diamond', 'odiamond', 'cdiamond'

Note that the letter 'o' stands for outline only, and the letter 'c' stands for contrast and adds an outline with the 'foreground' color (black by default).

The non-primitive glyph types and their creator functions are:

<table>
<thead>
<tr>
<th>Type</th>
<th>R creator function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Text</td>
<td>l_glyph_add_text</td>
</tr>
<tr>
<td>Serialaxes</td>
<td>l_glyph_add_serialaxes</td>
</tr>
<tr>
<td>Pointranges</td>
<td>l_glyph_add_pointrange</td>
</tr>
<tr>
<td>Images</td>
<td>l_glyph_add_image</td>
</tr>
<tr>
<td>Polygon</td>
<td>l_glyph_add_polygon</td>
</tr>
</tbody>
</table>

When adding non-primitive glyphs to a display, the number of glyphs needs to match the dimension n of the plot. In other words, a glyph needs to be defined for each observation. See in the examples.
Currently loon does not support compound glyphs. However, it is possible to construct an arbitrary glyph using any system and save it as a png and then re-import them as as image glyphs using `l_glyph_add_image`.

For more information run: `l_help("learn_R_display_plot.html#glyphs")`

**Value**

String with glyph id. Every set of non-primitive glyphs has an id (character).

**See Also**

`l_glyph_add_text`, `l_make_glyphs`

Other glyph functions: `l_glyph_add.default()`, `l_glyph_add_image()`, `l_glyph_add_pointrange()`, `l_glyph_add_polygon()`, `l_glyph_add_serialaxes()`, `l_glyph_add_text()`, `l_glyph_delete()`, `l_glyph_getLabel()`, `l_glyph_getType()`, `l_glyph_ids()`, `l_glyph_relabel()`, `l_primitiveGlyphs()`

**Examples**

```r
if(interactive()){

# Simple Example with Text Glyphs
p <- with(olive, l_plot(stearic, eicosenoic, color=Region))
g <- l_glyph_add_text(p, text=olive$Area, label="Area")
p['glyph'] <- g

## Not run:
demo("l_glyphs", package="loon")

## End(Not run)

# create a plot that demonstrates the primitive glyphs and the text glyphs
p <- l_plot(x=1:15, y=rep(0,15), size=10, showLabels=FALSE)
text_glyph <- l_glyph_add_text(p, text=letters[1:15])
p['glyph'] <- c(
    'circle', 'ocircle', 'ccircle',
    'square', 'osquare', 'csquare',
    'triangle', 'otriangle', 'ctriangle',
    'diamond', 'odiamond', 'cdiamond',
)
)
```

---

**Description**

Generic function to write new glyph types using loon’s primitive glyphs
Usage

```r
## Default S3 method:
l_glyph_add(widget, type, label = "", ...)  
```

Arguments

- `widget` : widget path as a string or as an object handle
- `type` : loon-native non-primitive glyph type, one of 'text', 'serialaxes', 'image', '[polygon]', or 'pointrange'
- `label` : label of a glyph (currently shown only in the glyph inspector)
- `...` : state arguments

See Also

Other glyph functions: `l_glyph_add_image()`, `l_glyph_add_pointrange()`, `l_glyph_add_polygon()`, `l_glyph_add_serialaxes()`, `l_glyph_add_text()`, `l_glyph_add()`, `l_glyph_delete()`, `l_glyph_getLabel()`, `l_glyph_getType()`, `l_glyph_ids()`, `l_glyph_relabel()`, `l_primitiveGlyphs()`

---

**l_glyph_add_image**

Add an image glyphs

---

Description

Image glyphs are useful to show pictures or other sophisticated compound glyphs. Note that images in the Tk canvas support transparency.

Usage

```r
l_glyph_add_image(widget, images, label = "", ...)  
```

Arguments

- `widget` : widget path as a string or as an object handle
- `images` : Tk image references, see the `l_image_import_array` and `l_image_import_files` helper functions.
- `label` : label of a glyph (currently shown only in the glyph inspector)
- `...` : state arguments

Details

For more information run: `l_help("learn_R_display_plot.html#images")`
See Also

l_glyph_add, l_image_import_array, l_image_import_files, l_make_glyphs

Other glyph functions: l_glyph_add.default(), l_glyph_add_pointrange(), l_glyph_add_polygon(), l_glyph_add_serialaxes(), l_glyph_add_text(), l_glyph_add(), l_glyph_delete(), l_glyph_getLabel(), l_glyph_getType(), l_glyph_ids(), l_glyph_relabel(), lPrimitiveGlyphs()

Examples

if(interactive()){
  p <- with(olive, l_plot(palmitic ~ stearic, color = Region))
  img_paths <- list.files(file.path(find.package(package = 'loon'), "images"), full.names = TRUE)
  imgs <- setNames(l_image_import_files(img_paths),
                  tools::file_path_sans_ext(basename(img_paths)))
  i <- pmatch(gsub("^[[:alpha:]][-]","", olive$Area), names(imgs), duplicates.ok = TRUE)

  g <- l_glyph_add_image(p, imgs[i], label="Flags")
  p['glyph'] <- g
}

---

l_glyph_add_pointrange

Add a Pointrange Glyph

Description

Pointrange glyphs show a filled circle at the x-y location and also a y-range.

Usage

l_glyph_add_pointrange(
  widget,
  ymin,
  ymax,
  linewidth = 1,
  showArea = TRUE,
  label = "",
  ...
)

Arguments

- **widget**: widget path as a string or as an object handle
- **ymin**: vector with lower y-value of the point range.
- **ymax**: vector with upper y-value of the point range.
- **linewidth**: line with in pixel.
Add one Polygon Glyph

Description

Add one polygon per scatterplot point.

Usage

```r
l_glyph_add_polygon(
  widget,
  x,
  y,
  linewidth = 1,
  showArea = TRUE,
  label = "",
  ...
)
```

Arguments

- `widget`: widget path as a string or as an object handle
- `x`: nested list of x-coordinates of polygons (relative to `widget`), one list element for each scatterplot point.
- `y`: nested list of y-coordinates of polygons, one list element for each scatterplot point.

See Also

- `l_glyph_add`
- Other glyph functions: `l_glyph_add.default()`, `l_glyph_add_image()`, `l_glyph_add_polygon()`, `l_glyph_add_serialaxes()`, `l_glyph_add_text()`, `l_glyph_add()`, `l_glyph_delete()`, `l_glyph_getLabel()`, `l_glyph_getType()`, `l_glyph_ids()`, `l_glyph_relabel()`, `l_primitiveGlyphs()`
linewidth
  linewidth of outline.
showArea
  boolean, show a filled polygon or just the outline
label
  label of a glyph (currently shown only in the glyph inspector)
... 
  state arguments

Details

A polygon can be a useful point glyph to visualize arbitrary shapes such as airplanes, animals and shapes that are not available in the primitive glyph types (e.g. cross). The lGlyphs demo has an example of polygon glyphs which we reuse here.

See Also

l_glyph_add

Other glyph functions: l_glyph_add.default(), l_glyph_add_image(), l_glyph_add_pointrange(),
  l_glyph_add_serialaxes(), l_glyph_add_text(), l_glyph_add(), l_glyph_delete(), l_glyph_getLabel(),
  l_glyph_getType(), l_glyph_ids(), l_glyph_relabel(), l_primitiveGlyphs()

Examples

if(interactive()){

  x_star <-
    c(-0.000864304235090734, 0.292999135695765, 0.949870354364736, 
      0.474503025664823, 0.586862575626621, -0.000864304235090734, 
      -0.586430423509075, -0.474070872947277, -0.949438202247191, 
      -0.29256698357822)

  y_star <-
    c(-1, -0.403630077787381, -0.308556611927398, 0.153846153846154, 
      0.808556611927398, 0.499567847882455, 0.808556611927398, 
      0.153846153846154, -0.308556611927398, -0.403630077787381)

  x_cross <-
    c(-0.258931143762604, -0.258931143762604, -0.950374531835206, 
      -0.950374531835206, -0.258931143762604, -0.258931143762604, 
      0.259651397291847, 0.259651397291847, 0.948934024776722, 
      0.948934024776722, 0.259651397291847, 0.259651397291847)

  y_cross <-
    c(-0.950374531835206, -0.258931143762604, -0.258931143762604, 
      -0.258931143762604, -0.258931143762604, -0.258931143762604, 
      0.259651397291847, 0.259651397291847, 0.948934024776722, 
      0.948934024776722, 0.259651397291847, 0.259651397291847)

  x_hexagon <-
    c(0.773552290406223, 0, -0.773552290406223, -0.773552290406223, 
      0, 0.773552290406223)

  y_hexagon <-
    c(0.446917314894843, 0.8941947555307, 0.446917314894843, 
      -0.447637568424085, -0.892754249495822, -0.447637568424085)

  p <- l_plot(1:3, 1:3)
l_glyph_add_serialaxes

Add a Serialaxes Glyph

Description
Serialaxes glyph show either a star glyph or a parallel coordinate glyph for each point.

Usage
l_glyph_add_serialaxes(
  widget,
  data,
  sequence,
  linewidth = 1,
  scaling = "variable",
  axesLayout = "radial",
  showAxes = FALSE,
  andrews = FALSE,
  axesColor = "gray70",
  showEnclosing = FALSE,
  bboxColor = "gray70",
  label = "",
  ...
)

Arguments

  widget
    widget path as a string or as an object handle

  data
    a data frame with numerical data only

  sequence
    vector with variable names that defines the axes sequence

  linewidth
    linewidth of outline

  scaling
    one of 'variable', 'data', 'observation' or 'none' to specify how the data is scaled. See Details and Examples for more information.

  axesLayout
    either "radial" or "parallel"

  showAxes
    boolean to indicate whether axes should be shown or not

  andrews
    Andrew's curve (a 'Fourier' transformation)
l_glyph_add_text

Add a Text Glyph

Description
Each text glyph can be a multiline string.

Usage
l_glyph_add_text(widget, text, label = "", ...)

Arguments
- widget: widget path as a string or as an object handle
- text: the text strings for each observation. If the object is a factor then the labels get extracted with as.character.
- label: label of a glyph (currently shown only in the glyph inspector)
- ...: state arguments

See Also
l_glyph_add
Other glyph functions: l_glyph_add.default(), l_glyph_add_image(), l_glyph_add_pointrange(), l_glyph_add_polygon(), l_glyph_add_text(), l_glyph_add(), l_glyph_delete(), l_glyph_getLabel(), l_glyph_getType(), l_glyph_ids(), l_glyph_relabel(), l_primitiveGlyphs()
Examples

if(interactive()){

   p <- l_plot(iris, color = iris$Species)
   g <- l_glyph_add_text(p, iris$Species, "test_label")
   p['glyph'] <- g
}

l_glyph_delete  
Delete a Glyph

Description

Delete a glyph from the plot.

Usage

l_glyph_delete(widget, id)

Arguments

widget widget path as a string or as an object handle
id glyph id

See Also

l_glyph_add

Other glyph functions: l_glyph_add.default(), l_glyph_add_image(), l_glyph_add_pointrange(),
l_glyph_add_polygon(), l_glyph_add_serialaxes(), l_glyph_add_text(), l_glyph_add(),
l_glyph_getLabel(), l_glyph_getType(), l_glyph_ids(), l_glyph_relabel(), l_primitiveGlyphs()

l_glyph_getLabel  
Get Glyph Label

Description

Returns the label of a glyph

Usage

l_glyph_getLabel(widget, id)

Arguments

widget widget path as a string or as an object handle
id glyph id
**l_glyph_getType**

*Get Glyph Type*

**Description**

Query the type of a glyph

**Usage**

```c
l_glyph_getType(widget, id)
```

**Arguments**

- `widget`: widget path as a string or as an object handle
- `id`: glyph id

**See Also**

`l_glyph_add`, `l_glyph_ids`, `l_glyph_relabel`

Other glyph functions: `l_glyph_add.default()`, `l_glyph_add_image()`, `l_glyph_add_pointrange()`, `l_glyph_add_polygon()`, `l_glyph_add_serialaxes()`, `l Glyph_add_text()`, `l_glyph_add()`, `l_glyph_delete()`, `lGlyph_getLabel()`, `l_glyph_ids()`, `l_glyph_relabel()`, `l_primitiveGlyphs()`

---

**l_glyph_ids**

*List glyphs ids*

**Description**

List all the non-primitive glyph ids attached to display.

**Usage**

```c
l_glyph_ids(widget)
```

**Arguments**

- `widget`: widget path as a string or as an object handle

**See Also**

`l_glyph_add()`, `l_glyph_add_image()`, `l_glyph_add_pointrange()`, `l_glyph_add_polygon()`, `l_glyph_add_serialaxes()`, `lGlyph_add_text()`, `l_glyph_add()`, `l_glyph_delete()`, `l_glyph_getLabel()`, `l_glyph_ids()`, `l_glyph_relabel()`, `l_primitiveGlyphs()`
See Also

l_glyph_add

Other glyph functions: l_glyph_add.default(), l_glyph_add_image(), l_glyph_add_pointrange(), l_glyph_add_polygon(), l_glyph_add_serialaxes(), l Glyph_add_text(), l_glyph_add(), l_glyph_delete(), l_glyph_getLabel(), l_glyph_getType(), l_glyph_relabel(), lPrimitiveGlyphs()

---

l_glyph_relabel Relabel Glyph

Description

Change the label of a glyph. Note that the label is only displayed in the glyph inspector.

Usage

l_glyph_relabel(widget, id, label)

Arguments

widget widget path as a string or as an object handle
id glyph id
label new label

See Also

Other glyph functions: l_glyph_add.default(), l_glyph_add_image(), l Glyph_add_pointrange(), lGlyph_add_polygon(), l_glyph_add_serialaxes(), l Glyph_add_text(), l_glyph_add(), l_glyph_delete(), l_glyph_getLabel(), l_glyph_getType(), l_glyph_relabel(), lPrimitiveGlyphs()

Examples

if(interactive()){

  p <- l_plot(iris, color = iris$Species)
  g <- l_glyph_add_text(p, iris$Species, "test_label")
  p['glyph'] <- g
  l Glyph_relabel(p, g, "Species")
}

### l_graph

**Generic function to create an interactive graph display**

#### Description

Interactive graphs in loon are currently most often used for navigation graphs.

#### Usage

```r
l_graph(nodes, ...)
```

#### Arguments

- `nodes`  
  object for method dispatch
- `...`  
  arguments passed on to methods
- `from`  
  vector with node names of the from-to pairs for edges
- `to`  
  vector with node names of the from-to pairs for edges
- `isDirected`  
  a boolean state to specify whether these edges have directions
- `parent`  
  parent widget of graph display

#### Details

For more information run: `l_help("learn_R_display_graph.html#graph")`

#### Value

graph handle

#### See Also

Other related graph objects, `loongraph, completegraph, linegraph, complement, as.graph`

Advanced usage `l_navgraph, l_ng_plots, l_ng_ranges`
Examples

```r
if(interactive()) {
    G <- completegraph(nodes=names(iris))
    LG <- linegraph(G, sep=":")
    g <- l_graph(LG)
}
```

---

**l_graphswitch**

Create a graphswitch widget

---

**Description**

The graphswitch provides a graphical user interface for changing the graph in a graph display interactively.

**Usage**

```r
l_graphswitch(activewidget = "", parent = NULL, ...)
```

**Arguments**

- `activewidget`: widget handle of a graph display
- `parent`: parent widget path
- `...`: widget states

**Details**

For more information run: `l_help("learn_R_display_graph.html#graph-switch-widget")`

**See Also**

- `l_graphswitch_add`, `l_graphswitch_ids`, `l_graphswitch_delete`, `l_graphswitch_relabel`,
- `l_graphswitch_getLabel`, `l_graphswitch_move`, `l_graphswitch_reorder`, `l_graphswitch_set`,
- `l_graphswitch_get`
l_graphswitch_add

Add a graph to a graphswitch widget

Description

This is a generic function to add a graph to a graphswitch widget.

Usage

l_graphswitch_add(widget, graph, ...)

Arguments

widget  widget path as a string or as an object handle
graph   a graph or a loongraph object
...     arguments passed on to method

Details

For more information run: l_help("learn_R_display_graph.html#graph-switch-widget")

Value

id for graph in the graphswitch widget

See Also

l_graphswitch

l_graphswitch_add.default

Add a graph that is defined by node names and a from-to edges list

Description

This default method uses the loongraph display states as arguments to add a graph to the graphswitch widget.
Usage

```r
## Default S3 method:
l_graphswitch_add(
  widget,
  graph,
  from,
  to,
  isDirected,
  label = "",
  index = "end",
  ...
)
```

Arguments

- `widget`: graphswitch widget handle (or widget path)
- `graph`: a vector with the node names, i.e. this argument gets passed on as the nodes argument to create a loongraph like object
- `from`: vector with node names of the from-to pairs for edges
- `to`: vector with node names of the from-to pairs for edges
- `isDirected`: boolean to indicate whether the from-to-list defines directed or undirected edges
- `label`: string with label for graph
- `index`: position of graph in the graph list
- `...`: additional arguments are not used for this method

Value

id for graph in the graphswitch widget

See Also

- `l_graphswitch`

---

### l_graphswitch_add.graph

Add a graph to the graphswitch widget using a graph object

Description

Graph objects are defined in the graph R package.

Usage

```r
## S3 method for class 'graph'
l_graphswitch_add(widget, graph, label = "", index = "end", ...)
```
Arguments

widget  
graphswitch widget handle (or widget path)

graph  
a graph object created with the functions in the graph R package.

label  
string with label for graph

index  
position of graph in the graph list

...  
additional arguments are not used for this method

Value

id for graph in the graphswitch widget

See Also

l_graphswitch

---

l_graphswitch_add.loongraph

Add a graph to the graphswitch widget using a loongraph object

Description

Loongraphs can be created with the loongraph function.

Usage

```r
## S3 method for class 'loongraph'
l_graphswitch_add(widget, graph, label = "", index = "end", ...)
```

Arguments

- widget  
  graphswitch widget handle (or widget path)

- graph  
  a loongraph object

- label  
  string with label for graph

- index  
  position of graph in the graph list

- ...  
  additional arguments are not used for this method

Value

id for graph in the graphswitch widget

See Also

l_graphswitch
l_graphswitch_delete   Delete a graph from the graphswitch widget

Description
Remove a graph from the graphswitch widget.

Usage
l_graphswitch_delete(widget, id)

Arguments
widget       graphswitch widget handle (or widget path)
id           of the graph

See Also
l_graphswitch

l_graphswitch_get   Return a Graph as a loongraph Object

Description
Graphs can be extracted from the graphswitch widget as loongraph objects.

Usage
l_graphswitch_get(widget, id)

Arguments
widget       graphswitch widget handle (or widget path)
id           of the graph

See Also
l_graphswitch, loongraph
**_l_graphswitch_getLabel_**

*Query Label of a Graph in the Graphswitch Widget*

**Description**

The graphs in the graphswitch widgets have labels. Use this function to query the label of a graph.

**Usage**

```
l_graphswitch_getLabel(widget, id)
```

**Arguments**

- `widget` | graphswitch widget handle (or widget path)
- `id` | of the graph

**See Also**

- `l_graphswitch`

---

**_l_graphswitch_ids_**

*List the ids of the graphs in the graphswitch widget*

**Description**

Every graph in the graphswitch widget has an id. This function returns these ids preserving the order of how the graphs are listed in the graphswitch.

**Usage**

```
l_graphswitch_ids(widget)
```

**Arguments**

- `widget` | graphswitch widget handle (or widget path)
l_graphswitch_move  
*Move a Graph in the Graph List*

**Description**
Change the position in of a graph in the graphswitch widget.

**Usage**
```
l_graphswitch_move(widget, id, index)
```

**Arguments**
- `widget`: graphswitch widget handle (or widget path)
- `id`: of the graph
- `index`: position of the graph as a positive integer, "start" and "end" are also valid keywords.

**See Also**
- `l_graphswitch`

l_graphswitch_relabel  
*Relabel a Graph in the Graphswitch Widget*

**Description**
The graphs in the graphswitch widgets have labels. Use this function to relabel a graph.

**Usage**
```
l_graphswitch_relabel(widget, id, label)
```

**Arguments**
- `widget`: graphswitch widget handle (or widget path)
- `id`: of the graph
- `label`: string with label of graph

**See Also**
- `l_graphswitch`
**1_graphswitch_reorder**  
*Reorder the Positions of the Graphs in the Graph List*

**Description**

Define a new graph order in the graph list.

**Usage**

1_graphswitch_reorder(widget, ids)

**Arguments**

- **widget**  
  graphswitch widget handle (or widget path)
- **ids**  
  vector with all graph ids from the graph widget. Use 1_graphswitch_ids to query the ids.

**See Also**

1_graphswitch

---

**1_graphswitch_set**  
*Change the Graph shown in the Active Graph Widget*

**Description**

The activewidget state holds the widget handle of a graph display. This function replaces the graph in the activewidget with one of the graphs in the graphswitch widget.

**Usage**

1_graphswitch_set(widget, id)

**Arguments**

- **widget**  
  graphswitch widget handle (or widget path)
- **id**  
  of the graph

**See Also**

1_graphswitch
l_graph_inspector

Create a Graph Inspector

Description
Inspectors provide graphical user interfaces to oversee and modify plot states

Usage
l_graph_inspector(parent = NULL, ...)

Arguments
parent parent widget path
...
state arguments

Value
widget handle

See Also
l_create_handle

Examples
if(interactive()){
  i <- l_graph_inspector()
}

l_graph_inspector_analysis

Create a Graph Analysis Inspector

Description
Inspectors provide graphical user interfaces to oversee and modify plot states

Usage
l_graph_inspector_analysis(parent = NULL, ...)

Arguments
parent parent widget path
...
state arguments
Value

widget handle

See Also

l_create_handle

Examples

if(interactive()){
  i <- l_graph_inspector_navigators()
}
1_help

Open a browser with loon’s combined (TCL and R) documentation website

Description

1_help opens a browser with the relevant page on the official combined loon documentation website at https://great-northern-diver.github.io/loon/1_help/.

Usage

1_help(page = "index", ...)

Arguments

  page  relative path to a page, the .html part may be omitted

...  arguments forwarded to browseURL, e.g. to specify a browser

See Also

help, 1_web for R manual or web R manual

Examples

## Not run:

1_help()
1_help("learn_R_intro")
1_help("learn_R_display_hist")
1_help("learn_R_bind")
# jump to a section
1_help("learn_R_bind.html#list-reorder-delete-bindings")

## End(Not run)

1_hexcolor

Convert color names to their 12 digit hexadecimal color representation

Description

Color names in loon will be mapped to colors according to the Tk color specifications and are normalized to a 12 digit hexadecimal color representation.

Usage

1_hexcolor(color)
l_hist

Create an interactive histogram

Description

l_hist is a generic function for creating interactive histogram displays that can be linked with loon’s other displays.

Usage

l_hist(x, ...)

## Default S3 method:
l_hist(
x,  
yshows = c("frequency", "density"),  
by = NULL,  
on,  
layout = c("grid", "wrap", "separate"),  
connectedScales = c("cross", "row", "column", "both", "x", "y", "none"),  
origin = NULL,  
binwidth = NULL,  
showStackedColors = TRUE,  
showBinHandle = FALSE,  
color = l_getOption("color"),  
active = TRUE,
selected = FALSE,
xlabel = NULL,
showLabels = TRUE,
showScales = FALSE,
showGuides = TRUE,
parent = NULL,
...)

## S3 method for class 'factor'
l_hist(
  x,
  showFactors = length(unique(x)) < 25L,
  factorLabelAngle,
  factorLabelSize = 12,
  factorLabelColor = l_getOption("foreground"),
  factorLabelY = 0,
  ...
)

## S3 method for class 'character'
l_hist(
  x,
  showFactors = length(unique(x)) < 25L,
  factorLabelAngle,
  factorLabelSize = 12,
  factorLabelColor = l_getOption("foreground"),
  factorLabelY = 0,
  ...
)

## S3 method for class 'data.frame'
1_hist(x, ...)

## S3 method for class 'matrix'
1_hist(x, ...)

## S3 method for class 'list'
1_hist(x, ...)

## S3 method for class 'table'
1_hist(x, ...)

## S3 method for class 'array'
1_hist(x, ...)

Arguments

x vector with numerical data to perform the binning on x,
..., named arguments to modify the histogram plot states or layouts, see details.

**yshow**
- one of "frequency" (default) or "density"

**by**
- loon plot can be separated by some variables into multiple panels. This argument can take a formula, n dimensional state names (see `l_nDimStateNames`) an n-dimensional vector and data.frame or a list of same lengths n as input.

**on**
- if the x or by is a formula, an optional data frame containing the variables in the x or by. If the variables are not found in data, they are taken from environment, typically the environment from which the function is called.

**layout**
- layout facets as 'grid', 'wrap' or 'separate'

**connectedScales**
- Determines how the scales of the facets are to be connected depending on which layout is used. For each value of layout, the scales are connected as follows:
  - **layout = "wrap"**: Across all facets, when connectedScales is
    - "x", then only the "x" scales are connected
    - "y", then only the "y" scales are connected
    - "both", both "x" and "y" scales are connected
    - "none", neither "x" nor "y" scales are connected. For any other value, only the "y" scale is connected.
  - **layout = "grid"**: Across all facets, when connectedScales is
    - "cross", then only the scales in the same row and the same column are connected
    - "row", then both "x" and "y" scales of facets in the same row are connected
    - "column", then both "x" and "y" scales of facets in the same column are connected
    - "x", then all of the "x" scales are connected (regardless of column)
    - "y", then all of the "y" scales are connected (regardless of row)
    - "both", both "x" and "y" scales are connected in all facets
    - "none", neither "x" nor "y" scales are connected in any facets.

**origin**
- numeric scalar to define the binning origin

**binwidth**
- a numeric scalar to specify the binwidth. If NULL, binwidth is set using David Scott’s rule when x is numeric (namely 3.49 * sd(x)/(n ^ (1/3)) if sd(x) > 0 and 1 if sd(x) == 0) and using the minimum numerical difference between factor levels when x is a factor or a character vector (coerced to factor).

**showStackedColors**
- if TRUE (default) then bars will be coloured according to colours of the points; if FALSE, then the bars will be a uniform colour except for highlighted points.

**showBinHandle**
- If TRUE, then an interactive "bin handle" appears on the plot whose movement resets the origin and the binwidth. Default is FALSE.

**color**
- colour fills of bins; colours are repeated until matching the number x. Default is found using `l_getOption("color")`.

**active**
- a logical determining whether points appear or not (default is TRUE for all points). If a logical vector is given of length equal to the number of points, then it identifies which points appear (TRUE) and which do not (FALSE).
selected a logical determining whether points appear selected at first (default is FALSE for all points). If a logical vector is given of length equal to the number of points, then it identifies which points are (TRUE) and which are not (FALSE).

xlabel label to be used on the horizontal axis. If NULL, an attempt at a meaningful label inferred from x will be made.

showLabels logical to determine whether axes label (and title) should be presented.

showScales logical to determine whether numerical scales should be presented on both axes.

showGuides logical to determine whether to present background guidelines to help determine locations.

parent a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like tkpack or tkplace in order to be displayed. See the examples below.

showFactors whether to show the factor labels (unique strings in x) as a layer on the plot. If FALSE, the factor labels are hidden and can be turned on from the "layers" tab on the inspector.

factorLabelAngle is the angle of rotation (in degrees) for the factor labels. If not specified, an angle of 0 is chosen if there are fewer than 10 labels; labels are rotated 90 degrees if there are 10 or more. This can also be a numeric vector of length equal to the number of factor labels.

factorLabelSize is the font size for the factor labels (default 12).

factorLabelColor is the colour to be used for the factor labels. (default is l_getOption("foreground"). Can also be a vector equal to that of the number of factor labels.

factorLabelY either a single number, or a numeric vector of length equal to the number of factor labels, determining the y coordinate(s) for the factor labels.

Details
For more information run: l_help("learn_R_display_hist")

• Note that when changing the yshows state from 'frequency' to 'density' you might have to use l_scaleto_world to show the complete histogram in the plotting region.

• Some arguments to modify layouts can be passed through, e.g. "separate", "byrow", etc. Check l_facet to see how these arguments work.

Value
if the argument by is not set, a loon widget will be returned; else an l_facet object (a list) will be returned and each element is a loon widget displaying a subset of interest.

See Also
Turn interactive loon plot static loonGrob, grid.loon, plot.loon.

Other loon interactive states: l_info_states(), l_plot(), l_serialaxes(), l_state_names(), names.loon()
Examples

```r
if(interactive()){

  h <- l_hist(iris$Sepal.Length)

  names(h)
  h["xlabel"] <- "Sepal length"
  h["showOutlines"] <- FALSE

  h["yshows"]
  h["yshows"] <- "density"
  l_scaleto_plot(h)

  h["showStackedColors"] <- TRUE
  h["color"] <- iris$Species
  h["showStackedColors"] <- FALSE
  h["showOutlines"] <- TRUE
  h["showGuides"] <- FALSE

  # link another plot with the previous plot
  h["linkingGroup"] <- "iris_data"
  h2 <- with(iris, l_hist(Petal.Width,
                           linkingGroup="iris_data",
                           showStackedColors = TRUE))

  # Get an R (grid) graphics plot of the current loon plot
  plot(h)
  # or with more control about grid parameters
  grid.loon(h)
  # or to save the grid data structure (grob) for later use
  hg <- loonGrob(h)
}
```

---

**l_hist_inspector**  
Create a Histogram Inspector

---

**Description**

Inspectors provide graphical user interfaces to oversee and modify plot states

**Usage**

```r
l_hist_inspector(parent = NULL, ...)
```

**Arguments**

- `parent`  
  parent widget path
- `...`  
  state arguments
**l_hist_inspector_analysis**

Create a Histogram Analysis Inspector

**Description**

Inspectors provide graphical user interfaces to oversee and modify plot states

**Usage**

```r
l_hist_inspector_analysis(parent = NULL, ...)
```

**Arguments**

- **parent**
  - parent widget path
- **...**
  - state arguments

**Value**

widget handle

**See Also**

`l_create_handle`

**Examples**

```r
if(interactive()){
  i <- l_hist_inspector()
}
```
Display Tcl Images in a Simple Image Viewer

Description

Loon provides a simple image viewer to browse through the specified tcl image objects. The simple GUI supports either the use of the mouse or left and right arrow keys to switch the images to the previous or next image in the specified image vector. The images are resized to fill the viewer window.

Usage

`l_imageviewer(tclimages)`

Arguments

tclimages Vector of tcl image object names.

Value

the tclimages vector is returned

Examples

```r
if(interactive()){

  img2 <- tkimage.create('photo', width=200, height=150)
  tcl(img2, 'put', 'yellow', '-to', 0, 0, 199, 149)
  tcl(img2, 'put', 'green', '-to', 40, 20, 130, 40)
  img3 <- tkimage.create('photo', width=500, height=100)
  tcl(img3, 'put', 'orange', '-to', 0, 0, 499, 99)
  tcl(img3, 'put', 'green', '-to', 40, 80, 350, 95)

  l_imageviewer(c(tclvalue(img2), tclvalue(img3)))
}
```

Import Greyscale Images as Tcl images from an Array

Description

Import image grayscale data (0-255) with each image saved as a row or column of an array.
Usage

l_image_import_array(
    array,
    width,
    height,
    img_in_row = TRUE,
    invert = FALSE,
    rotate = 0
)

Arguments

array       of 0-255 grayscale value data.
width       of images in pixels.
height      of images in pixels.
img_in_row  logical, TRUE if every row of the array represents an image
invert      logical, for 'invert=FALSE' 0=white, for 'invert=TRUE' 0=black
rotate      the image: one of 0, 90, 180, or 270 degrees.

Details

Images in tcl are managed by the tcl interpreter and made accessible to the user via a handle, i.e. a function name of the form image1, image2, etc.

For more information run: l_help("learn_R_display_plot.html#images")

Value

vector of image object names

Examples

## Not run:
# see
demo("I_ng_images_frey_LLE")

## End(Not run)
Usage

l_image_import_files(paths)

Arguments

paths vector with paths to image files that are supported

Details

For more information run: l_help("learn_R_display_plot.html#load-images")

Value

vector of image object names

See Also

l_image_import_array, l_imageviewer

l_info_states

Retrieve Information about the States of a Loon Widget

Description

Loon’s built-in object documentation. Can be used with every loon object that has plot states including plots, layers, navigators, contexts. This is a generic function.

Usage

l_info_states(target, states = "all")

Arguments

target either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. '.10.plot'), the remaining objects by their ids.

states vector with names of states. 'all' is treated as a keyword and results in returning information on all plot states

Value

a named nested list with one element per state. The list elements are also named lists with type, dimension, defaultvalue, and description elements containing the respective information.

See Also

Other loon interactive states: l_hist(), l_plot(), l_serialaxes(), l_state_names(), names.loon()
Examples

if(interactive()){

p <- l_plot(iris, linkingGroup="iris")
i <- l_info_states(p)
names(p)
names(i)
i$selectBy

l <- l_layer_rectangle(p, x=range(iris[,1]), y=range(iris[,2]), color="")
l_info_states(l)

h <- l_hist(iris$Sepal.Length, linkingGroup="iris")
l_info_states(h)
}


l_isLoonWidget  
Check if a widget path is a valid loon widget

Description

This function can be useful to check whether a loon widget is has been closed by the user.

Usage

l_isLoonWidget(widget)

Arguments

widget  
widget path as a string or as an object handle

Value

boolean, TRUE if the argument is a valid loon widget path, FALSE otherwise

l_layer  
Loon layers

Description

Loon supports layering of visuals and groups of visuals. The l_layer function is a generic method.

Usage

l_layer(widget, x, ...)

Arguments

widget widget path as a string or as an object handle
x for UseMethod: an object whose class will determine the method to be dispatched.
...
additional arguments, often state definition for the basic layering function

Details

loon’s displays that use the main graphics model (i.e. histogram, scatterplot and graph displays) support layering of visual information. The following table lists the layer types and functions for layering on a display.

<table>
<thead>
<tr>
<th>Type</th>
<th>Description</th>
<th>Creator Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>group</td>
<td>a group can be a parent of other layers</td>
<td>l_layer_group</td>
</tr>
<tr>
<td>polygon</td>
<td>one polygon</td>
<td>l_layer_polygon</td>
</tr>
<tr>
<td>text</td>
<td>one text string</td>
<td>l_layer_text</td>
</tr>
<tr>
<td>line</td>
<td>one line (i.e. connected line segments)</td>
<td>l_layer_line</td>
</tr>
<tr>
<td>rectangle</td>
<td>one rectangle</td>
<td>l_layer_rectangle</td>
</tr>
<tr>
<td>oval</td>
<td>one oval</td>
<td>l_layer_oval</td>
</tr>
<tr>
<td>points</td>
<td>n points (filled) circle</td>
<td>l_layer_points</td>
</tr>
<tr>
<td>texts</td>
<td>n text strings</td>
<td>l_layer_text</td>
</tr>
<tr>
<td>polygons</td>
<td>n polygons</td>
<td>l_layer_polygons</td>
</tr>
<tr>
<td>rectangles</td>
<td>n rectangles</td>
<td>l_layer_rectangles</td>
</tr>
<tr>
<td>lines</td>
<td>n sets of connected line segments</td>
<td>l_layer_lines</td>
</tr>
<tr>
<td>smooth</td>
<td>fitted smooth line</td>
<td>l_layer_smooth</td>
</tr>
<tr>
<td>rasterImage</td>
<td>one raster image</td>
<td>l_layer_rasterImage</td>
</tr>
<tr>
<td>heatImage</td>
<td>one heat image</td>
<td>l_layer_heatImage</td>
</tr>
<tr>
<td>contourLines</td>
<td>contour lines</td>
<td>l_layer_contourLines</td>
</tr>
</tbody>
</table>

Every layer within a display has a unique id. The visuals of the data in a display present the default layer of that display and has the layer id ‘model’. For example, the ‘model’ layer of a scatterplot display visualizes the scatterplot glyphs. Functions useful to query layers are

Function | Description
--- | ---
1_layer_ids | List layer ids
1_layer_getType | Get layer type

Layers are arranged in a tree structure with the tree root having the layer id ‘root’. The rendering order of the layers is according to a depth-first traversal of the layer tree. This tree also maintains a label and a visibility flag for each layer. The layer tree, layer ids, layer labels and the visibility of each layer are visualized in the layers inspector. If a layer is set to be invisible then it is not rendered on the display. If a group layer is set to be invisible then all its children are not rendered; however, the visibility flag of the children layers remain unchanged. Relevant functions are:

Function | Description
--- | ---
1_layer_getParent | Get parent layer id of a layer
All layers have states that can be queried and modified using the same functions as the ones used for displays (i.e. `l_cget, l_configure, `\` and `\`[<<]`). The last group of layer types in the above table have n-dimensional states, where the actual value of n can be different for every layer in a display.

The difference between the model layer and the other layers is that the model layer has a selected state, responds to selection gestures and supports linking.

For more information run: `l_help("learn_R_layer")`

### Value

layer object handle, layer id

### See Also

`l_info_states, l_scaleto_layer, l_scaleto_world`


### Examples

```r
if(interactive()){
  # l_layer is a generic method
  newFoo <- function(x, y, ...) {
    r <- list(x=x, y=y, ...)
    class(r) <- 'foo'
    return(r)
}
l_layer.density

Layer Method for Kernel Density Estimation

Description

Layer a line that represents a kernel density estimate.

Usage

## S3 method for class 'density'

l_layer(widget, x, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>widget</td>
<td>widget path as a string or as an object handle</td>
</tr>
<tr>
<td>x</td>
<td>object from density of class &quot;density&quot;</td>
</tr>
<tr>
<td>...</td>
<td>additional arguments, often state definition for the basic layering function</td>
</tr>
</tbody>
</table>

Value

layer object handle, layer id

See Also

density
Examples

```r
if(interactive()){
  d <- density(faithful$eruptions, bw = "sj")
  h <- l_hist(x = faithful$eruptions, yshows="density")
  l <- l_layer.density(h, d, color="steelblue", linewidth=3)
  # or l <- l_layer(h, d, color="steelblue", linewidth=3)
}
```

---

**l_layer.Line**  
*Layer line in Line object*

Description

Methods to plot map data defined in the sp package

Usage

```r
## S3 method for class 'Line'
1_layer(widget, x, ...)
```

Arguments

- `widget` widget widget path as a string or as an object handle
- `x` an object defined in the sp class
- `...` arguments forwarded to the relative `l_layer` function

Details

Note that currently loon does neither support holes and ring directions.

Value

layer id

References

Applied Spatial Data Analysis with R by Bivand, Roger S. and Pebesma, Edzer and Gomez-Rubio and Virgilio

See Also

sp, l_layer
Examples

```r
if (interactive()) {
    if (requireNamespace("rworldmap", quietly = TRUE)) {
        world <- rworldmap::getMap(resolution = "coarse")
        p <- l_plot()
        lmap <- l_layer(p, world, asSingleLayer=TRUE)
        l_scaleto_world(p)
        attr(lmap, 'hole')
        attr(lmap, 'NAME')
    }
}
```

l_layer.Lines

Layer lines in Lines object

Description

Methods to plot map data defined in the sp package

Usage

```r
## S3 method for class 'Lines'
l_layer(widget, x, asSingleLayer = TRUE, ...)
```

Arguments

- `widget`: widget widget path as a string or as an object handle
- `x`: an object defined in the sp class
- `asSingleLayer`: If TRUE then prefer a single layer over groups with nested 1-dimensinal layers
- `...`: arguments forwarded to the relative l_layer function

Details

Note that currently loon does neither support holes and ring directions.

Value

layer id

References

Applied Spatial Data Analysis with R by Bivand, Roger S. and Pebesma, Edzer and Gomez-Rubio and Virgilio
See Also

sp, l_layer

Examples

```r
if (interactive()) {
  if (requireNamespace("rworldmap", quietly = TRUE)) {
    world <- rworldmap::getMap(resolution = "coarse")
    p <- l_plot()
    lmap <- l_layer(p, world, asSingleLayer=TRUE)
    l_scaleto_world(p)
    attr(lmap, 'hole')
    attr(lmap, 'NAME')
  }
}
```

---

### l_layer.map

**Add a Map of class map as Drawings to Loon plot**

#### Description

The `maps` library provides some map data in polygon which can be added as drawings (currently with polygons) to Loon plots. This function adds map objects with class `map` from the `maps` library as background drawings.

#### Usage

```r
## S3 method for class 'map'
l_layer(
  widget,  # widget path as a string or as an object handle
  x,  # a map object of class `map` as defined in the `maps` R package
  color = "",  # string: color
  linecolor = "black",  # string: linecolor
  linewidth = 1,  # numeric
  label,  # string, label
  parent = "root",  # string, parent
  index = 0,  # numeric
  asSingleLayer = TRUE,  
  ...
)
```

#### Arguments

- `widget`
- `x`
color fill color, if empty string "", then the fill is transparant
linenormal outline color
linewidth linewidth of outline
label label used in the layers inspector
parent a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like `tkpack` or `tkplace` in order to be displayed. See the examples below.
index position among its siblings. valid values are 0, 1, 2, ..., 'end'
asSingleLayer if TRUE then all the polygons get placed in a n-dimension layer of type polygons. Otherwise, if FALSE, each polygon gets its own layer.
... additional arguments are not used for this method

Value

If asSingleLayer=TRUE then returns layer id of polygons layer, otherwise group layer that contains polygon children layers.

Examples

```r
if(interactive()){
  if (requireNamespace("maps", quietly = TRUE)) {
    canada <- maps::map("world", "Canada",
                        fill=TRUE, plot=FALSE)
    p <- l_plot()
    l_map <- l_layer(p, canada,
                     asSingleLayer=TRUE, color = "cornsilk")
    l_map['color'] <- ifelse(grepl("lake", canada$names, TRUE),
                            "lightblue", "cornsilk")
    l_scaleto_layer(p, l_map)
    l_map['active'] <- FALSE
    l_map['active'] <- TRUE
    l_map['tag']
  }
}
```

Description

Methods to plot map data defined in the `sp` package

Usage

```r
## S3 method for class 'Polygon'
l_layer(widget, x, ...)
```
### Arguments

- **widget**: widget widget path as a string or as an object handle
- **x**: an object defined in the `sp` class
- **...**: arguments forwarded to the relative `l_layer` function

### Details

Note that currently loon does neither support holes and ring directions.

### Value

layer id

### References

Applied Spatial Data Analysis with R by Bivand, Roger S. and Pebesma, Edzer and Gomez-Rubio and Virgilio

### See Also

`sp`, `l_layer`

### Examples

```r
if (interactive()) {
  if (requireNamespace("rworldmap", quietly = TRUE)) {
    world <- rworldmap::getMap(resolution = "coarse")
    p <- l_plot()
    lmap <- l_layer(p, world, asSingleLayer=TRUE)
    l_scaleto_world(p)
    attr(lmap, "hole")
    attr(lmap, "NAME")
  }
}
```

### Description

Methods to plot map data defined in the `sp` package

### Usage

```r
## S3 method for class 'Polygons'
l_layer(widget, x, asSingleLayer = TRUE, ...)
```
Arguments

- **widget**: widget widget path as a string or as an object handle
- **x**: an object defined in the `sp` class
- **asSingleLayer**: If TRUE then prefer a single layer over groups with nested 1-dimensional layers
- **...**: arguments forwarded to the relative `l_layer` function

Details

Note that currently loon does neither support holes and ring directions.

Value

layer id

References

Applied Spatial Data Analysis with R by Bivand, Roger S. and Pebesma, Edzer and Gomez-Rubio and Virgilio

See Also

- `sp`, `l_layer`

Examples

```r
if (interactive()) {
  if (requireNamespace("rworldmap", quietly = TRUE)) {
    world <- rworldmap::getMap(resolution = "coarse")
    p <- l_plot()
    lmap <- l_layer(p, world, asSingleLayer=TRUE)
    l_scaleto_world(p)
    attr(lmap,'hole')
    attr(lmap,'NAME')
  }
}
```

---

**l_layer.SpatialLines**  
*Layer lines in SpatialLines object*

Description

Methods to plot map data defined in the `sp` package

Usage

```r
## S3 method for class 'SpatialLines'
l_layer(widget, x, asSingleLayer = TRUE, ...)
```
**Arguments**

- **widget**: widget widget path as a string or as an object handle
- **x**: an object defined in the `sp` class
- **asSingleLayer**: If TRUE then prefer a single layer over groups with nested 1-dimensional layers
- **...**: arguments forwarded to the relative `l_layer` function

**Details**

Note that currently loon does neither support holes and ring directions.

**Value**

layer id

**References**

Applied Spatial Data Analysis with R by Bivand, Roger S. and Pebesma, Edzer and Gomez-Rubio and Virgilio

**See Also**

`sp`, `l_layer`

**Examples**

```r
if (interactive()) {
  if (requireNamespace("rworldmap", quietly = TRUE)) {
    world <- rworldmap::getMap(resolution = "coarse")
    p <- l_plot()
    lmap <- l_layer(p, world, asSingleLayer=TRUE)
    l_scaleto_world(p)
    attr(lmap, 'hole')
    attr(lmap, 'NAME')
  }
}
```

---

**Description**

Methods to plot map data defined in the `sp` package
Usage

```r
## S3 method for class 'SpatialLinesDataFrame'
l_layer(widget, x, asSingleLayer = TRUE, ...)
```

Arguments

- `widget` widget widget path as a string or as an object handle
- `x` an object defined in the `sp` class
- `asSingleLayer` If TRUE then prefer a single layer over groups with nested 1-dimensinal layers
- `...` arguments forwarded to the relative `l_layer` function

Details

Note that currently loon does neither support holes and ring directions.

Value

layer id

References

Applied Spatial Data Analysis with R by Bivand, Roger S. and Pebesma, Edzer and Gomez-Rubio and Virgilio

See Also

`sp`, `l_layer`

Examples

```r
if (interactive()) {
  if (requireNamespace("rworldmap", quietly = TRUE)) {
    world <- rworldmap::getMap(resolution = "coarse")
    p <- l_plot()
    lmap <- l_layer(p, world, asSingleLayer=TRUE)
    l_scaleto_world(p)
    attr(lmap, 'hole')
    attr(lmap, 'NAME')
  }
}
```
### Description

Methods to plot map data defined in the *sp* package.

### Usage

```r
## S3 method for class 'SpatialPoints'
l_layer(widget, x, asMainLayer = FALSE, ...)
```

### Arguments

- `widget` widget widget path as a string or as an object handle
- `x` an object defined in the *sp* class
- `asMainLayer` if TRUE and the widget is a scatterplot widget, then points can be chosen to be added to the 'model' layer
- `...` arguments forwarded to the relative `l_layer` function

### Details

Note that currently loon does neither support holes and ring directions.

### Value

layer id

### References

Applied Spatial Data Analysis with R by Bivand, Roger S. and Pebesma, Edzer and Gomez-Rubio and Virgilio

### See Also

* `sp`, `l_layer`

### Examples

```r
if (interactive()) {
  if (requireNamespace("rworldmap", quietly = TRUE)) {
    world <- rworldmap::getMap(resolution = "coarse")
    p <- l_plot()
    lmap <- l_layer(p, world, asSingleLayer=TRUE)
    l_scaleto_world(p)
    attr(lmap,'hole')
  }
}
```
Description

Methods to plot map data defined in the sp package

Usage

## S3 method for class 'SpatialPointsDataFrame'
l_layer(widget, x, asMainLayer = FALSE, ...)

Arguments

widget
gradient widget path as a string or as an object handle

x
an object defined in the sp class

asMainLayer
if TRUE and the widget is a scatterplot widget, then points can be chosen to be added to the 'model' layer

...arguments forwarded to the relative l_layer function

Details

Note that currently loon does neither support holes and ring directions.

Value

layer id

References

Applied Spatial Data Analysis with R by Bivand, Roger S. and Pebesma, Edzer and Gomez-Rubio and Virgilio

See Also

sp, l_layer
Examples

```r
if (interactive()) {
  if (requireNamespace("rworldmap", quietly = TRUE)) {
    world <- rworldmap::getMap(resolution = "coarse")
    p <- l_plot()
    lmap <- l_layer(p, world, asSingleLayer=TRUE)
    l_scaleto_world(p)
    attr(lmap, 'hole')
    attr(lmap, 'NAME')
  }
}
```

---

**l_layer.SpatialPolygons**

Layer polygons in SpatialPolygons object

---

**Description**

Methods to plot map data defined in the sp package

**Usage**

```r
## S3 method for class 'SpatialPolygons'
l_layer(widget, x, asSingleLayer = TRUE, ...)
```

**Arguments**

- `widget` widget widget path as a string or as an object handle
- `x` an object defined in the sp class
- `asSingleLayer` If TRUE then prefer a single layer over groups with nested 1-dimensinal layers
- `...` arguments forwarded to the relative `l_layer` function

**Details**

Note that currently loon does neither support holes and ring directions.

**Value**

layer id

**References**

Applied Spatial Data Analysis with R by Bivand, Roger S. and Pebesma, Edzer and Gomez-Rubio and Virgilio
l_layer.SpatialPolygonsDataFrame

Description

Methods to plot map data defined in the sp package

Usage

```r
## S3 method for class 'SpatialPolygonsDataFrame'
l_layer(widget, x, asSingleLayer = TRUE, ...)
```

Arguments

- `widget` widget widget path as a string or as an object handle
- `x` an object defined in the sp class
- `asSingleLayer` If TRUE then prefer a single layer over groups with nested 1-dimensional layers
- `...` arguments forwarded to the relative `l_layer` function

Details

Note that currently loon does neither support holes and ring directions.

Value

layer id
l_layers_inspector

Create a Layers Inspector

Description

Inspectors provide graphical user interfaces to oversee and modify plot states

Usage

l_layers_inspector(parent = NULL, ...)

Arguments

parent  

parent widget path

...  

state arguments

Value

widget handle

See Also

l_create_handle
Examples

```r
if(interactive()){
  i <- l_layers_inspector()
}
```

---

**l_layer_bbox**

Get the bounding box of a layer.

**Description**

The bounding box of a layer returns the coordinates of the smallest rectangle that encloses all the elements of the layer.

**Usage**

```r
l_layer_bbox(widget, layer = "root")
```

**Arguments**

- `widget` widget path or layer object of class `l_layer`
- `layer` layer id. If the widget argument is of class `l_layer` then the layer argument is not used

**Value**

Numeric vector of length 4 with (xmin, ymin, xmax, ymax) of the bounding box

**Examples**

```r
if(interactive()){
  p <- with(iris, l_plot(Sepal.Length ~ Sepal.Width, color=Species))
  l_layer_bbox(p, layer = "model")
  l <- l_layer_rectangle(p, x=0:1, y=30:31)
  l_layer_bbox(p, l)
  l_layer_bbox(p, 'root')
}
```
Layer Contour Lines

Description

This function is a wrapper around `contourLines` that adds the contourlines to a loon plot which is based on the cartesian coordinate system.

Usage

```r
l_layer_contourLines(
  widget, 
  x = seq(0, 1, length.out = nrow(z)), 
  y = seq(0, 1, length.out = ncol(z)), 
  z, 
  nlevels = 10, 
  levels = pretty(range(z, na.rm = TRUE), nlevels), 
  asSingleLayer = TRUE, 
  parent = "root", 
  index = "end", 
  ...
)
```

Arguments

- `widget` widget path as a string or as an object handle
- `x` locations of grid lines at which the values in `z` are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If `x` is a list, its components `x$x` and `x$y` are used for `x` and `y`, respectively. If the list has component `z` this is used for `z`.
- `y` see description for the `x` argument
- `z` a matrix containing the values to be plotted (NAs are allowed). Note that `x` can be used instead of `z` for convenience.
- `nlevels` number of contour levels desired if levels is not supplied.
- `levels` numeric vector of levels at which to draw contour lines.
- `asSingleLayer` if TRUE a lines layer is used for the line, otherwise if FALSE a group with nested line layers for each line is created
- `parent` a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like `tkpack` or `tkplace` in order to be displayed. See the examples below.
- `index` position among its siblings. valid values are 0, 1, 2, ..., 'end'
- `...` arguments forwarded to `l_layer_line`
Details

For more information run: l_help("learn_R_layer.html#countourlines-heatimage-rasterimage")

Value

layer id of group or lines layer

Examples

```r
if(interactive()){
    p <- l_plot()
x <- 10*1:nrow(volcano)
y <- 10*1:ncol(volcano)
lcl <- l_layer_contourLines(p, x, y, volcano)
l_scale_to_world(p)
    
    if (requireNamespace("MASS", quietly = TRUE)) {
        p1 <- with(iris, l_plot(Sepal.Length~Sepal.Width, color=Species))
lcl <- with(iris, l_layer_contourLines(p1, MASS::kde2d(Sepal.Width,Sepal.Length)))

        p2 <- with(iris, l_plot(Sepal.Length~Sepal.Width, color=Species))
layers <- sapply(split(cbind(iris, color=p2['color']), iris$Species), function(dat) {
            kest <- with(dat, MASS::kde2d(Sepal.Width,Sepal.Length))
l_layer_contourLines(p2, kest, color=as.character(dat$color[1]), linewidth=2,
                label=paste0(as.character(dat$Species[1]), " contours"))
        })
    }
}
```

Description

All but the 'model' and the 'root' layer can be dynamically deleted. If a group layer gets deleted with `l_layer_delete` then all its children layers get moved into their grandparent group layer.

Usage

`l_layer_delete(widget, layer)`

Arguments

- **widget**: widget path or layer object of class 'l_layer'
- **layer**: layer id. If the widget argument is of class 'l_layer' then the layer argument is not used
Value

0 if success otherwise the function throws an error

See Also

l_layer, l_info_states

Examples

if(interactive()){

  p <- l_plot()
  l1 <- l_layer_rectangle(p, x = 0:1, y = 0:1, color='red')
  l_layer_delete(l1)

  l2 <- l_layer_rectangle(p, x = 0:1, y = 0:1, color='yellow')
  l_layer_delete(p,l2)
}

l_layer_demote

Moves the layer to be a child of its right group layer sibling

Description

Moves the layer up the layer tree (away from the root layer) if there is a sibling group layer to the right of the layer.

Usage

l_layer_demote(widget, layer)

Arguments

  widget  widget path or layer object of class 'l_layer'
  layer   layer id. If the widget argument is of class 'l_layer' then the layer argument is not used

Value

0 if success otherwise the function throws an error
**l_layer_expunge**

*Delete a layer and all its descendants*

**Description**

Delete a group layer and all its descendants. Note that the 'model' layer cannot be deleted.

**Usage**

```r
l_layer_expunge(widget, layer)
```

**Arguments**

- `widget` widget path or layer object of class 'l_layer'
- `layer` layer id. If the widget argument is of class 'l_layer' then the layer argument is not used

**Value**

0 if success otherwise the function throws an error

**See Also**

`l_layer, l_layer_delete`
Examples

```r
if(interactive()){
  p <- l_plot()
  g <- l_layer_group(p)
  l1 <- l_layer_rectangle(p, x=0:1, y=0:1, parent=g, color="", linecolor="orange", linewidth=2)
  l2 <- l_layer_line(p, x=c(0,.5,1), y=c(0,1,0), parent=g, color="blue")

  l_layer_expunge(p, g)
  # or l_layer_expunge(g)
}
```

---

`l_layer_getChildren`  
*Get children of a group layer*

Description

Returns the ids of a group layer's children.

Usage

```r
l_layer_getChildren(widget, layer = "root")
```

Arguments

- `widget`: widget path or layer object of class `l_layer`
- `layer`: layer id. If the `widget` argument is of class `l_layer` then the `layer` argument is not used.

Value

Character vector with ids of the childrens. To create layer handles (i.e. objects of class `l_layer`) use the `l_create_handle` function.

See Also

- `l_layer`, `l_layer_getParent`

Examples

```r
if(interactive()){
  p <- l_plot()
  g <- l_layer_group(p)
  l1 <- l_layer_rectangle(p, x=0:1, y=0:1, parent=g)
```
l2 <- l_layer_oval(p, x=0:1, y=0:1, color='thistle', parent=g)
l_layer_getChildren(p, g)
}

Description

Layer labels are useful to identify layer in the layer inspector. The layer label can be initially set at layer creation with the label argument.

Usage

l_layer_getLabel(widget, layer)

Arguments

(widget) widget path or layer object of class 'l_layer'
(layer) layer id. If the widget argument is of class 'l_layer' then the layer argument is not used

Details

Note that the layer label is not a state of the layer itself, instead is information that is part of the layer collection (i.e. its parent widget).

Value

Named vector of length 1 with layer label as value and layer id as name.

See Also

l_layer, l_layer_relabel

Examples

if(interactive()){
p <- l_plot()
l1 <- l_layer_rectangle(p, x=0:1, y=0:1, label="a rectangle")
l_layer_getLabel(p, 'model')
l_layer_getLabel(p, l1)
}
\texttt{l\_layer\_getParent} \hspace{1em} \textit{Get parent layer id of a layer}

\begin{itemize}
  \item \textbf{Description}
  \begin{itemize}
    \item The toplevel parent is the 'root' layer.
  \end{itemize}
  \item \textbf{Usage}
  \begin{itemize}
    \item \texttt{l\_layer\_getParent(widget, layer)}
  \end{itemize}
  \item \textbf{Arguments}
  \begin{itemize}
    \item \texttt{widget} \hspace{1em} \text{widget path or layer object of class 'l\_layer'}
    \item \texttt{layer} \hspace{1em} \text{layer id. If the widget argument is of class 'l\_layer' then the layer argument is not used}
  \end{itemize}
  \item \textbf{See Also}
  \begin{itemize}
    \item \texttt{l\_layer, l\_layer\_getChildren}
  \end{itemize}
  \item \textbf{Examples}
  \begin{itemize}
    \item \texttt{if(interactive()){}
      \begin{itemize}
        \item \texttt{p <- with(iris, l\_plot(Sepal.Length ~ Sepal.Width, color=Species))}
        \item \texttt{l\_layer\_getParent(p, 'model')}
      \end{itemize}
    \}
  \end{itemize}
\end{itemize}

\texttt{l\_layer\_getType} \hspace{1em} \textit{Get layer type}

\begin{itemize}
  \item \textbf{Description}
  \begin{itemize}
    \item To see the manual page of \texttt{l\_layer} for all the primitive layer types.
  \end{itemize}
  \item \textbf{Usage}
  \begin{itemize}
    \item \texttt{l\_layer\_getType(widget, layer)}
  \end{itemize}
  \item \textbf{Arguments}
  \begin{itemize}
    \item \texttt{widget} \hspace{1em} \text{widget path or layer object of class 'l\_layer'}
    \item \texttt{layer} \hspace{1em} \text{layer id. If the widget argument is of class 'l\_layer' then the layer argument is not used}
  \end{itemize}
\end{itemize}
Details

For more information run: l_help("learn_R_layer")

Value

One of: 'group', 'polygon', 'text', 'line', 'rectangle', 'oval', 'points', 'texts', 'polygons', 'rectangles', 'lines' and 'scatterplot', 'histogram', 'serialaxes' and 'graph'.

See Also

l_layer

Examples

if(interactive()){
  p <- l_plot()
  l <- l_layer_rectangle(p, x=0:1, y=0:1)
  l_layer_getType(p, l)
  l_layer_getType(p, 'model')
}

l_layer_group

layer a group node

Description

Loon's displays that are based on Cartesian coordinates (i.e. scatterplot, histogram and graph display) allow for layering visual information including polygons, text and rectangles.

A group layer can contain other layers. If the group layer is invisible, then so are all its children.

Usage

l_layer_group(widget, label = "group", parent = "root", index = 0)

Arguments

widget widget path name as a string
label label used in the layers inspector
parent group layer
index of the newly added layer in its parent group

Details

For more information run: l_help("learn_R_layer")
Value

layer object handle, layer id

See Also

l_layer, l_info_states

Examples

```r
if (interactive()){
  p <- l_plot(x=c(1,10,1.5,7,4.3,9,5,2,8),
              y=c(1,10,7,3,4,3.3,8,3,4),
              title="Demo Layers")

  id.g <- l_layer_group(p, "A Layer Group")
  id.pts <- l_layer_points(p, x=c(3,6), y=c(4,7), color="red", parent=id.g)
  l_scaleto_layer(p, id.pts)
  l_configure(id.pts, x=c(-5,5,12), y=c(-2,-5,18), color="lightgray")
}
```

l_layer_groupVisibility

Queries visibility status of descendants

Description

Query whether all, part or none of the group layers descendants are visible.

Usage

l_layer_groupVisibility(widget, layer)

Arguments

- **widget**: widget path or layer object of class 'l_layer'
- **layer**: layer id. If the widget argument is of class 'l_layer' then the layer argument is not used

Details

Visible layers are rendered, invisible ones are not. If any ancestor of a layer is set to be invisible then the layer is not rendered either. The layer visibility flag can be checked with `l_layer_isVisible` and the actual visibility (i.e. are all the ancestors visible too) can be checked with `l_layer_layerVisibility`.

Note that layer visibility is not a state of the layer itself, instead is information that is part of the layer collection (i.e. its parent widget).
Value

'all', 'part' or 'none' depending on the visibility status of the descendants.

See Also

l_layer, l_layer_show, l_layer_hide, l_layer_isVisible, l_layer_layerVisibility

Examples

if(interactive()){
  p <- l_plot()
  g <- l_layer_group(p)
  l1 <- l_layer_rectangle(p, x=0:1, y=0:1, parent=g)
  l2 <- l_layer_oval(p, x=0:1, y=0:1, parent=g)

  l_layer_groupVisibility(p, g)
  l_layer_hide(p, l2)
  l_layer_groupVisibility(p, g)
  l_layer_hide(p, l1)
  l_layer_groupVisibility(p, g)
  l_layer_hide(p, g)
  l_layer_groupVisibility(p, g)

}

l_layer_heatImage

Display a Heat Image

Description

This function is very similar to the image function. It works with every loon plot which is based on the cartesian coordinate system.

Usage

l_layer_heatImage(
  widget,
  x = seq(0, 1, length.out = nrow(z)),
  y = seq(0, 1, length.out = ncol(z)),
  z,
  zlim = range(z[is.finite(z)]),
  xlim = range(x),
  ylim = range(y),
  col = grDevices::heat.colors(12),
  breaks,
oldstyle = FALSE,
useRaster,
index = "end",
parent = "root",
...)

Arguments

widget widget path as a string or as an object handle
x locations of grid lines at which the values in z are measured. These must be finite, non-missing and in (strictly) ascending order. By default, equally spaced values from 0 to 1 are used. If x is a list, its components x$x and x$y are used for x and y, respectively. If the list has component z this is used for z.
y see description for the x argument above
z a numeric or logical matrix containing the values to be plotted (NAs are allowed). Note that x can be used instead of z for convenience.
zlim the minimum and maximum z values for which colors should be plotted, defaulting to the range of the finite values of z. Each of the given colors will be used to color an equispaced interval of this range. The midpoints of the intervals cover the range, so that values just outside the range will be plotted.
xlim range for the plotted x values, defaulting to the range of x
ylim range for the plotted y values, defaulting to the range of y
col a list of colors such as that generated by hcl.colors, gray.colors or similar functions.
breaks a set of finite numeric breakpoints for the colours: must have one more breakpoint than colour and be in increasing order. Unsorted vectors will be sorted, with a warning.
oldstyle logical. If true the midpoints of the colour intervals are equally spaced, and zlim[1] and zlim[2] were taken to be midpoints. The default is to have colour intervals of equal lengths between the limits.
useRaster logical; if TRUE a bitmap raster is used to plot the image instead of polygons. The grid must be regular in that case, otherwise an error is raised. For the behaviour when this is not specified, see ‘Details’.
index position among its siblings. valid values are 0, 1, 2, ..., 'end'
parent a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like tkpack or tkplace in order to be displayed. See the examples below.
...

Details

For more information run: l_help("learn_R_layer.html#countourlines-heatimage-rasterimage")
### Value

layer id of group or rectangles layer

### Examples

```r
if(interactive()){
  if (requireNamespace("MASS", quietly = TRUE)) {
    kest <- with(iris, MASS::kde2d(Sepal.Width,Sepal.Length))
    image(kest)
    contour(kest, add=TRUE)

    p <- l_plot()
    lcl <- l_layer_contourLines(p, kest, label="contour lines")
    limg <- l_layer_heatImage(p, kest, label="heatmap")
    l_scaleto_world(p)
  }
  # from examples(image)
  x <- y <- seq(-4*pi, 4*pi, len = 27)
  r <- sqrt(outer(x^2, y^2, "+"))
  p1 <- l_plot()
  l_layer_heatImage(p1, z = z <- cos(r^2)*exp(-r/6), col = gray((0:32)/32))
  l_scaleto_world(p1)

  image(z = z <- cos(r^2)*exp(-r/6), col = gray((0:32)/32))
}
```

---

### l_layer_hide

#### Hide a Layer

### Description

A hidden layer is not rendered. If a group layer is set to be hidden then all its descendants are not rendered either.

### Usage

```r
l_layer_hide(widget, layer)
```

### Arguments

- **widget**: widget path or layer object of class 'l_layer'
- **layer**: layer id. If the widget argument is of class 'l_layer' then the layer argument is not used
Details

Visible layers are rendered, invisible ones are not. If any ancestor of a layer is set to be invisible then the layer is not rendered either. The layer visibility flag can be checked with `l_layer_isVisible` and the actual visibility (i.e. are all the ancestors visible too) can be checked with `l_layer_layerVisibility`.

Note that layer visibility is not a state of the layer itself, instead is information that is part of the layer collection (i.e. its parent widget).

Value

0 if success otherwise the function throws an error

See Also

`l_layer`, `l_layer_show`, `l_layer_isVisible`, `l_layer_layerVisibility`, `l_layer_groupVisibility`

Examples

```r
if(interactive()){
  p <- l_plot()
  l <- l_layer_rectangle(p, x=0:1, y=0:1, color="steelblue")
  l_layer_hide(p, l)
}
```

---

R Interface

```r
l_layer_ids(widget)
```

Arguments

- `widget` widget path as a string or as an object handle

Details

For more information run: `l_help("learn_R_layer.html#add-move-delete-layers")`

Value

vector with layer ids in rendering order. To create a layer handle object use `l_create_handle`.
See Also

l_layer, l_info_states

Examples

```r
if (interactive()){  
  set.seed(500)  
x <- rnorm(30)  
y <- 4 + 3*x + rnorm(30)  
fit <- lm(y~x)  
xseq <- seq(min(x)-1, max(x)+1, length.out = 50)  
fit_line <- predict(fit, data.frame(x=xseq))  
ci <- predict(fit, data.frame(x=xseq),  
        interval="confidence", level=0.95)  
pi <- predict(fit, data.frame(x=xseq),  
        interval="prediction", level=0.95)  

  p <- l_plot(y~x, color='black', showScales=TRUE, showGuides=TRUE)  
gLayer <- l_layer_group(  
    p, label="simple linear regression",  
    parent="root", index="end"  
)  
fitLayer <- l_layer_line(  
    p, x=range(xseq), y=fit_line, color="#04327F",  
    linewidth=4, label="fit", parent=gLayer  
)  

  ciLayer <- l_layer_polygon(  
      p,  
      x = c(xseq, rev(xseq)),  
      y = c(ci[, 'lwr'], rev(ci[, 'upr'])),  
      color = "#96BDFF", linecolor="",  
      label = "95 % confidence interval",  
      parent = gLayer, index='end'  
  )  

  piLayer <- l_layer_polygon(  
      p,  
      x = c(xseq, rev(xseq)),  
      y = c(pi[, 'lwr'], rev(pi[, 'upr'])),  
      color = "#E2EDFF", linecolor="",  
      label = "95 % prediction interval",  
      parent = gLayer, index='end'  
  )  

  l_info_states(piLayer)  
}
```
### l_layer_index

*Get the order index of a layer among its siblings*

**Description**

The index determines the rendering order of the children layers of a parent. The layer with index=0 is rendered first.

**Usage**

```python
l_layer_index(widget, layer)
```

**Arguments**

- `widget`: widget path or layer object of class `'l_layer'`
- `layer`: layer id. If the widget argument is of class `'l_layer'` then the layer argument is not used.

**Details**

Note that the index for layers is 0 based.

**Value**

numeric value

**See Also**

`l_layer, l_layer_move`

---

### l_layer_isVisible

*Return visibility flag of layer*

**Description**

Hidden or invisible layers are not rendered. This function queries whether a layer is visible/rendered or not.

**Usage**

```python
l_layer_isVisible(widget, layer)
```

**Arguments**

- `widget`: widget path or layer object of class `'l_layer'`
- `layer`: layer id. If the widget argument is of class `'l_layer'` then the layer argument is not used.
Details

Visibile layers are rendered, invisible ones are not. If any ancestor of a layer is set to be invisible then
the layer is not rendered either. The layer visibility flag can be checked with `l_layer_isVisible`
and the actual visibility (i.e. are all the ancestors visible too) can be checked with `l_layer_layerVisibility`.

Note that layer visibility is not a state of the layer itself, instead is information that is part of the
layer collection (i.e. its parent widget).

Value

TRUE or FALSE depending whether the layer is visible or not.

See Also

`l_layer`, `l_layer_show`, `l_layer_hide`, `l_layer_layerVisibility`, `l_layer_groupVisibility`

Examples

```r
if(interactive()){
  p <- l_plot()
  l <- l_layer_rectangle(p, x=0:1, y=0:1)
  l_layer_isVisible(p, l)
  l_layer_hide(p, l)
  l_layer_isVisible(p, l)
}
```

---

**l_layer_layerVisibility**

*Returns logical value for whether layer is actually seen*

Description

Although the visibility flag for a layer might be set to TRUE it won’t be rendered as on of its ancestor
group layer is set to be invisible. The `l_layer_visibility` returns TRUE if the layer and all its
ancestor layers have their visibility flag set to true and the layer is actually rendered.

Usage

`l_layer_layerVisibility(widget, layer)`

Arguments

- **widget**: widget path or layer object of class 'l_layer'
- **layer**: layer id. If the widget argument is of class 'l_layer' then the layer argument
  is not used
Details

Visible layers are rendered, invisible ones are not. If any ancestor of a layer is set to be invisible then the layer is not rendered either. The layer visibility flag can be checked with `l_layer_isVisible` and the actual visibility (i.e. are all the ancestors visible too) can be checked with `l_layer_layerVisibility`.

Note that layer visibility is not a state of the layer itself, instead is information that is part of the layer collection (i.e. its parent widget).

Value

TRUE if the layer and all its ancestor layers have their visibility flag set to true and the layer is actually rendered, otherwise FALSE.

See Also

`l_layer`, `l_layer_show`, `l_layer_hide`, `l_layer_isVisible`, `l_layer_groupVisibility`

---

### l_layer_line

**Layer a line**

Description

Loon’s displays that are based on Cartesian coordinates (i.e. scatterplot, histogram and graph display) allow for layering visual information including polygons, text and rectangles.

Usage

```r
l_layer_line(
  widget,  # widget path name as a string
  x,       # the coordinates of line. Alternatively, a single plotting structure, function or any R object with a plot method can be provided as x and y are passed on to
  y = NULL, # the y coordinates of the line, optional if x is an appropriate structure.
  color = "black", # color
  linewidth = 1,  # line width
  dash = "",      # dash pattern
  label = "line", # label
  parent = "root", # parent
  index = 0,      # index
  ...
)
```

Arguments

- **widget**: widget path name as a string
- **x**: the coordinates of line. Alternatively, a single plotting structure, function or any R object with a plot method can be provided as x and y are passed on to `xy.coords`
- **y**: the y coordinates of the line, optional if x is an appropriate structure.
**color**
- color of line

**linewidth**
- linewidth of outline

**dash**
- dash pattern of line, see [https://www.tcl.tk/man/tcl8.6/TkCmd/canvas.htm#M26](https://www.tcl.tk/man/tcl8.6/TkCmd/canvas.htm#M26)

**label**
- label used in the layers inspector

**parent**
- group layer

**index**
- of the newly added layer in its parent group

...  
- additional state initialization arguments, see `l_info_states`

**Details**

For more information run: `l_help("learn_R_layer")`

**Value**

layer object handle, layer id

**See Also**

`l_layer, l_info_states`

**Examples**

```r
if(interactive()){
  p <- l_plot()
  l <- l_layer_line(p, x=c(1,2,3,4), y=c(1,3,2,4), color="red", linewidth=2)
  l_scaleto_world(p)

  # object
  p <- l_plot()
  l <- l_layer_line(p, x=nhtemp)
  l_scaleto_layer(l)
}
```

---

**Description**

Loon's displays that are based on Cartesian coordinates (i.e. scatterplot, histogram and graph display) allow for layering visual information including polygons, text and rectangles.
Usage

```r
l_layer_lines(
  widget,
  x,
  y,
  color = "black",
  linewidth = 1,
  label = "lines",
  parent = "root",
  index = 0,
  group = NULL,
  active = TRUE,
  ...)
```

Arguments

- `widget`: widget path name as a string
- `x`: list with vectors with x coordinates
- `y`: list with vectors with y coordinates
- `color`: color of lines
- `linewidth`: vector with line widths
- `label`: label used in the layers inspector
- `parent`: group layer
- `index`: of the newly added layer in its parent group
- `group`: separate x vector or y vector into a list by group.
- `active`: a logical determining whether objects appear or not (default is `TRUE` for all).
- `...`: additional state initialization arguments, see `l_info_states`

Details

For more information run: `l_help("learn_R_layer")`

Value

layer object handle, layer id

See Also

`l_layer, l_info_states`
if(interactive()){  

s <- Filter(function(df) nrow(df) > 1, split(UsAndThem, UsAndThem$Country))  
sUaT <- Map(function(country){country[order(country$Year),]}, s)  
xcoords <- Map(function(x)x$Year, sUaT)  
ycoords <- Map(function(x)x$LifeExpectancy, sUaT)  
region <- sapply(sUaT, function(x) as.character(x$Geographic.Region[1]))  

p <- l_plot(showItemLabels=TRUE)  
l <- l_layer_lines(p, xcoords, ycoords, itemLabel=names(sUaT), color=region)  
l_scaleto_layer(l)

# Set groups  
p <- l_plot(showItemLabels=TRUE)  
l <- l_layer_lines(p,  
  x = c((0:4)/10, rep(.5, 5), (10:6)/10, rep(.5, 5)),  
  y = c(rep(.5, 5), (10:6/10), rep(.5, 5), (0:4)/10),  
  group = rep(1:5, 4),  
  linewidth = 4,  
  col = l_getColorList()[1:5])  
l_scaleto_layer(l)

}

1_layer_lower

Switch the layer place with its sibling to the right

Description

Change the layers position within its parent layer group by increasing the index of the layer by one if possible. This means that the raised layer will be rendered before (or on below) of its sibling layer to the right.

Usage

1_layer_lower(widget, layer)

Arguments

widget      widget path or layer object of class 'l_layer'
layer       layer id. If the widget argument is of class 'l_layer' then the layer argument is not used

Value

0 if success otherwise the function throws an error
See Also

`l_layer, l_layer_raise, l_layer_move`

Examples

```r
if(interactive()){
  p <- l_plot()
  l1 <- l_layer_rectangle(p, x=0:1, y=0:1)
  l2 <- l_layer_oval(p, x=0:1, y=0:1, color='thistle')
  l_aspect(p) <- 1
  l_layer_lower(p, l2)
}
```

### Description

The position of a layer in the layer tree determines the rendering order. That is, the non-group layers are rendered in order of a Depth-first traversal of the layer tree. The toplevel group layer is called 'root'.

### Usage

```r
l_layer_move(widget, layer, parent, index = "0")
```

### Arguments

- **widget**: widget path or layer object of class 'l_layer'
- **layer**: layer id. If the widget argument is of class 'l_layer' then the layer argument is not used
- **parent**: if parent layer is not specified it is set to the current parent layer of the layer
- **index**: position among its siblings. Valid values are 0, 1, 2, ..., 'end'

### Value

0 if success otherwise the function throws an error

### See Also

`l_layer, l_layer_printTree, l_layer_index`
Examples

```r
if(interactive()){

  p <- l_plot()

  l <- l_layer_rectangle(p, x=0:1, y=0:1, color="steelblue")
  g <- l_layer_group(p)
  l_layer_printTree(p)

  l_layer_move(l, parent=g)
  l_layer_printTree(p)

  l_layer_move(p, 'model', parent=g)
  l_layer_printTree(p)

}
```

---

### l_layer_oval

**Layer a oval**

#### Description

Loon's displays that are based on Cartesian coordinates (i.e. scatterplot, histogram and graph display) allow for layering visual information including polygons, text and rectangles.

#### Usage

```r
l_layer_oval(
  widget,
  x,
  y,
  color = "gray80",
  linecolor = "black",
  linewidth = 1,
  label = "oval",
  parent = "root",
  index = 0,
  ...
)
```

#### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>widget</td>
<td>widget path name as a string</td>
</tr>
<tr>
<td>x</td>
<td>x coordinates</td>
</tr>
<tr>
<td>y</td>
<td>y coordinates</td>
</tr>
<tr>
<td>color</td>
<td>fill color, if empty string &quot;&quot; , then the fill is transparant</td>
</tr>
<tr>
<td>linecolor</td>
<td>outline color</td>
</tr>
</tbody>
</table>
\begin{verbatim}
linewidth  linewidth of outline
label      label used in the layers inspector
parent     group layer
index      of the newly added layer in its parent group
...        additional state initialization arguments, see \texttt{l_info_states}
\end{verbatim}

\section*{Details}

For more information run: \texttt{l_help("learn_R_layer")}

\section*{Value}

layer object handle, layer id

\section*{See Also}

\texttt{l_layer}, \texttt{l_info_states}

\section*{Examples}

\begin{verbatim}
if(interactive()){  
  p <- \texttt{l_plot()}  
  l <- \texttt{l_layer_oval(p, c(1,5), c(2,12), color='steelblue')}  
  l_configure(p, panX=0, panY=0, deltaX=20, deltaY=20)
  }
\end{verbatim}

\section*{Description}

Loon's displays that are based on Cartesian coordinates (i.e. scatterplot, histogram and graph display) allow for layering visual information including polygons, text and rectangles.

Scatter points layer

\section*{Usage}

\begin{verbatim}
\texttt{l_layer_points(}
  \hspace{1em} \texttt{widget,}
  \hspace{1em} \texttt{x,}
  \hspace{1em} \texttt{y = NULL,}
  \hspace{1em} \texttt{color = "gray60",}
  \hspace{1em} \texttt{size = 6,}
  \hspace{1em} \texttt{label = "points",}
  \hspace{1em} \texttt{parent = "root"},
\end{verbatim}
index = 0,
active = TRUE,
...
)

Arguments

widget widget path name as a string
x the coordinates of line. Alternatively, a single plotting structure, function or any R object with a plot method can be provided as x and y are passed on to xy.coords
y the y coordinates of the line, optional if x is an appropriate structure.
color color of points
size size point, as for scatterplot model layer
label label used in the layers inspector
parent group layer
index of the newly added layer in its parent group
active a logical determining whether objects appear or not (default is TRUE for all).
... additional state initialization arguments, see \texttt{l\_info\_states}

Details

For more information run: l\_help("learn\_R\_layer")

Value

layer object handle, layer id

See Also

\texttt{l\_layer, l\_info\_states}

Description

Loon’s displays that are based on Cartesian coordinates (i.e. scatterplot, histogram and graph display) allow for layering visual information including polygons, text and rectangles.
Usage

```r
l_layer_polygon(
    widget,
    x, 
    y, 
    color = "gray80",
    linecolor = "black",
    linewidth = 1,
    label = "polygon",
    parent = "root",
    index = 0,
    ...
)
```

Arguments

- `widget`: widget path name as a string
- `x`: x coordinates
- `y`: y coordinates
- `color`: fill color, if empty string "", then the fill is transparent
- `linecolor`: outline color
- `linewidth`: linewidth of outline
- `label`: label used in the layers inspector
- `parent`: group layer
- `index`: of the newly added layer in its parent group
- `...`: additional state initialization arguments, see `l_info_states`

Details

For more information run: `l_help("learn_R_layer")`

Value

layer object handle, layer id

See Also

- `l_layer`, `l_info_states`

Examples

```r
if (interactive()){ 
    set.seed(500)
    x <- rnorm(30)
    y <- 4 + 3*x + rnorm(30)
    fit <- lm(y~x)
```
Layer polygons

Description

Loon’s displays that are based on Cartesian coordinates (i.e. scatterplot, histogram and graph display) allow for layering visual information including polygons, text and rectangles.

Usage

l_layer_polygons(
    widget,
l_layer_polygons

x,
y,
color = "gray80",
linecolor = "black",
linewidth = 1,
label = "polygons",
parent = "root",
index = 0,
group = NULL,
active = TRUE,
...
)

Arguments

widget widget path name as a string
x list with vectors with x coordinates
y list with vectors with y coordinates
color vector with fill colors, if empty string "", then the fill is transparant
linecolor vector with outline colors
linewidth vector with line widths
label label used in the layers inspector
parent group layer
index of the newly added layer in its parent group
group separate x vector or y vector into a list by group.
active a logical determining whether objects appear or not (default is TRUE for all).
... additional state initialization arguments, see l_info_states

Details

For more information run: l_help("learn_R_layer")

Value

layer object handle, layer id

See Also

l_layer, l_info_states

Examples

if(interactive()){
  p <- l_plot()
  l <- l_layer_polygons(}
p,
x = list(c(1,2,1.5), c(3,4,6,5,2), c(1,3,5,3)),
y = list(c(1,1.2), c(1,1.5,1,4,2), c(3,5,6,4)),
color = c('red', 'green', 'blue'),
linecolor = ""
)
l_scaleto_world(p)
l_info_states(l, "color")

# Set groups
p <- l_plot()
l_layer_polygons(p,
    x = c(1, 2, 1.5, 3, 4, 6, 5, 2, 1, 3, 5, 3),
    y = c(1, 1, 2, 1, 1.5, 1, 4, 2, 3, 5, 6, 4),
    group = c(rep(1,3), rep(2,5), rep(3, 4))
)
l_scaleto_world(p)
}

l_layer_printTree

Print the layer tree

Description
Prints the layer tree (i.e. the layer ids) to the prompt. Group layers are prefixed with a '+'. The 'root' layer is not listed.

Usage
l_layer_printTree(widget)

Arguments
widget    widget path as a string or as an object handle

Value
empty string

See Also
l_layer, l_layer_getChildren, l_layer_getParent
Examples

```r
if(interactive()){
  p <- l_plot()
l_layer_rectangle(p, x=0:1, y=0:1)
g <- l_layer_group(p)
l_layer_oval(p, x=0:1, y=0:1, parent=g)
l_layer_line(p, x=0:1, y=0:1, parent=g)
l_layer_printTree(p)
}
```

---

`l_layer_promote`  
*Moves the layer up to be a left sibling of its parent*

Description

Moves the layer down the layer tree (towards the root layer) if the parent layer is not the root layer.

Usage

```r
l_layer_promote(widget, layer)
```

Arguments

- `widget` widget path or layer object of class 'l_layer'
- `layer` layer id. If the widget argument is of class 'l_layer' then the layer argument is not used

Value

0 if success otherwise the function throws an error

Examples

```r
if(interactive()){
  p <- l_plot()
  g1 <- l_layer_group(p)
g2 <- l_layer_group(p, parent=g1)
l1 <- l_layer_oval(p, x=0:1, y=0:1, parent=g2)
  l_layer_printTree(p)
l_layer_promote(p, l1)
l_layer_printTree(p)
l_layer_promote(p, l1)
l_layer_printTree(p)
  }
```
`l_layer_raise`  
*Switch the layer place with its sibling to the left*

**Description**
Change the layers position within its parent layer group by decreasing the index of the layer by one if possible. This means that the raised layer will be rendered after (or on top) of its sibling layer to the left.

**Usage**

```r
l_layer_raise(widget, layer)
```

**Arguments**
- `widget`: widget path or layer object of class 'l_layer'
- `layer`: layer id. If the widget argument is of class 'l_layer' then the layer argument is not used

**Value**
0 if success otherwise the function throws an error

**See Also**
- `l_layer`, `l_layer_lower`, `l_layer_move`

**Examples**

```r
if(interactive()){
  p <- l_plot()
  l1 <- l_layer_rectangle(p, x=0:1, y=0:1)
  l2 <- l_layer_oval(p, x=0:1, y=0:1, color='thistle')
  l_aspect(p) <- 1
  l_layer_raise(p, l1)
}
```
Description

This function is very similar to the `rasterImage` function. It works with every loon plot which is based on the cartesian coordinate system.

Usage

```r
l_layer_rasterImage(
  widget,
  image,
  xleft,
  ybottom,
  xright,
  ytop,
  angle = 0,
  interpolate = FALSE,
  parent = "root",
  index = "end",
  ...
)
```

Arguments

- `widget` widget path as a string or as an object handle
- `image` a raster object, or an object that can be coerced to one by `as.raster`.
- `xleft` a vector (or scalar) of left x positions.
- `ybottom` a vector (or scalar) of bottom y positions.
- `xright` a vector (or scalar) of right x positions.
- `ytop` a vector (or scalar) of top y positions.
- `angle` angle of rotation (in degrees, anti-clockwise from positive x-axis, about the bottom-left corner).
- `interpolate` a logical vector (or scalar) indicating whether to apply linear interpolation to the image when drawing.
- `parent` a valid Tk parent widget path. When the parent widget is specified (i.e. not `NULL`) then the plot widget needs to be placed using some geometry manager like `tkpack` or `tkplace` in order to be displayed. See the examples below.
- `index` position among its siblings. valid values are 0, 1, 2, ..., 'end'
- `...` arguments forwarded to `l_layer_line`

Details

For more information run: `l_help("learn_R_layer.html#countourlines-heatimage-rasterimage")`
l_layer_rectangle

Layer a rectangle

Description

Loon’s displays that are based on Cartesian coordinates (i.e. scatterplot, histogram and graph display) allow for layering visual information including polygons, text and rectangles.

Usage

l_layer_rectangle(
  widget,
  x,
  y,
)
color = "gray80",
linecolor = "black",
linewidth = 1,
label = "rectangle",
parent = "root",
index = 0,
...
)

Arguments

widget widget path name as a string
x x coordinates
y y coordinates
color fill color, if empty string "," then the fill is transparent
linecolor outline color
linewidth linewidth of outline
label label used in the layers inspector
parent group layer
index of the newly added layer in its parent group
... additional state initialization arguments, see l_info_states

Details

For more information run: l_help("learn_R_layer")

Value

layer object handle, layer id

See Also

l_layer, l_info_states

Examples

if(interactive()){

p <- l_plot()

l <- l_layer_rectangle(p, x=c(2,3), y=c(1,10), color=quotesingle.Varsteelblue/quotesingle.Var)
l_scaleto_layer(l)

}
Description

Loon’s displays that are based on Cartesian coordinates (i.e. scatterplot, histogram and graph display) allow for layering visual information including polygons, text and rectangles.

Usage

```r
l_layer_rectangles(
  widget,
  x,
  y,
  color = "gray80",
  linecolor = "black",
  linewidth = 1,
  label = "rectangles",
  parent = "root",
  index = 0,
  group = NULL,
  active = TRUE,
  ...
)
```

Arguments

- `widget` : widget path name as a string
- `x` : list with vectors with x coordinates
- `y` : list with vectors with y coordinates
- `color` : vector with fill colors, if empty string """, then the fill is transparent
- `linecolor` : vector with outline colors
- `linewidth` : vector with line widths
- `label` : label used in the layers inspector
- `parent` : group layer
- `index` : of the newly added layer in its parent group
- `group` : separate x vector or y vector into a list by group.
- `active` : a logical determining whether objects appear or not (default is TRUE for all).
- `...` : additional state initialization arguments, see `l_info_states`

Details

For more information run: `l_help("learn_R_layer")`
Value

layer object handle, layer id

See Also

l_layer, l_info_states

Examples

```r
if(interactive()){
  p <- l_plot()
  l <- l_layer_rectangles(
    p,
    x = list(c(0,1), c(1,2), c(2,3), c(5,6)),
    y = list(c(0,1), c(1,2), c(0,1), c(3,4)),
    color = c('red', 'blue', 'green', 'orange'),
    linecolor = "black"
  )
  l_scaleto_world(p)
  l_info_states(l)

  # Set groups
  pp <- l_plot(x = c(0,1,1,2,2,3,5,6),
               y = c(0,1,1,2,0,1,3,4))
  # x and y are inherited from pp
  ll <- l_layer_rectangles(
    pp,
    group = rep(1:4, each = 2),
    color = c('red', 'blue', 'green', 'orange'),
    linecolor = "black"
  )
  l_scaleto_world(pp)
}
```

---

l_layer_relabel

Change layer label

Description

Layer labels are useful to identify layer in the layer inspector. The layer label can be initially set at layer creation with the label argument.

Usage

l_layer_relabel(widget, layer, label)
Arguments

- **widget**: widget path or layer object of class 'l_layer'
- **layer**: layer id. If the widget argument is of class 'l_layer' then the layer argument is not used
- **label**: new label of layer

Details

Note that the layer label is not a state of the layer itself, instead is information that is part of the layer collection (i.e. its parent widget).

Value

0 if success otherwise the function throws an error

See Also

l_layer, l_layer_getLabel

Examples

```r
if(interactive()){  
p <- l_plot()  
  l <- l_layer_rectangle(p, x=0:1, y=0:1, label="A rectangle")  
  l_layer_getLabel(p, l)  
  l_layer_relabel(p, l, label="A relabelled rectangle")  
  l_layer_getLabel(p, l)  
}
```

---

**Description**

Hidden or invisible layers are not rendered. This function unhides invisible layer so that they are rendered again.

**Usage**

```
l_layer_show(widget, layer)
```
**Arguments**

- **widget**: widget path or layer object of class 'l_layer'
- **layer**: layer id. If the widget argument is of class 'l_layer' then the layer argument is not used.

**Details**

Visible layers are rendered, invisible ones are not. If any ancestor of a layer is set to be invisible then the layer is not rendered either. The layer visibility flag can be checked with `l_layer_isVisible` and the actual visibility (i.e. are all the ancestors visible too) can be checked with `l_layer_layerVisibility`.

Note that layer visibility is not a state of the layer itself, instead is information that is part of the layer collection (i.e. its parent widget).

**Value**

0 if success otherwise the function throws an error

**See Also**

`l_layer, l_layer_hide, l_layer_isVisible, l_layer_layerVisibility, l_layer_groupVisibility`

**Examples**

```r
if(interactive()){
  p <- l_plot()
  l <- l_layer_rectangle(p, x=0:1, y=0:1, color="steelblue")
  l_layer_hide(p, l)
  l_layer_show(p, l)
}
```

**Description**

Display a smooth line layer
Usage

```r
l_layer_smooth(
  widget,
  x = NULL,
  y = NULL,
  method = "loess",
  group = "",
  formula = y ~ x,
  interval = c("none", "confidence", "prediction"),
  n = 80,
  span = 0.75,
  level = 0.95,
  methodArgs = list(),
  linecolor = "steelblue",
  linewidth = 2,
  linedash = "",
  confidenceIntervalArgs = list(linecolor = "gray80", linewidth = 4, linedash = ""),
  predictionIntervalArgs = list(linecolor = "gray50", linewidth = 3, linedash = 1),
  label = "smooth",
  parent = "root",
  index = 0,
  ...
)
```

Arguments

- **widget**: widget path name as a string
- **x**: The x coordinates of line. If it is not provided, x will be inherited from widget
- **y**: The y coordinates of line. If it is not provided, y will be inherited from widget
- **method**: Smoothing method (function) to use, accepts either a character vector, e.g. "lm", "glm", "loess" or a function, e.g. MASS::rlm or mgcv::gam, stats::lm, or stats::loess.
- **group**: Data can be grouped by n dimensional aesthetics attributes, e.g. "color", "size". In addition, any length n vector or data.frame is accommodated.
- **formula**: Formula to use in smoothing function, e.g. y ~ x, y ~ poly(x, 2), y ~ log(x)
- **interval**: type of interval, could be "none", "confidence" or "prediction" (not for glm)
- **n**: Number of points at which to evaluate smoother.
- **span**: Controls the amount of smoothing for the default loess smoother. Smaller numbers produce wigglier lines, larger numbers produce smoother lines.
- **level**: Level of confidence interval to use (0.95 by default).
- **methodArgs**: List of additional arguments passed on to the modelling function defined by method.
- **linecolor**: fitted line color.
- **linewidth**: fitted line width
- **linedash**: fitted line dash
confidenceIntervalArgs
  the line color, width and dash for confidence interval
predictionIntervalArgs
  the line color, width and dash for prediction interval
label
  label used in the layers inspector
parent
  group layer
index
  index of the newly added layer in its parent group
...
  additional state initialization arguments, see l_info_states

Examples

```r
if(interactive()) {
  # loess fit
  p <- l_plot(iris, color = iris$Species)
  l1 <- l_layer_smooth(p, interval = "confidence")
  l_layer_hide(l1)
  
  # the fits are grouped by points color
  l2 <- l_layer_smooth(p, group = "color",
                      method = "lm")

  # so far, all intervals are hidden
  ls <- l_layer_getChildren(l2)
  intervals <- l_layer_getChildren(l_create_handle(c(p,ls[3])))
  ci <- l_create_handle(c(p,intervals[3]))
  l_layer_show(ci)
  
  # show prediction interval
  pi <- l_create_handle(c(p,intervals[2]))
  l_layer_show(pi)
  
  # hide all
  l_layer_hide(l2)

  # Draw a fitted line based on a new data set
  shortSepalLength <- (iris$Sepal.Length < 5)
  l3 <- l_layer_smooth(p, 
                      x = iris$Sepal.Length[shortSepalLength],
                      y = iris$Sepal.Width[shortSepalLength],
                      method = "lm",
                      linecolor = "firebrick",
                      interval = "prediction")
  l_layer_hide(l3)

  if(require(mgcv)) {
    # a full tensor product smooth
    ## linecolor is the same with the points color
    l4 <- l_layer_smooth(p, 
                        method = "gam",
                        formula = y~te(x))
    l_layer_hide(l4)
  }
}
```
# facets
fp <- l_facet(p, by = iris$Species, inheritLayers = FALSE)
l5 <- l_layer_smooth(fp, method = "lm")

# generalized linear model
if(require("loon.data")) {
  data("SAheart")
  # logit regression
  chd <- as.numeric(SAheart$chd) - 1
  age <- SAheart$age
  p1 <- l_plot(age, chd, title = "logit regression")
  gl1 <- l_layer_smooth(p1, method = "glm",
                       methodArgs = list(family = binomial()),
                       interval = "conf")
  # log linear regression
  counts <- c(18,17,15,20,10,20,25,13,12)
  age <- c(40,35,53,46,20,33,48,25,23)
  p2 <- l_plot(age, counts, title = "log-linear regression")
  gl2 <- l_layer_smooth(p2, method = "glm",
                        methodArgs = list(family = poisson()),
                        interval = "conf")
}
}

---

### l_layer_text

**Layer a text**

**Description**

Loon’s displays that are based on Cartesian coordinates (i.e. scatterplot, histogram and graph display) allow for layering visual information including polygons, text and rectangles.

**layer a single character string**

**Usage**

```r
l_layer_text(
  widget,
  x,
  y,
  text,
  color = "gray60",
  size = 6,
  angle = 0,
  label = "text",
```
parent = "root",
index = 0,
...
)

Arguments

widget                 widget path name as a string
x                      coordinate
y                      coordinate
text                   character string
color                  color of text
size                   size of the font
angle                  rotation of text
label                  label used in the layers inspector
parent                 group layer
index                  of the newly added layer in its parent group
...                    additional state initialization arguments, see l_info_states

Details

As a side effect of Tcl’s text-based design, it is best to use l_layer_text if one would like to layer
a single character string (and not l_layer_texts with n=1).
For more information run: l_help("learn_R_layer")

Value

layer object handle, layer id

See Also

l_layer, l_info_states

Examples

if(interactive()){

  p <- l_plot()
  l <- l_layer_text(p, 0, 0, "Hello World")
}


**Description**

Loon’s displays that are based on Cartesian coordinates (i.e., scatterplot, histogram and graph display) allow for layering visual information including polygons, text and rectangles.

Layer a vector of character strings.

**Usage**

```r
l_layer_texts(
  widget,  
  x,    
  y,    
  text,  
  color = "gray60",  
  size = 6,  
  angle = 0,  
  anchor = "center",  
  justify = "center",  
  label = "texts",  
  parent = "root",  
  index = 0,  
  active = TRUE,  
  ...  
)
```

**Arguments**

- `widget`  
  widget path name as a string
- `x`  
  vector of x coordinates
- `y`  
  vector of y coordinates
- `text`  
  vector with text strings
- `color`  
  color of text
- `size`  
  font size
- `angle`  
  text rotation
- `anchor`  
  specifies how the information in a text is to be displayed in the widget. Must be one of the values c("n", "ne", "e", "se", "s", "sw", "w", "nw", "center"). For example, "nw" means display the information such that its top-left corner is at the top-left corner of the widget.
- `justify`  
  when there are multiple lines of text displayed in a widget, this option determines how the lines line up with each other. Must be one of c("left", "center", "right"). "Left" means that the lines’ left edges all line up, "center" means that
the lines’ centers are aligned, and "right" means that the lines’ right edges line up.

- **label**: label used in the layers inspector
- **parent**: group layer
- **index**: of the newly added layer in its parent group
- **active**: a logical determining whether objects appear or not (default is TRUE for all).
- ... additional state initialization arguments, see `l_info_states`

### Details

As a side effect of Tcl’s text-based design, it is best to use `l_layer_text` if one would like to layer a single character string (and not `l_layer_texts` with `n=1`).

For more information run: `l_help("learn_R_layer")`

### Value

layer object handle, layer id

### See Also

`l_layer`, `l_info_states`

### Examples

```r
if(interactive()){
  p <- l_plot()
  l <- l_layer_texts(p, x=1:3, y=3:1, text=c("This is", "a", "test"), size=20)
  l_scaleto_world(p)
}
```

---

```r
l_loonWidgets
```

**Get all active top level loon plots.**

---

### Description

Loon’s plots are constructed in TCL and identified with a path string appearing in the window containing the plot.

If the plots were not saved on a variable, this function will look for all loon plots displayed and return their values in a list whose elements may then be assigned to `R` variables.

### Usage

```r
l_loonWidgets(pathTypes, inspector = FALSE)
```
Arguments

pathTypes an optional argument identifying the collection of path types that are to be returned (if displayed).

inspector whether to return the loon inspector widget or not

This must be a subset of the union of `l_basePaths()` and `l_compoundPaths()`. If it is missing, all `l_basePaths()` and `l_compoundPaths()` will be returned.

Value

list whose elements are named by, and contain the values of, the loon plot widgets. The list can be nested when loon plots (like `l_pairs`) are compound in that they consist of more than one base loon plot.

See Also

`l_basePaths` `l_compoundPaths` `l_getFromPath`

Examples

```r
if(interactive()){
  l_plot(iris)
l_hist(iris)
l_hist(mtcars)
l_pairs(iris)
  # The following will not be loonWidgets (neither is the inspector)
t <- tktoplevel()
tkpack(l1 <- tklabel(tt, text = "Heave"), l2<- tklabel(tt, text = "Ho"))
  # This will return loon widgets corresponding to plots
loonPlots <- l_loonWidgets()
names(loonPlots)
firstPlot <- loonPlots[[1]]
firstPlot["color"] <- "red"
histograms <- l_loonWidgets("hist")
lapply(histograms,
       FUN = function(hist) {
         hist["binwidth"] <- hist["binwidth"]/2
         l_scaleto_world(hist)
       })
}
```

---

Create a loon inspector
l_make_glyphs

Description

Loon’s primitive glyph types are limited in terms of compound shapes. With this function you can create each point glyph as a png and re-import it as a tk img object to be used as point glyphs in loon. See the examples.

Usage

l_make_glyphs(data, draw_fun, width = 50, height = 50, ...)

Arguments

data

state arguments, see l_info_states.

Details

For more information run: l_help("learn_R_display_inspectors")

Value

a loon widget

Examples

if(interactive()){
  i <- l_loon_inspector()
}

l_make_glyphs

Make arbitrary glyphs with R graphic devices

Description

The loon inspector is a singleton widget that provides an overview to view and modify the active plot.

Usage

l_loon_inspector(parent = NULL, ...)

Arguments

parent

a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like tkpack or tkplace in order to be displayed. See the examples below.

Details

For more information run: l_help("learn_R_display_inspectors")

Value

a loon widget

Examples

if(interactive()){
  i <- l_loon_inspector()
}

Arguments

- **data**: list where each element contains a data object used for the `draw_fun`
- **draw_fun**: function that draws a glyph using R base graphics or the grid (including ggplot2 and lattice) engine
- **width**: width of each glyph in pixel
- **height**: height of each glyph in pixel
- **...**: additional arguments passed on to the `png` function Note: type is not allowed in this list.

Value

- vector with tk img object references

Examples

```r
if(interactive()){

  ## Not run:
  if (requireNamespace("maps", quietly = TRUE)) {
    data(minority)
    p <- l_plot(minority$long, minority$lat)
    canada <- maps::map("world", "Canada", fill=TRUE, plot=FALSE)
    l_map <- l_layer(p, canada, asSingleLayer=TRUE)
    l_scaleto_world(p)

    img <- l_make_glyphs(lapply(1:nrow(minority), function(i)minority[i,]), function(m) {
      par(mar=c(1,1,1,1)*.5)
      mat <- as.matrix(m[1,1:10]/max(m[1:10]))
      barplot(height = mat,
              beside = FALSE,
              ylim = c(0,1),
              axes= FALSE,
              axisnames=FALSE)
    }), width=120, height=120)
  l_imageviewer(img)

  g <- l_glyph_add_image(p, img, "barplot")
  p["glyph"] <- g

  }

  ## with grid
  if (requireNamespace("grid", quietly = TRUE)) {

    li <- l_make_glyphs(runif(6), function(x) {
      if(any(x>1 | x<0))
        stop("out of range")
      grid::pushViewport(grid::plotViewport(grid::unit(c(1,1,1)*0, "points")))

```
grid::grid.rect(gp=grid::gpar(fill=NA))
grid::grid.rect(0, 0, height = grid::unit(x, "npc"), just = c("left", "bottom"),
               gp=grid::gpar(col=NA, fill="steelblue"))
}

l_imageviewer(li)

p <- l_plot(1:6)
g <- l_glyph_add_image(p, li, "bars")
p["glyph"] <- g
}

## End(Not run)

## A more familiar example?
## The periodic table

data("elements", package = "loon.data")

# A draw function for each element
draw_element_box <- function(symbol,
                              name, number,
                              mass_number,
                              mass, col) {
  if (missing(col)) col <- "white"
  oldPar <- par(bg = col, mar = rep(1, 4))
  plot(NA, xlim = c(0,1), ylim = c(0, 1), axes=FALSE, ann = FALSE)
  text(0.5, 0.6, labels = symbol, cex = 18)
  text(0.15, 1, labels = number, cex = 6, adj= c(0.5,1))
  text(0.5, 0.25, labels = name, cex = 6)
  text(0.5, 0.11, labels = mass_number, cex = 3)
  text(0.5, 0.01, labels = mass, cex = 3)
  box()
  par(oldPar)
}

# Get the categories
colIDs <- paste(elements$Category, elements$Subcategory)
# Get a loon palette function
colFn <- color_loon()
# Get colors identified with categories
tableCols <- colFn(colIDs)

# A function to an element box image for each element.
make_element_boxes <- function(elements, cols, width = 500, height = 500) {
  if (missing(cols)) cols <- rep("white", nrow(elements))
  listOfElements <- lapply(1:nrow(elements),
                           FUN = function(i) {
                             list(vals = elements[i],
                             width = width, height = height,
                             col = cols[i],
                             symbol = elements[i, "symbol"],
                             category = elements[i, "Category"],
                             subcategory = elements[i, "Subcategory"]
                           })
  return(listOfElements)
}
l_make_glyphs

197
col = cols[i])

})

# glyphs created here
l_make_glyphs(listOfElements,
draw_fun = function(element){
x <- element$vals
col <- element$col
draw_element_box(symbol = x$Symbol,
name = x$Name,
number = x$Number,
mass_number = x$Mass_number,
mass = x$Mass,
col = col)
},
width = width,
height = height)
}
# Construct the glyphs
boxGlyphs <- make_element_boxes(elements, cols = tableCols)
# Get a couple of plots
periodicTable <- l_plot(x = elements$x, y = elements$y,
xlabel = "", ylabel = "",
title = "Periodic Table of the Elements",
linkingGroup = "elements",
color = tableCols)
# Add the images as possible glyphs
bg <- l_glyph_add_image(periodicTable,
images = boxGlyphs,
label = "Symbol boxes")
# Set this to be the glyph
periodicTable['glyph'] <- bg
#
# Get a second plot that shows the
#
# First some itemlabels
elementLabels <- with(elements,
paste("
",
"
",
"
",
)
)
periodicPlot

periodicity

Number, Symbol, "\n",
Name, "\n",
Mass

<- l_plot(x = elements$Mass, y = elements$Density,
xlabel = "Mass", ylabel = "Density",
itemLabel = elementLabels,
showItemLabels = TRUE,
linkingGroup = "elements",
color = tableCols)


# Add the images as possible glyphs to this plot as well
bg2 <- l_glyph_add_image(periodicPlot, 
    images = boxGlyphs, 
    label = "Symbol boxes")

# Could set this to be the glyph
periodicPlot[['glyph']] <- bg2

}
and b are the same or close numbers) and then by taking the a smallest values in the y direction and arrange them by their x order in the first row, then repeat for the remaining points.

Also note the the loon inspector also has buttons for these temporary points/nodes movements.

See Also

l_move_valign, l_move_halign, l_move_vdist, l_move_hdist, l_move_grid, l_move_jitter, l_move_reset

1_move_halign

Horizontally Align Points or Nodes

Description

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

Usage

1_move_halign(widget, which = "selected")

Arguments

widget plot or graph widget handle or widget path name
which either one of 'selected', 'active', 'all', or a boolean vector with a value for each point.

Details

Moving the points temporarily saves the new point coordinates to the states xTemp and yTemp. The dimension of xTemp and yTemp is either 0 or n. If xTemp or yTemp are not of length 0 then they are required to be of length n, and the scatterplot will display those coordinates instead of the coordinates in x or y.

Note that the points can also be temporally relocated using mouse and keyboard gestures. That is, to move a single point or node press the CTRL key while dragging a the point. To move the selected points press down the CTRL and Shift keys while dragging one of the selected points.

When distributing points horizontally or vertically, their order remains the same. When distributing points horizontally or vertically, their order remains the same. For example, when you distribute the point both horizontally and vertically, then the resulting scatterplot will be a plot of the y ranks versus the x ranks. The correlation on that plot will be Spearman’s rho. When arranging points on a grid, some of the spatial ordering is preserved by first determining a grid size (i.e. a x b where a and b are the same or close numbers) and then by taking the a smallest values in the y direction and arrange them by their x order in the first row, then repeat for the remaining points.

Also note the the loon inspector also has buttons for these temporary points/nodes movements.
_l_move_hdist_

**See Also**

`l_move_valign, l_move_halign, l_move_vdist, l_move_hdist, l_move_grid, l_move_jitter, l_move_reset`

---

### l_move_hdist

*Horizontally Distribute Points or Nodes*

**Description**

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

**Usage**

```r
l_move_hdist(widget, which = "selected")
```

**Arguments**

- `widget`: plot or graph widget handle or widget path name
- `which`: either one of 'selected', 'active', 'all', or a boolean vector with a value for each point.

**Details**

Moving the points temporarily saves the new point coordinates to the states `xTemp` and `yTemp`. The dimension of `xTemp` and `yTemp` is either 0 or n. If `xTemp` or `yTemp` are not of length 0 then they are required to be of length n, and the scatterplot will display those coordinates instead of the coordinates in `x` or `y`.

Note that the points can also be temporally relocated using mouse and keyboard gestures. That is, to move a single point or node press the CTRL key while dragging a the point. To move the selected points press down the CTRL and Shift keys while dragging one of the selected points.

When distributing points horizontally or vertically, their order remains the same. When distributing points horizontally or vertically, their order remains the same. For example, when you distribute the point both horizontally and vertically, then the resulting scatterplot will be a plot of the y ranks versus the x ranks. The correlation on that plot will be Spearman’s rho. When arranging points on a grid, some of the spatial ordering is preserved by first determining a grid size (i.e. a x b where a and b are the same or close numbers) and then by taking the a smallest values in the y direction and arrange them by their x order in the first row, then repeat for the remaining points.

Also note the loon inspector also has buttons for these temporary points/nodes movements.

**See Also**

`l_move_valign, l_move_halign, l_move_vdist, l_move_hdist, l_move_grid, l_move_jitter, l_move_reset`
**Description**

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

**Usage**

```r
l_move_jitter(widget, which = "selected", factor = 1, amount = "")
```

**Arguments**

- `widget`: plot or graph widget handle or widget path name
- `which`: either one of 'selected', 'active', 'all', or a boolean vector with a value for each point.
- `factor`: numeric.
- `amount`: numeric; if positive, used as `amount` (see below), otherwise, if `= 0` the default is `factor * z/50`.
  
  Default (NULL): `factor * d/5` where `d` is about the smallest difference between x values.

**Details**

Moving the points temporarily saves the new point coordinates to the states `xTemp` and `yTemp`. The dimension of `xTemp` and `yTemp` is either 0 or `n`. If `xTemp` or `yTemp` are not of length 0 then they are required to be of length `n`, and the scatterplot will display those coordinates instead of the coordinates in `x` or `y`.

Note that the points can also be temporally relocated using mouse and keyboard gestures. That is, to move a single point or node press the CTRL key while dragging a the point. To move the selected points press down the CTRL and Shift keys while dragging one of the selected points.

When distributing points horizontally or vertically, their order remains the same. When distributing points horizontally or vertically, their order remains the same. For example, when you distribute the point both horizontally and vertically, then the resulting scatterplot will be a plot of the y ranks versus the x ranks. The correlation on that plot will be Spearman’s rho. When arranging points on a grid, some of the spatial ordering is preserved by first determining a grid size (i.e. \( a \times b \) where \( a \) and \( b \) are the same or close numbers) and then by taking the a smallest values in the y direction and arrange them by their x order in the first row, then repeat for the remaining points.

Also note the the loon inspector also has buttons for these temporary points/nodes movements.

**See Also**

- `l_move_valign`
- `l_move_halign`
- `l_move_vdist`
- `l_move_hdist`
- `l_move_grid`
- `l_move_jitter`
- `l_move_reset`
Description

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

Usage

```r
l_move_reset(widget, which = "selected")
```

Arguments

- **widget**: plot or graph widget handle or widget path name
- **which**: either one of 'selected', 'active', 'all', or a boolean vector with a value for each point.

Details

Moving the points temporarily saves the new point coordinates to the states `xTemp` and `yTemp`. The dimension of `xTemp` and `yTemp` is either 0 or `n`. If `xTemp` or `yTemp` are not of length 0 then they are required to be of length `n`, and the scatterplot will display those coordinates instead of the coordinates in `x` or `y`.

Note that the points can also be temporally relocated using mouse and keyboard gestures. That is, to move a single point or node press the CTRL key while dragging a the point. To move the selected points press down the CTRL and Shift keys while dragging one of the selected points.

When distributing points horizontally or vertically, their order remains the same. When distributing points horizontally or vertically, their order remains the same. For example, when you distribute the point both horizontally and vertically, then the resulting scatterplot will be a plot of the `y` ranks versus the `x` ranks. The correlation on that plot will be Spearman's rho. When arranging points on a grid, some of the spatial ordering is preserved by first determining a grid size (i.e. `a x b` where `a` and `b` are the same or close numbers) and then by taking the a smallest values in the `y` direction and arrange them by their `x` order in the first row, then repeat for the remaining points.

Also note that the loon inspector also has buttons for these temporary points/nodes movements.

See Also

`l_move_valign, l_move_halign, l_move_vdist, l_move_hdist, l_move_grid, l_move_jitter, l_move_reset`
Vertically Align Points or Nodes

Description

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

Usage

```r
l_move_valign(widget, which = "selected")
```

Arguments

- `widget` plot or graph widget handle or widget path name
- `which` either one of 'selected', 'active', 'all', or a boolean vector with a value for each point.

Details

Moving the points temporarily saves the new point coordinates to the states `xTemp` and `yTemp`. The dimension of `xTemp` and `yTemp` is either 0 or `n`. If `xTemp` or `yTemp` are not of length 0 then they are required to be of length `n`, and the scatterplot will display those coordinates instead of the coordinates in `x` or `y`.

Note that the points can also be temporally relocated using mouse and keyboard gestures. That is, to move a single point or node press the CTRL key while dragging a the point. To move the selected points press down the CTRL and Shift keys while dragging one of the selected points.

When distributing points horizontally or vertically, their order remains the same. When distributing points horizontally or vertically, their order remains the same. For example, when you distribute the point both horizontally and vertically, then the resulting scatterplot will be a plot of the `y` ranks versus the `x` ranks. The correlation on that plot will be Spearman's rho. When arranging points on a grid, some of the spatial ordering is preserved by first determining a grid size (i.e. `a x b` where `a` and `b` are the same or close numbers) and then by taking the `a` smallest values in the `y` direction and arrange them by their `x` order in the first row, then repeat for the remaining points.

Also note the the loon inspector also has buttons for these temporary points/nodes movements.

See Also

```
l_move_valign, l_move_halign, l_move_vdist, l_move_hdist, l_move_grid, l_move_jitter, l_move_reset
```
Vertically Distribute Points or Nodes

Description

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

Usage

```r
l_move_vdist(widget, which = "selected")
```

Arguments

- `widget` plot or graph widget handle or widget path name
- `which` either one of 'selected', 'active', 'all', or a boolean vector with a value for each point.

Details

Moving the points temporarily saves the new point coordinates to the states `xTemp` and `yTemp`. The dimension of `xTemp` and `yTemp` is either 0 or `n`. If `xTemp` or `yTemp` are not of length 0 then they are required to be of length `n`, and the scatterplot will display those coordinates instead of the coordinates in `x` or `y`.

Note that the points can also be temporally relocated using mouse and keyboard gestures. That is, to move a single point or node press the CTRL key while dragging a the point. To move the selected points press down the CTRL and Shift keys while dragging one of the selected points.

When distributing points horizontally or vertically, their order remains the same. When distributing points horizontally or vertically, their order remains the same. For example, when you distribute the point both horizontally and vertically, then the resulting scatterplot will be a plot of the y ranks versus the x ranks. The correlation on that plot will be Spearman’s rho. When arranging points on a grid, some of the spatial ordering is preserved by first determining a grid size (i.e. a x b where a and b are the same or close numbers) and then by taking the a smallest values in the y direction and arrange them by their x order in the first row, then repeat for the remaining points.

Also note the loon inspector also has buttons for these temporary points/nodes movements.

See Also

`l_move_valign`, `l_move_halign`, `l_move_vdist`, `l_move_hdist`, `l_move_grid`, `l_move_jitter`, `l_move_reset`
Explore a dataset with the canonical 2d navigation graph setting

Description

Creates a navigation graph, a graphswitch, a navigator and a geodesic2d context added, and a scatterplot.

Usage

l_navgraph(data, separator = " ", graph = NULL, ...)

Arguments

data a data.frame with numeric variables only
separator string the separates variable names in 2d graph nodes
graph optional, graph or loongraph object with navigation graph. If the graph argument
is not used then a 3d and 4d transition graph and a complete transition graph is added.
... arguments passed on to modify the scatterplot plot states

Details

For more information run: l_help("learn_R_display_graph.html#l_navgraph")

Value

named list with graph handle, plot handle, graphswitch handle, navigator handle, and context handle.

Examples

if(interactive()){
  ng <- l_navgraph(oliveAcids, color=olive$Area)
  ng2 <- l_navgraph(oliveAcids, separator='-', color=olive$Area)
}
Add a Navigator to a Graph

Description

To turn a graph into a navigation graph you need to add one or more navigators. Navigator have their own set of states that can be queried and modified.

Usage

```r
l_navigator_add(
    widget,
    from = "",
    to = "",
    proportion = 0,
    color = "orange",
    ...
)
```

Arguments

- `widget`: graph widget
- `from`: The position of the navigator on the graph is defined by the states `from`, `to` and `proportion`. The states `from` and `to` hold vectors of node names of the graph. The `proportion` state is a number between and including 0 and 1 and defines how far the navigator is between the last element of `from` and the first element of `to`. The `to` state can also be an empty string `'` if there is no further node to go to. Hence, the concatenation of `from` and `to` define a path on the graph.
- `to`: see description above for `from`
- `proportion`: see description above for `from`
- `color`: see description above for `from`
- `...`: named arguments passed on to modify navigator states

Details

For more information run: `l_help("learn_R_display_graph.html#navigators")`

Value

- navigator handle with navigator id

See Also

- `l_navigator_delete`, `l_navigator_ids`, `l_navigator_walk_path`, `l_navigator_walk_forward`, `l_navigator_walk_backward`, `l_navigator_relabel`, `l_navigator_getLabel`
Delete a Navigator

Description

Removes a navigator from a graph widget

Usage

l_navigator_delete(widget, id)

Arguments

widget        graph widget
id            navigator handle or navigator id

See Also

l_navigator_add

Query the Label of a Navigator

Description

Returns the label of a navigator

Usage

l_navigator_getLabel(widget, id)

Arguments

widget        graph widget handle
id            navigator id

See Also

l_navigator_add
**l_navigator_getPath**  
*Get the sequence of nodes of a navigator's current path*

**Description**
Determines and returns the current path of the navigator.

**Usage**

```plaintext
l_navigator_getPath(navigator)
```

**Arguments**
- **navigator**  
navigator handle

**Value**
a vector of node names for the current path of the navigator

---

**l_navigator_ids**  
*List Navigators*

**Description**
Lists all navigators that belong to a graph

**Usage**

```plaintext
l_navigator_ids(widget)
```

**Arguments**
- **widget**  
graph widget

**See Also**

```plaintext
l_navigator_add
```
\_\_l\_navigator\_relabel

Modify the Label of a Navigator

**Description**

Change the navigator label

**Usage**

\_\_l\_navigator\_relabel(widget, id, label)

**Arguments**

- **widget**: graph widget handle
- **id**: navigator id
- **label**: new label of navigator

**See Also**

- \_\_l\_navigator\_add

\_\_l\_navigator\_walk\_backward

Have the Navigator Walk Backward on the Current Path

**Description**

Animate a navigator by having it walk on a path on the graph

**Usage**

\_\_l\_navigator\_walk\_backward(navigator, to = \\\\\\\"")

**Arguments**

- **navigator**: navigator handle
- **to**: node name that is part of the active path backward where the navigator should stop.

**Details**

Note that navigators have the states animationPause and animationProportionIncrement to control the animation speed. Further, you can stop the animation when clicking somewhere on the graph display or by using the mouse scroll wheel.
Have the Navigator Walk Forward on the Current Path

Description
Animate a navigator by having it walk on a path on the graph.

Usage
\[
\text{l\_navigator\_walk\_forward(navigator, to = "")}
\]

Arguments
- **navigator**: navigator handle
- **to**: node name that is part of the active path forward where the navigator should stop.

Details
Note that navigators have the states animationPause and animationProportionIncrement to control the animation speed. Further, you can stop the animation when clicking somewhere on the graph display or by using the mouse scroll wheel.

See Also
- \text{l\_navigator\_add}

Have the Navigator Walk a Path on the Graph

Description
Animate a navigator by having it walk on a path on the graph.

Usage
\[
\text{l\_navigator\_walk\_path(navigator, path)}
\]

Arguments
- **navigator**: navigator handle
- **path**: vector with node names of the host graph that form a valid path on that graph.
\textit{l_nDimStateNames} \hspace{1cm} \textit{N dimensional state names access}

\textbf{Description}

Get all n dimensional state names

\textbf{Usage}

\begin{verbatim}
l_nDimStateNames(loon_plot)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{loon_plot} \hspace{1cm} A loon widget or the class name of a loon plot
\end{itemize}

\textbf{Examples}

\begin{verbatim}
if(interactive()){
  p <- l_plot()
  l_nDimStateNames(p)
  l_nDimStateNames("l_plot")
}
\end{verbatim}

\textit{l_nestedTclList2Rlist} \hspace{1cm} \textit{Convert a Nested Tcl List to an R List}

\textbf{Description}

Helper function to work with \textbf{R} and \textbf{Tcl}

\textbf{Usage}

\begin{verbatim}
l_nestedTclList2Rlist(tclobj, transform = function(x) {
  as.numeric(x)
})
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{tclobj} \hspace{1cm} a tcl object as returned by \texttt{tcl} or \texttt{.Tcl}.
  \item \texttt{transform} \hspace{1cm} a function to transform the string output to another data type
\end{itemize}
Value

a nested R list

See Also

`l_Rlist2nestedTclList`

Examples

```r
tclobj <- .Tcl('set a {{1 2 3} {2 3 4 4} {3 5 3 3}}')
l_nestedTclList2Rlist(tclobj)
```

---

### Description

Generic function to create a navigation graph environment where user can filter graph nodes by selecting 2d spaces based on 2d measures displayed in a scatterplot matrix.

### Usage

```r
l_ng_plots(measures, ...)
```

### Arguments

- `measures` object with measures are stored
- `...` argument passed on to methods

### Details

For more information run: `l_help("learn_R_display_graph.html#l_ng_plots")`

### See Also

`l_ng_plots.default, l_ng_plots.measures, l_ng_plots.scagnostics, measures1d, measures2d, scagnostics2d, l_ng_ranges`
Description

Measures object is a matrix or data.frame with measures (columns) for variable pairs (rows) and rownames of the two variates separated by separator.

Usage

```r
## Default S3 method:
lng_plots(measures, data, separator = ":", ...)
```

Arguments

- `measures`: matrix or data.frame with measures (columns) for variable pairs (rows) and rownames of the two variates separated by separator.
- `data`: data frame for scatterplot.
- `separator`: a string that separates the variable pair string into the individual variables.
- `...`: arguments passed on to configure the scatterplot.

Details

For more information run: `l_help("learn_R_display_graph.html#lng_plots")`

Value

named list with plots-, graph-, plot-, navigator-, and context handle. The list also contains the environment of the the function call in `env`.

See Also

- `lng_plots`, `lng_plots.measures`, `lng_plots.scagnostics`, `measures1d`, `measures2d`, `scagnostics2d`, `lng_ranges`

Examples

```r
if(interactive()){

## Not run:
n <- 100
data <- data.frame(
    A = rnorm(n), B = rnorm(n), C = rnorm(n),
    D = rnorm(n), E = rnorm(n)
)
m2d <- data.frame(
```
cov = with(dat, c(cov(A,B), cov(A,C), cov(B,D), cov(D,E), cov(A,E))),
measure_1 = c(1, 3, 2, 1, 4),
row.names = c('A:B', 'A:C', 'B:D', 'D:E', 'A:E')
)

# or m2d <- as.matrix(m2d)

nav <- l_ng_plots(measures=m2d, data=dat)

# only one measure
m <- m2d[,1]
names(m) <- row.names(m2d)
nav <- l_ng_plots(measures=m, data=dat)

m2d[c(1,2),1]

# one d measures
m1d <- data.frame(
  mean = sapply(dat, mean),
  median = sapply(dat, median),
  sd = sapply(dat, sd),
  q1 = sapply(dat, function(x)quantile(x, probs=0.25)),
  q3 = sapply(dat, function(x)quantile(x, probs=0.75)),
  row.names = names(dat)
)

nav <- l_ng_plots(m1d, dat)

## more involved
q1 <- function(x)as.vector(quantile(x, probs=0.25))

# be careful that the vector names are correct
nav <- l_ng_plots(sapply(oliveAcids, q1), oliveAcids)

## End(Not run)

\hline
\hspace{0cm}
\hline
\multicolumn{2}{c}{l_ng_plots.measures} & 2d Navigation Graph Setup with dynamic node filtering using a scatterplot matrix \\
\hline
\multicolumn{3}{c}{Description} \\
\multicolumn{3}{c}{Measures object is of class measures. When using measure objects then the measures can be dynamically re-calculated for a subset of the data.
Usage
## S3 method for class 'measures'
1_ng_plots(measures, ...)

Arguments
measures object of class measures, see measures1d, measures2d.
...
arguments passed on to configure the scatterplot

Details
Note that we provide the scagnostics2d function to create a measures object for the scagnostics
measures.
For more information run: l_help("learn_R_display_graph.html#l_ng_plots")

Value
named list with plots-, graph-, plot-, navigator-, and context handle. The list also contains the
environment of the the function call in env.

See Also
measures1d, measures2d, scagnostics2d, 1_ng_plots, 1_ng_ranges

Examples
if(interactive()){

## Not run:
# 2d measures
scags <- scagnostics2d(oliveAcids, separator='**')
scags()
ng <- 1_ng_plots(scags, color=olive$Area)

# 1d measures
scale01 <- function(x)(x-min(x))/diff(range(x))
m1d <- measures1d(sapply(iris[-5], scale01),
  mean=mean, median=median, sd=sd,
  q1=function(x)as.vector(quantile(x, probs=0.25)),
  q3=function(x)as.vector(quantile(x, probs=0.75)))
m1d()

nav <- 1_ng_plots(m1d, color=iris$Species)

# with only one measure
nav <- 1_ng_plots(measures1d(oliveAcids, sd))

# with two measures
nav <- 1_ng_plots(measures1d(oliveAcids, sd=sd, mean=mean))
## End(Not run)

### Usage

```r
## S3 method for class 'scagnostics'
lng_plots(measures, data, separator = ":", ...)  
```

### Arguments

- **measures**: objects from the `scagnostics` function from the scagnostics R package
- **data**: data frame for scatterplot
- **separator**: a string that separates the variable pair string into the individual variables
- **...**: arguments passed on to configure the scatterplot

### Value

- named list with plots-, graph-, plot-, navigator-, and context handle. The list also contains the environment of the the function call in `env`.

### See Also

- `lng_plots`, `lng_plots.default`, `lng_plots.measures`, `measures1d`, `measures2d`, `scagnostics2d`, `lng_ranges`

### Examples

```r
if(interactive()){
  ## Not run:
  library(scagnostics)
  scags <- scagnostics::scagnostics(oliveAcids)
  lng_plots(scags, oliveAcids, color=olive$Area)
```
## l_ng_ranges

2d navigation graph setup with dynamic node filtering using a slider

### Description

Generic function to create a navigation graph environment where user can filter graph nodes using as slider to select 2d spaces based on 2d measures.

### Usage

```r
l_ng_ranges(measures, ...)```

### Arguments

- `measures`: object with measures are stored
- `...`: argument passed on to methods

### Details

For more information run: `l_help("learn_R_display_graph.html#l_ng_ranges")`

### See Also

- `l_ng_ranges.default`
- `l_ng_ranges.measures`
- `l_ng_ranges.scagnostics`
- `measures1d`
- `measures2d`
- `scagnostics2d`

---

## l_ng_ranges.default

Select 2d spaces with variable associated measures using a slider

### Description

Measures object is a matrix or data.frame with measures (columns) for variable pairs (rows) and rownames of the two variates separated by separator

### Usage

```r
## Default S3 method:
l_ng_ranges(measures, data, separator = ":", ...)```

---
Arguments

- **measures**: matrix or data.frame with measures (columns) for variable pairs (rows) and row-names of the two variates separated by separator
- **data**: data frame for scatterplot
- **separator**: a string that separates the variable pair string into the individual variables
- **...**: arguments passed on to configure the scatterplot

Details

For more information run: `l Help("learn_R_display_graph.html#l_ng_ranges")`

Value

named list with plots-, graph-, plot-, navigator-, and context handle. The list also contains the environment of the the function call in env.

See Also

`l_ng_ranges, l_ng_ranges.measures, l_ng_ranges.scagnostics, measures1d, measures2d, scagnostics2d, l_ng_ranges`

Examples

```r
if (interactive()){  
  # Simple example with generated data  
  n <- 100  
  dat <- data.frame(  
    A = rnorm(n), B = rnorm(n), C = rnorm(n),  
    D = rnorm(n), E = rnorm(n)  
  )  
  m2d <- data.frame(  
    cor = with(dat, c(cor(A,B), cor(A,C), cor(B,D), cor(D,E), cor(A,E))),  
    my_measure = c(1, 3, 2, 1, 4),  
    row.names = c('A:B', 'A:C', 'B:D', 'D:E', 'A:E')  
  )  
  # or m2d <- as.matrix(m2d)  
  nav <- l_ng_ranges(measures=m2d, data=dat)  
  # With 1d measures  
  m1d <- data.frame(  
    mean = sapply(dat, mean),  
    median = sapply(dat, median),  
    sd = sapply(dat, sd),  
    q1 = sapply(dat, function(x)quantile(x, probs=0.25)),  
    q3 = sapply(dat, function(x)quantile(x, probs=0.75)),  
    row.names = names(dat)  
  )
```
Description

Measures object is of class measures. When using measure objects then the measures can be dynamically re-calculated for a subset of the data.

Usage

```r
## S3 method for class 'measures'
1_ng_ranges(measures, ...)
```

Arguments

- `measures` object of class measures, see `measures1d`, `measures2d`.
- `...` arguments passed on to configure the scatterplot

Details

Note that we provide the `scagnostics2d` function to create a measures object for the scagnostics measures.

For more information run: `?l_help("learn_R_display_graph.html#1_ng_ranges")`

Value

named list with plots-, graph-, plot-, navigator-, and context handle. The list also contains the environment of the the function call in `env`.

See Also

- `measures1d`, `measures2d`, `scagnostics2d`, `1_ng_ranges`, `1_ng_plots`

Examples

```r
if (interactive()){
    # 2d measures
    # s <- scagnostics2d(oliveAcids)
    # nav <- 1ng_ranges(s, color=olive$Area)
    # 1d measures
    scale01 <- function(x)((x-min(x))/diff(range(x)))
}
m1d <- measures1d(sapply(iris[-5], scale01),
    mean=mean, median=median, sd=sd,
    q1=function(x)as.vector(quantile(x, probs=0.25)),
    q3=function(x)as.vector(quantile(x, probs=0.75)))

m1d()

nav <- l_ng_ranges(m1d, color=iris$Species)

---

l_ng_ranges.scagnostics

2d Navigation Graph Setup with dynamic node filtering based on scagnostic measures and using a slider

Description

This method is useful when working with objects from the `scagnostics` function from the scagnostics R package. In order to dynamically re-calculate the scagnostic measures for a subset of the data use the `scagnostics2d` measures creature function.

Usage

```r
## S3 method for class 'scagnostics'
l_ng_ranges(scagnostics, data, separator = "::", ...)
```

Arguments

- `measures`: objects from the `scagnostics` function from the scagnostics R package
- `data`: data frame for scatterplot
- `separator`: a string that separates the variable pair string into the individual variables
- `...`: arguments passed on to configure the scatterplot

Details

For more information run: `?l_help("learn_R_display_graph.html#l_ng_ranges")`

Value

named list with plots-, graph-, plot-, navigator-, and context handle. The list also contains the environment of the the function call in `env`.

See Also

`l_ng_ranges, l_ng_ranges.default, l_ng_ranges.measures, measures1d, measures2d, scagnostics2d, l_ng_ranges`
### l_pairs

**An interactive scatterplot matrix**

**Description**

Function creates a scatterplot matrix using loon’s scatterplot widgets

**Usage**

```r
l_pairs(
data,
connectedScales = c("cross", "none"),
linkingGroup,
linkingKey,
showItemLabels = TRUE,
itemLabel,
showHistograms = FALSE,
histLocation = c("edge", "diag"),
histHeightProp = 1,
histArgs = list(),
showSerialAxes = FALSE,
serialAxesArgs = list(),
parent = NULL,
plotWidth = 100,
plotHeight = 100,
span = 10L,
showProgressBar = TRUE,
...
)
```

**Arguments**

- **data**
  - a data.frame with numerical data to create the scatterplot matrix

- **connectedScales**
  - Determines how the scales of the panels are to be connected.
    - "cross": only the scales in the same row and the same column are connected;
    - "none": neither "x" nor "y" scales are connected in any panels.
linkingGroup  string giving the linkingGroup for all plots. If missing, a default linkingGroup will be determined from deparsing the data.

linkingKey  a vector of strings to provide a linking identity for each row of the data data.frame. If missing, a default linkingKey will be 0:(nrows(data)-1).

showItemLabels  TRUE, logical indicating whether its itemLabel pops up over a point when the mouse hovers over it.

itemLabel  a vector of strings to be used as pop up information when the mouse hovers over a point. If missing, the default itemLabel will be the row.names(data).

showHistograms  logical (default FALSE) to show histograms of each variable or not

histLocation  one "edge" or "diag", when showHistograms = TRUE

histHeightProp  a positive number giving the height of the histograms as a proportion of the height of the scatterplots

histArgs  additional arguments to modify the ‘l_hist’ states

showSerialAxes  logical (default FALSE) indication of whether to show a serial axes plot in the bottom left of the pairs plot (or not)

serialAxesArgs  additional arguments to modify the ‘l_serialaxes’ states

parent  a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like tkpack or tkplace in order to be displayed. See the examples below.

plotWidth  default plot width (in pixel)

plotHeight  default plot height (in pixel)

span  How many column/row occupies for each widget

showProgressBar  Logical; show progress bar or not

...  named arguments to modify the ‘l_plot’ states of the scatterplots

Value

an ‘l_pairs’ object (an ‘l_compound’ object), being a list with named elements, each representing a separate interactive plot. The names of the plots should be self explanatory and a list of all plots can be accessed from the ‘l_pairs’ object via ‘l_getPlots()’. All plots are linked by default (name taken from data set if not provided). Panning and zooming are constrained to work together within the scatterplot matrix (and histograms).

See Also

l_plot and l_getPlots

Examples

if(interactive()){  
  p <- l_pairs(iris[,-5], color=iris$Species, linkingGroup = "iris")
  p <- l_pairs(iris[,-5], color=iris$Species, linkingGroup = "iris",

showHistograms = TRUE, showSerialAxes = TRUE)

# plot names
names(p)

# Each plot must be accessed to make changes not managed through
# linking.
# E.g. to change the glyph on all scatterplots to open circles
for (plot in l_getPlots(p)) {
  if (is(plot, "l_plot")) {
    plot["glyph"] <- "ocircle"
  }
}

---

**l_plot**

Create an interactive loon plot widget

---

**Description**

l_plot is a generic function for creating an interactive visualization environments for R objects.

**Usage**

l_plot(x, y, ...)

## Default S3 method:
l_plot(
x,
y = NULL,
by = NULL,
on,
layout = c("grid", "wrap", "separate"),
connectedScales = c("cross", "row", "column", "both", "x", "y", "none"),
color = l_getOption("color"),
glyph = l_getOption("glyph"),
size = l_getOption("size"),
active = TRUE,
selected = FALSE,
xlabel,
ylabel,
title,
showLabels = TRUE,
showScales = FALSE,
showGuides = TRUE,
guidelines = l_getOption("guidelines"),
guidesBackground = l_getOption("guidesBackground"),
foreground = l_getOption("foreground"),
background = l_getOption("background"),
224

```r

## S3 method for class 'decomposed.ts'

l_plot(
  x,
  y = NULL,
  xlabel = NULL,
  ylabel = NULL,
  title = NULL,
  tk_title = NULL,
  color = l_getOption("color"),
  size = l_getOption("size"),
  lineloc = l_getOption("color"),
  linewidth = l_getOption("linewidth"),
  linkingGroup,
  showScales = TRUE,
  showGuides = TRUE,
  showLabels = TRUE,
...
)

## S3 method for class 'density'

l_plot(
  x,
  y = NULL,
  xlabel = NULL,
  ylabel = NULL,
  title = NULL,
  linewidth = l_getOption("linewidth"),
  linecolor = l_getOption("color"),
...
)

## S3 method for class 'map'

l_plot(x, y = NULL, ...)

## S3 method for class 'stl'

l_plot(
  x,
  y = NULL,
  xlabel = NULL,
  ylabel = NULL,
  title = NULL,
  tk_title = NULL,
  color = l_getOption("color"),
  size = l_getOption("size"),
  ...)
```

```
l_plot

```r
linecolor = l_getOption("color"),
linewidth = l_getOption("linewidth"),
linkingGroup,
showScales = TRUE,
showGuides = TRUE,
showLabels = TRUE,
...
```

Arguments

- **x**: the coordinates of points in the `l_plot`. Alternatively, a single plotting structure (see the function `xy.coords` for details), `formula`, or any R object (e.g. `density`, `stl`, etc) is accommodated.
- **y**: the y coordinates of points in the `l_plot`, optional if x is an appropriate structure.
- **...**: named arguments to modify plot states. See `l_info_states` of any instantiated `l_plot` for examples of names and values.
- **by**: loon plot can be separated by some variables into multiple panels. This argument can take a `formula`, n dimensional state names (see `l_nDimStateNames`) an n-dimensional vector and `data.frame` or a list of same lengths n as input.
- **on**: if the x or by is a formula, an optional data frame containing the variables in the x or by. If the variables are not found in data, they are taken from environment, typically the environment from which the function is called.

- **layout**: layout facets as 'grid', 'wrap' or 'separate'
- **connectedScales**: Determines how the scales of the facets are to be connected depending on which layout is used. For each value of layout, the scales are connected as follows:
  - layout = "wrap": Across all facets, when connectedScales is
    - "x", then only the "x" scales are connected
    - "y", then only the "y" scales are connected
    - "both", both "x" and "y" scales are connected
    - "none", neither "x" nor "y" scales are connected. For any other value, only the "y" scale is connected.
  - layout = "grid": Across all facets, when connectedScales is
    - "cross", then only the scales in the same row and the same column are connected
    - "row", then both "x" and "y" scales of facets in the same row are connected
    - "column", then both "x" and "y" scales of facets in the same column are connected
    - "x", then all of the "x" scales are connected (regardless of column)
    - "y", then all of the "y" scales are connected (regardless of row)
    - "both", both "x" and "y" scales are connected in all facets
    - "none", neither "x" nor "y" scales are connected in any facets.
color: colours of points; colours are repeated until matching the number points. Default is found using \texttt{l_getOption("color").}

glyph: the visual representation of the point. Argument values can be any of

- the string names of primitive glyphs:
  - circles: "circle", "ccircle", "ocircle";
  - squares or boxes: "square", "csquare", "osquare";
  - triangles: "triangle", "ctriangle", "otriangle";
  - diamonds: "diamond", "cdiamond", or "odiamond".

  Note that prefixes "c" and "o" may be thought of as closed and open, respectively. The set of values are returned by \texttt{l_primitiveGlyphs()}. 

- the string names of constructed glyphs:
  - text as glyphs: see \texttt{l_glyph_add_text()}
  - point ranges: see \texttt{l_glyph_add_pointrange()}
  - polygons: see \texttt{l_glyph_add_polygon()}
  - parallel coordinates: see \texttt{l_glyph_add_serialaxes()}
  - star or radial axes: see \texttt{l_glyph_add_serialaxes()}
  - or any plot created using R: see \texttt{l_make_glyphs()}

  Note that glyphs are constructed and given a stringname to be used in the inspector.

size: size of the symbol (roughly in terms of area). Default is found using \texttt{l_getOption("size").}

active: a logical determining whether points appear or not (default is \texttt{TRUE} for all points). If a logical vector is given of length equal to the number of points, then it identifies which points appear (\texttt{TRUE}) and which do not (\texttt{FALSE}).

selected: a logical determining whether points appear selected at first (default is \texttt{FALSE} for all points). If a logical vector is given of length equal to the number of points, then it identifies which points are (\texttt{TRUE}) and which are not (\texttt{FALSE}).

xlabel: Label for the horizontal (x) axis. If missing, one will be inferred from \texttt{x} if possible.

ylabel: Label for the vertical (y) axis. If missing, one will be inferred from \texttt{y} (or \texttt{x}) if possible.

title: Title for the plot, default is an empty string.

showLabels: logical to determine whether axes label (and title) should be presented.

showScales: logical to determine whether numerical scales should be presented on both axes.

showGuides: logical to determine whether to present background guidelines to help determine locations.

guidelines: colour of the guidelines shown when \texttt{showGuides = TRUE}. Default is found using \texttt{l_getOption("guidelines").}

guidesBackground: colour of the background to the guidelines shown when \texttt{showGuides = TRUE}. Default is found using \texttt{l_getOption("guidesBackground").}

foreground: foreground colour used by all other drawing. Default is found using \texttt{l_getOption("foreground").}

background: background colour used for the plot. Default is found using \texttt{l_getOption("background").}
parent  a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like tkpack or tkplace in order to be displayed. See the examples below.

tk_title  provides an alternative window name to Tk's wm title. If NULL, stl will be used.

tlinecolor  line colour of all time series. Default given by l_getOption("color").

linewidth  line width of all time series (incl. original and decomposed components. Default given by l_getOption("linewidth").

linkingGroup  string giving the linkingGroup for all plots. If missing, a default linkingGroup will be determined from deparsing the input x.

Details

Like plot in R, l_plot is the generic plotting function for objects in loon. The default method l_plot.default produces the interactive scatterplot in loon. This is the workhorse of 'loon' and is often a key part of many other displays (e.g. l_pairs and l_navigraph).

For example, the methods include l_plot.default (the basic interactive scatterplot), l_plot.density (layers output of density in an empty scatterplot), l_plot.map (layers a map in an empty scatterplot), and l_plot.stl (a compound display of the output of stl).

A complete list is had from methods(l_plot).

To get started with loon it is recommended to follow the introductory loon vignette vignette(topic = "introduction",package = "loon") and to explore loon's website accessible via l_help().

The general direct manipulation and interaction gestures are outlined in the following figures.

Zooming and Panning

Selecting Points/Objects

Moving Points on the Scatterplot Display

The scatterplot displays a number of direct interactions with the mouse and keyboard, these include: zooming towards the mouse cursor using the mouse wheel, panning by right-click dragging and various selection methods using the left mouse button such as sweeping, brushing and individual point selection. See the documentation for l_plot for more details about the interaction gestures.

Some arguments to modify layouts can be passed through, e.g. "separate", "ncol", "nrow", etc. Check l_facet to see how these arguments work.

Value

- The input is a stl or a decomposed.ts object, a structure of class "l_ts" containing four loon plots each representing a part of the decomposition by name: "original", "trend", "seasonal", and "remainder"
- The input is a vector, formula, data.frame, ...
  - by = NULL: a loon widget will be returned
  - by is not NULL: an l_facet object (a list) will be returned and each element is a loon widget displaying a subset of interest.
See Also

Turn interactive loon plot static \texttt{loonGrob}, \texttt{grid.loon}, \texttt{plot.loon}.

Density layer \texttt{l_layer.density}

Map layer \texttt{l_layer, l_layer.map, map}

Other loon interactive states: \texttt{l_hist()}, \texttt{l_info_states()}, \texttt{l_serialaxes()}, \texttt{l_state_names()}, \texttt{names.loon()}

Examples

\begin{verbatim}
if(interactive()) {
   ########################## l_plot.default ##########################
   # default use as scatterplot
   p1 <- with(iris, l_plot(Sepal.Length, Sepal.Width, color=Species,
                            title = "First plot"))
   # The names of the info states that can be
   # accessed or set. They can also be given values as
   # arguments to \texttt{l_plot.default()}
   names(p1)
   p1["size"] <- 10

   p2 <- with(iris, l_plot(Petal.Length ~ Petal.Width,
                            linkingGroup="iris_data",
                            title = "Second plot",
                            showGuides = FALSE))
   p2["showScales"] <- TRUE

   # link first plot with the second plot requires
   # \texttt{l_configure} to coordinate the synchroniztion
   l_configure(p1, linkingGroup = "iris_data", sync = "push")

   p1['selected'] <- iris$Species == "versicolor"
   p2["glyph"][p1['selected']] <- "cdiamond"

   gridExtra::grid.arrange(loonGrob(p1), loonGrob(p2), nrow = 1)

   # Layout facets
   ### facet wrap
   p3 <- with(mtcars, l_plot(wt, mpg, by = cyl, layout = "wrap"))
   # it is equivalent to
   # p3 <- \texttt{l_plot}(mpg~wt, by = ~cyl, layout = "wrap", on = mtcars)

   ### facet grid
   p4 <- l_plot(x = 1:6, y = 1:6,
                 by = size ~ color,
                 size = c(rep(50, 2), rep(25, 2), rep(50, 2)),
                 color = c(rep("red", 3), rep("green", 3)))

   # Use with other tk widgets
   tt <- tktoplevel()
\end{verbatim}
tktitle(tt) <- "Loon plots with custom layout"

p1 <- l_plot(parent=tt, x=c(1,2,3), y=c(3,2,1))
p2 <- l_plot(parent=tt, x=c(4,3,1), y=c(6,8,4))

tkgrid(p1, row=0, column=0, sticky="nesw")
tkgrid(p2, row=0, column=1, sticky="nesw")

tkgrid.columnconfigure(tt, 0, weight=1)
tkgrid.columnconfigure(tt, 1, weight=1)

tkgrid.rowconfigure(tt, 0, weight=1)

############################ l_plot.decomposed.ts ############################
decompose <- decompose(co2)
p <- l_plot(decompose, title = "Atmospheric carbon dioxide over Mauna Loa")

# names of plots in the display
names(p)

# names of states associated with the seasonality plot
names(p$seasonal)

# which can be set
p$seasonal['color'] <- "steelblue"

############################ l_plot.stl ############################
co2_stl <- stl(co2, "per")
p <- l_plot(co2_stl, title = "Atmospheric carbon dioxide over Mauna Loa")

# names of plots in the display
names(p)

# names of states associated with the seasonality plot
names(p$seasonal)

# which can be set
p$seasonal['color'] <- "steelblue"

############################ l_plot.density ############################
# plot a density estimate
set.seed(314159)
ds <- density(rnorm(1000))
p <- l_plot(ds, title = "density estimate",
xlabel = "x", ylabel = "density",
showScales = TRUE)

############################ l_plot.map ############################
if (requireNamespace("maps", quietly = TRUE)) {
  p <- l_plot(maps::map('world', fill=TRUE, plot=FALSE))
}
}

l_plot3D

Create an interactive loon 3d plot widget

Description

l_plot3D is a generic function for creating interactive visualization environments for R objects.
Usage

l_plot3D(x, y, z, ...)

## Default S3 method:
l_plot3D(
x,
y = NULL,
z = NULL,
axisScaleFactor = 1,
by = NULL,
on,
layout = c("grid", "wrap", "separate"),
connectedScales = c("cross", "row", "column", "both", "x", "y", "none"),
color = l_getOption("color"),
glyph = l_getOption("glyph"),
size = l_getOption("size"),
active = TRUE,
selected = FALSE,
xlabel,
ylabel,
zlabel,
title,
showLabels = TRUE,
showScales = FALSE,
showGuides = TRUE,
guidelines = l_getOption("guidelines"),
guidesBackground = l_getOption("guidesBackground"),
foreground = l_getOption("foreground"),
background = l_getOption("background"),
parent = NULL,
...)

Arguments

x the x, y and z arguments provide the x, y and z coordinates for the plot. Any reasonable way of defining the coordinates is acceptable. See the function xyz.coords for details.

If supplied separately, they must be of the same length.

y the y coordinates of points in the plot, optional if x is an appropriate structure.

z the z coordinates of points in the plot, optional if x is an appropriate structure.

... named arguments to modify plot states.

axisScaleFactor the amount to scale the axes at the centre of the rotation. Default is 1. All numerical values are acceptable (0 removes the axes, < 0 inverts the direction of all axes.)
loon plot can be separated by some variables into multiple panels. This argument can take a formula, n dimensional state names (see \texttt{l_nDimStateNames}) an n-dimensional vector and \texttt{data.frame} or a list of same lengths n as input.

if the x or by is a formula, an optional data frame containing the variables in the x or by. If the variables are not found in data, they are taken from environment, typically the environment from which the function is called.

Determines how the scales of the facets are to be connected depending on which layout is used. For each value of layout, the scales are connected as follows:

- \texttt{layout = "wrap"}: Across all facets, when \texttt{connectedScales} is
  - "x", then only the "x" scales are connected
  - "y", then only the "y" scales are connected
  - "both", both "x" and "y" scales are connected
  - "none", neither "x" nor "y" scales are connected. For any other value, only the "y" scale is connected.

- \texttt{layout = "grid"}: Across all facets, when \texttt{connectedScales} is
  - "cross", then only the scales in the same row and the same column are connected
  - "row", then both "x" and "y" scales of facets in the same row are connected
  - "column", then both "x" and "y" scales of facets in the same column are connected
  - "x", then all of the "x" scales are connected (regardless of column)
  - "y", then all of the "y" scales are connected (regardless of row)
  - "both", both "x" and "y" scales are connected in all facets
  - "none", neither "x" nor "y" scales are connected in any facets.

colours of points; colours are repeated until matching the number points. Default is found using \texttt{l_getOption("color").

de the visual representation of the point. Argument values can be any of

- the string names of primitive glyphs:
  - circles: "circle", "ccircle", "ocircle";
  - squares or boxes: "square", "csquare", "osquare";
  - triangles: "triangle", "ctriangle", "otriangle";
  - diamonds: "diamond", "cdiamond", or "odiamond".
  Note that prefixes "c" and "o" may be thought of as closed and open, respectively. The set of values are returned by \texttt{l_primitiveGlyphs()).

- the string names of constructed glyphs:
  - text as glyphs: see \texttt{l_glyph_add_text()}
  - point ranges: see \texttt{l_glyph_add_pointrange()}
  - polygons: see \texttt{l_glyph_add_polygon()}
  - parallel coordinates: see \texttt{l_glyph_add_serialaxes()}
  - star or radial axes: see \texttt{l_glyph_add_serialaxes()}

\texttt{l_plot3D}
– or any plot created using R: see `l_make_glyphs()`

Note that glyphs are constructed and given a stringname to be used in the inspector.

- size: size of the symbol (roughly in terms of area). Default is found using `l_getOption("size")`.
- active: a logical determining whether points appear or not (default is TRUE for all points). If a logical vector is given of length equal to the number of points, then it identifies which points appear (TRUE) and which do not (FALSE).
- selected: a logical determining whether points appear selected at first (default is FALSE for all points). If a logical vector is given of length equal to the number of points, then it identifies which points are (TRUE) and which are not (FALSE).
- xlabel: Label for the horizontal (x) axis. If missing, one will be inferred from x if possible.
- ylabel: Label for the vertical (y) axis. If missing, one will be inferred from y (or x) if possible.
- zlabel: Label for the third (perpendicular to the screen) (z) axis. If missing, one will be inferred from z (or x) if possible.
- title: Title for the plot, default is an empty string.
- showLabels: logical to determine whether axes label (and title) should be presented.
- showScales: logical to determine whether numerical scales should be presented on both axes.
- showGuides: logical to determine whether to present background guidelines to help determine locations.
- guidelines: colour of the guidelines shown when showGuides = TRUE. Default is found using `l_getOption("guidelines")`.
- guidesBackground: colour of the background to the guidelines shown when showGuides = TRUE. Default is found using `l_getOption("guidesBackground")`.
- foreground: foreground colour used by all other drawing. Default is found using `l_getOption("foreground")`.
- background: background colour used for the plot. Default is found using `l_getOption("background")`.
- parent: a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like `tkpack` or `tkplace` in order to be displayed. See the examples below.

Details

To get started with loon it is recommended to read loons website which can be accessed via the `l_help()` function call.

The general direct manipulation and interaction gestures are outlined in the following figures.

Rotating

Press ‘R’ to toggle rotation mode. When rotation mode is active, either use the below mouse gestures or arrow keys to rotate the plot.

The centre of the rotation can be changed by panning the plot. To reset the rotation, use the tripod icon in the plot inspector.

Zooming and Panning
Selecting Points/Objects

Moving Points on the Scatterplot Display

NOTE: Although it is possible to programmatically add layers to an l_plot3D, these will not appear as part of the 3D plot’s display. There is no provision at present to incorporate rotation of 3D geometric objects other than point glyphs.

The scatterplot displays a number of direct interactions with the mouse and keyboard, these include: rotating, zooming towards the mouse cursor using the mouse wheel, panning by right-click dragging and various selection methods using the left mouse button such as sweeping, brushing and individual point selection. See the documentation for l_plot3D for more details about the interaction gestures.

Value

if the argument by is not set, a loon widget will be returned; else an l_facet object (a list) will be returned and each element is a loon widget displaying a subset of interest.

See Also

Turn interactive loon plot static loonGrob, grid.loon, plot.loon.

Other three-dimensional plotting functions: l_scale3D()

Examples

if(interactive()){

  with(quakes,
  l_plot3D(long, lat, depth, linkingGroup = "quakes")
  )

  with(l_scale3D(quakes),
  l_plot3D(long, lat, depth, linkingGroup = "quakes")
  )

  scaled_quakes <- l_scale3D(quakes)
  with(scaled_quakes,
  l_plot3D(long, lat, depth, linkingGroup = "quakes")
  )
  with(scaled_quakes,
  l_plot3D(mag, stations, depth, linkingGroup = "quakes")
  )
  with(scaled_quakes,
  l_plot3D(mag, stations, depth, linkingGroup = "quakes")
  )
  # Or together:
  with(scaled_quakes,{
    l_plot3D(long, lat, depth, linkingGroup = "quakes")
    l_plot3D(mag, stations, depth, linkingGroup = "quakes")
  })
}

##
if(interactive()){
  # default use as scatterplot
  p1 <- with(quakes,
             l_plot3D(long, lat, depth)
          )

  p2 <- with(quakes,
             l_plot3D(mag, stations, depth)
          )

  # link the two plots p1 and p2
  l_configure(p1, linkingGroup = "quakes", sync = "push")
  l_configure(p2, linkingGroup = "quakes", sync = "push")
}

---

### l_plot_arguments Arguments common to l_plot functions

#### Description

Like `plot` in R, `l_plot` is the generic plotting function for objects in `loon`.

This is the workhorse of `loon` and is often a key part of many other displays (e.g. `l_pairs` and `l_navgraph`).

Because plots in `loon` are interactive, the functions which create them have many arguments in common. The value of these arguments become ‘infostates’ once the plot is instantiated. These can be accessed and set using the usual R square bracket operators ‘[]’ and ‘[]<-’ using the statename as a string. The state names can be found from an instantiated `loon` plot either via `l_info_states()` or, more in keeping with the R programming style, via `names()` (uses the method `names.loon()` for `loon` objects).

The same state names can be passed as arguments with values to a `l_plot()` call. As arguments many of the common ones are described below.

#### Arguments

- **x**
  - the x and y arguments provide the x and y coordinates for the plot. Any reasonable way of defining the coordinates is acceptable. See the function `xy.coords` for details. If supplied separately, they must be of the same length.

- **y**
  - argument description is as for the x argument above.

- **by**
  - `loon` plots can be separated by some variables into multiple panels. This argument can take a `formula`, n dimensional state names (see `l_nDimStateNames`) an n-dimensional vector and `data.frame` or a list of same lengths n as input.

- **on**
  - if the x or y is a formula, an optional data frame containing the variables in the x or by. If the variables are not found in data, they are taken from environment, typically the environment from which the function is called.
### l_plot_arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>layout</td>
<td>layout facets as 'grid', 'wrap' or 'separate'</td>
</tr>
<tr>
<td>connectedScales</td>
<td>Determines how the scales of the facets are to be connected depending on which layout is used.</td>
</tr>
<tr>
<td>linkingGroup</td>
<td>a string naming a group of plots to be linked. All plots with the same linkingGroup will have the same values of their linked states (see l_getLinkedStates() and l_setLinkedStates()).</td>
</tr>
<tr>
<td>linkingKey</td>
<td>an n-dimensional character vector of unique entries. The entries identify which points match other points in other plots. Default is c(&quot;0&quot;,&quot;1&quot;,...,&quot;n-1&quot;) (for numerical n).</td>
</tr>
<tr>
<td>itemLabel</td>
<td>an n-dimensional character vector whose values are displayed in a pop-up box over any point whenever the mouse hovers over that point (provided showItemLabels = TRUE). This action is commonly known as providing a &quot;tool tip&quot;. Note that all objects drawn in any layer of a plot (e.g. maps) will have an itemLabel.</td>
</tr>
<tr>
<td>showItemLabels</td>
<td>a logical (default FALSE) which indicates whether the &quot;tool tip&quot; itemLabel is to be displayed whenever the mouse hovers over it.</td>
</tr>
<tr>
<td>color</td>
<td>colours of points (default &quot;grey60&quot;); colours are repeated until matching the number points,</td>
</tr>
<tr>
<td>glyph</td>
<td>the visual representation of the point. Argument values can be any of the string names of primitive glyphs &quot;circle&quot;, &quot;ccircle&quot;, &quot;ocircle&quot;, squares or boxes &quot;square&quot;, &quot;csquare&quot;, &quot;osquare&quot;, triangles &quot;triangle&quot;, &quot;ctriangle&quot;, &quot;otriangle&quot;, diamonds &quot;diamond&quot;, &quot;cdiamond&quot;, or &quot;odiamond&quot;. Note that prefixes &quot;c&quot; and &quot;o&quot; may be thought of as closed and open, respectively. The set of values are returned by l_primitiveGlyphs().</td>
</tr>
<tr>
<td>the string names of constructed glyphs text as glyphs</td>
<td>see l_glyph_add_text()</td>
</tr>
<tr>
<td>point ranges</td>
<td>see l_glyph_add_pointrange()</td>
</tr>
<tr>
<td>polygons</td>
<td>see l_glyph_add_polygon()</td>
</tr>
<tr>
<td>parallel coordinates</td>
<td>see l_glyph_add_serialaxes()</td>
</tr>
<tr>
<td>star or radial axes</td>
<td>see l_glyph_add_serialaxes()</td>
</tr>
<tr>
<td>or any plot created using R</td>
<td>see l_make_glyphs()</td>
</tr>
<tr>
<td>size</td>
<td>size of the symbol (roughly in terms of area)</td>
</tr>
<tr>
<td>active</td>
<td>a logical determining whether points appear or not (default is TRUE for all points). If a logical vector is given of length equal to the number of points, then it identifies which points appear (TRUE) and which do not (FALSE).</td>
</tr>
<tr>
<td>selected</td>
<td>a logical determining whether points appear selected at first (default is FALSE for all points). If a logical vector is given of length equal to the number of points, then it identifies which points are (TRUE) and which are not (FALSE).</td>
</tr>
<tr>
<td>xlabel</td>
<td>Label for the horizontal (x) axis. If missing, one will be inferred from x if possible.</td>
</tr>
</tbody>
</table>
ylabel Label for the vertical (y) axis. If missing, one will be inferred from y (or x) if possible.
title Title for the plot, default is an empty string.
minimumMargins the minimal size (in pixels) of the margins around the plot (bottom, left, top, right)
showLabels logical to determine whether axes label (and title) should be presented.
showScales logical to determine whether numerical scales should be presented on both axes.
showGuides logical to determine whether to present background guidelines to help determine locations.
guidelines colour of the guidelines shown when showGuides = TRUE (default "white").
guidesBackground colour of the background to the guidelines shown when showGuides = TRUE (default "grey92").
foreground foreground colour used by all other drawing (default "black").
background background colour used for the plot (default "white")
parent a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like tkpack or tkplace in order to be displayed. See the examples below.
... named arguments to modify plot states.

Details

The interactive displays permit a number of direct interactions using the mouse and keyboard, these include: zooming towards the mouse cursor using the mouse wheel, panning by right-click dragging and various selection methods using the left mouse button such as sweeping, brushing and individual point selection. See the documentation for \textit{l_plot} for more details about the interaction gestures.

See Also

the demos \texttt{demo(l_glyph_sizes,package = "loon")}, \texttt{demo(l_glyphs,package = "loon")}, and \texttt{demo(l_make_glyphs,package = "loon")}.

Examples

```r
## Not run:
# default use as scatterplot
p1 <- with(iris, l_plot(x = Sepal.Length,
  y = Sepal.Width,
  color=Species,
  title = "Sepal sizes"))
# The names of the info states that can be
# accessed or set. They can also be given values as
# arguments to l_plot.default()
names(p1)
versicolor <- (iris$Species == "versicolor")
```
Create a Scatterplot Inspector

Description

Inspectors provide graphical user interfaces to oversee and modify plot states.

Usage

l_plot_inspector(parent = NULL, ...)

Arguments

parent    parent widget path
...
     state arguments

Value

widget handle

See Also

l_create_handle

Examples

if(interactive()){
  i <- l_plot_inspector()
}
l_plot_inspector_analysis

Create a Scatterplot Analysis Inspector

Description

Inspectors provide graphical user interfaces to oversee and modify plot states

Usage

l_plot_inspector_analysis(parent = NULL, ...)

Arguments

parent    parent widget path
...
... state arguments

Value

widget handle

See Also

l_create_handle

Examples

if(interactive()){

  i <- l_plot_inspector_analysis()
}

l_plot_ts

Draw a decomposed time series loon plot

Description

l_plot_ts is a generic function for creating a decomposed time series plot. It is mainly used in
l_plot.decomposed.ts and l_plot.stl
Usage

l_plot_ts(
  x,
  color = l_getOption("color"),
  size = l_getOption("size"),
  linecolor = l_getOption("color"),
  linewidth = l_getOption("linewidth"),
  xlabel = NULL,
  ylabel = NULL,
  title = NULL,
  tk_title = NULL,
  linkingGroup,
  showScales = TRUE,
  showGuides = TRUE,
  showLabels = TRUE,
  call = match.call(),
  ...
)

Arguments

x Either an stl object or a decomposed.ts object.

color points colour of all time series. Default is given by l_getOption("color").

size points size of all time series. Default is given by l_getOption("size").

linecolor line colour of all time series. Default is given by l_getOption("color").

linewidth line width of all time series (incl. original and decomposed components. Default
is given by l_getOption("linewidth").

xlabel the labels for the x axes. This is a length four character vector one for each: of
the original time series, the trend component, the seasonality component, and
the remainder. If of length 1, the label is repeated; if NULL, xlabel is "time".

ylabel the labels for the vertical axes. This is a length four character vector one for
each: of the original time series, the trend component, the seasonality compo-
nent, and the remainder. If NULL, the default, ylabel will be c("data","trend","seasonality","remainder"
if a character vector of length 1, the label is repeated four times.

title an overall title for the entire display. If NULL (the default), the title will be
"Seasonal Trend Analysis".

tk_title provides an alternative window name to Tk’s wm title. If NULL, stl will be
used.

linkingGroup name of linking group. If missing, one is created from the data name and class
associated with stlOrDecomposedTS.

showScales a logical as to whether to display the scales on all axes, default is TRUE.

showGuides a logical as to whether to display background guide lines on all plots, default is
TRUE.

showLabels a logical as to whether to display axes labels on all plots, default is TRUE.
call a call in which all of the specified arguments are specified by their full names

... keyword value pairs passed off to \_plot() which constructs each loon scatter-plot component.

Value

A structure of class "l_ts" containing four loon plots each representing a part of the decomposition by name: "original", "trend", "seasonal", and "remainder".

See Also

\_plot.stl, \_plot.decomposed.ts, stl, or decompose.

---

**l_predict**  
*Model Prediction*

Description

It is entirely for the purpose of plotting fits and intervals on a scatterplot (or histogram). It is a generic function to predict models for loon smooth layer (a wrap of the function predict). However, the output is unified.

Usage

\_predict(model, \ldots)

## Default S3 method:
\_predict(model, \ldots)

## S3 method for class 'lm'
\_predict(
  model,
  newdata = NULL,
  interval = c("none", "confidence", "prediction"),
  level = 0.95,
  \ldots
)

## S3 method for class 'nls'
\_predict(
  model,
  newdata = NULL,
  interval = c("none", "confidence", "prediction"),
  level = 0.95,
  \ldots
)
l_predict

## S3 method for class 'glm'
l_predict(
  model,
  newdata = NULL,
  interval = c("none", "confidence"),
  level = 0.95,
  ...
)

## S3 method for class 'loess'
l_predict(
  model,
  newdata = NULL,
  interval = c("none", "confidence", "prediction"),
  level = 0.95,
  ...
)

### Arguments

- **model**: a model object for which prediction is desired
- **newdata**: optionally, a data frame in which to look for variables with which to predict. If omitted, the fitted linear predictors are used.
- **interval**: type of interval, could be "none", "confidence" or "prediction" (not for glm)
- **level**: confidence level

### Value

A data frame is returned with `x` (if `newdata` is given) and `y`. If the `interval` is not `none`, two more columns, `lower` (lower interval) and `upper` (upper interval) will be returned.

### Examples

```r
y <- rnorm(10)
x <- rnorm(10)
model1 <- lm(y ~ x)
# formal output
pre <- l_predict(model1, newdata = data.frame(x = sort(x)),
                 interval = "conf")
head(pre)
if(interactive()) {
p <- with(cars, l_plot(speed, dist))
# Example taken from
# https://stackoverflow.com/questions/23852505/how-to-get-confidence-interval-for-smooth-spline
# l_predict.smooth.spline <- function(model, interval = c("confidence", "none"),
```
level = 0.95, ...) {
  # confidence interval of `smooth.spline`
  interval <- match.arg(interval)

  res <- (model$yin - model$y)/(1 - model$lev) # jackknife residuals
  sigma <- sqrt(var(res)) # estimate sd
  std <- stats::qnorm(level / 2 + 0.5)
  upper <- model$y + std * sigma * sqrt(model$lev) # upper 95% conf. band
  lower <- model$y - std * sigma * sqrt(model$lev) # lower 95% conf. band

  data.frame(y = model$yin, lower = lower, upper = upper)
}
l <- l_layer_smooth(p, method = "smooth.spline", interval = "confidence")

---

l_primitiveGlyphs

The primitive glyphs available to a scatterplot or graph display

Description

Returns a vector of the available primitive glyphs.

Usage

l_primitiveGlyphs()

Details

The scatterplot and graph displays both have the n-dimensional state `glyph` that assigns each data point or graph node a glyph (i.e. a visual representation).

Looper distinguishes between primitive and non-primitive glyphs: the primitive glyphs are always available for use whereas the non-primitive glyphs need to be first specified and added to a plot before they can be used.

The primitive glyphs are:

'circle', 'ocircle', 'ccircle'
'square', 'osquare', 'csquare'
'triangle', 'otriangle', 'ctriangle'
'diamond', 'odiamond', 'cdiamond'

Note that the letter 'o' stands for outline only, and the letter 'c' stands for contrast and adds an outline with the 'foreground' color (black by default).

For more information run: l_help("learn_R_display_plot.html#glyphs")
**l_redraw**

Force a Content Redraw of a Plot

Description

Force redraw the plot to make sure that all the visual elements are placed correctly.

Usage

```
l_redraw(widget)
```

Arguments

- `widget` widget path as a string or as an object handle

Details

Note that this function is intended for debugging. If you find that the display does not display the data according to its plot states then please contact loon’s package maintainer.

Examples

```
if(interactive()){
  p <- l_plot(iris)
  l_redraw(p)
}
```
**l_resize**  
*Resize Plot Widget*

**Description**
Resizes the toplevel widget to a specific size.

**Usage**
```r
l_resize(widget, width, height)
```

**Arguments**
- `widget` widget path as a string or as an object handle
- `width` width in pixels
- `height` in pixels

**See Also**
- `l_size`, `l_size<-`

**Examples**
```r
if(interactive()){
  p <- l_plot(iris)
  l_resize(p, 300, 300)
  l_size(p) <- c(500, 500)
}
```

---

**l_Rlist2nestedTclList**  
*Convert an R list to a nested Tcl list*

**Description**
This is a helper function to create a nested Tcl list from an R list (i.e. a list of vectors).

**Usage**
```r
l_Rlist2nestedTclList(x)
```

**Arguments**
- `x` a list of vectors
Description

_\_saveStates_ uses saveRDS() to save the info states of a loon plot as an \texttt{R} object to the named file. This is helpful, for example, when using RMarkdown or some other notebooking facility to recreate an earlier saved loon plot so as to present it in the document.

Usage

\[
_\_saveStates_(
  \ p, \\
  \ \ \ \ \ \text{states} = \text{c("color", "active", "selected", "linkingKey", "linkingGroup")}, \\
  \ \ \ \ \ \text{file} = \text{stop("missing name of file")}, \\
  \ \ \ \ \ \text{...}
)
\]

Arguments

- \texttt{p} the \texttt{\_plot} object whose info states are to be saved.
- \texttt{states} either the logical \texttt{TRUE} or a character vector of info states to be saved. Default value \texttt{c("color", "active", "selected", "linkingKey", "linkingGroup")} consists of \texttt{n} dimensional states that are common to many \texttt{\_plot}'s and which are most important to reconstruct the plot's display in any summary. If \texttt{states} is the logical \texttt{TRUE}, by \texttt{names(p)} are saved.
- \texttt{file} is a string giving the file name where the saved information will be written (custom suggests this file name end in the suffix \texttt{.rds}).
- \texttt{...} further arguments passed to saveRDS().

Value

a list of class \texttt{\_savedStates} containing the states and their values. Also has an attribute \texttt{\_plot\_class} which contains the class vector of the plot \texttt{p}.
See Also

l_getSavedStates  l_copyStates  l_info_states  readRDS  saveRDS

Examples

if(interactive()){
  # Suppose you have some plot that you created like
  p <- l_plot(iris, showGuides = TRUE)
  #
  # and coloured groups by hand (using the mouse and inspector)
  # so that you ended up with these colours:
  p["color"] <- rep(c("lightgreen", "firebrick","skyblue"),
                   each = 50)
  #
  # Having determined the colours you could save them (and other states)
  # in a file of your choice, here some tempfile:
  myFileName <- tempfile("myPlot", fileext = ".rds")
  #
  # Save the named states of p
  l_saveStates(p,
               states = c("color", "active", "selected"),
               file = myFileName)
  #
  # These can later be retrieved and used on a new plot
  # (say in RMarkdown) to set the new plot's values to those
  # previously determined interactively.
  p_new <- l_plot(iris, showGuides = TRUE)
  p_saved_info <- l_getSavedStates(myFileName)
  #
  # We can tell what kind of plot was saved
  attr(p_saved_info, "l_plot_class")
  #
  # The result is a list of class "l_savedStates" which
  # contains the names of the
  p_new["color"] <- p_saved_info$color
  #
  # The result is that p_new looks like p did
  # (after your interactive exploration)
  # and can now be plotted as part of the document
  plot(p_new)
  #
  # For compound plots, the info_states are saved for each plot
  pp <- l_pairs(iris)
  myPairsFile <- tempfile("myPairsPlot", fileext = ".rds")
  #
  # Save the names states of pp
  l_saveStates(pp,
               states = c("color", "active", "selected"),
               file = myPairsFile)
  pairs_info <- l_getSavedStates(myPairsFile)
  #}
# For compound plots, the info states for all constituent plots are saved. The result is a list of class "l_savedStates" whose elements are the named plots as "l_savedStates" themselves.

# The names of the plots which were saved
names(pairs_info)

# And the names of the info states whose values were saved for the first plot
names(pairs_info$x2y1)

# While it is generally recommended to access (or assign) saved state values using the $ sign accessor, paying attention to the nested list structure of an "l_savedStates" object (especially for l_compound plots), R’s square bracket notation [ ] has also been specialized to allow a syntactically simpler (but less precise) access to the contents of an l_savedStates object.

# For example,
p_saved_info["color"]

# returns the saved "color" as a vector of colours.

# In contrast,
pairs_info["x2y1"]
# returns the l_savedStates object of the states of the plot named "x2y1", but
pairs_info["color"]
# returns a LIST of colour vectors, by plot as they were named in pairs_info

# As a consequence, the following two are equivalent,
pairs_info["x2y1"]["color"]
# finds the value of "color" from an "l_savedStates" object
# whereas
pairs_info["color"]["x2y1"]
# finds the value of "x2y1" from a "list" object

# Also, setting a state of an "l_savedStates" is possible (though not generally recommended; better to save the states again)

p_saved_info["color"] <- rep("red", 150)
# changes the saved state "color" on p_saved_info

# whereas
pairs_info["color"] <- rep("red", 150)
# will set the red color for any plot within pairs_info having "color" saved.
# In this way the assignment function via [ ] is trying to be clever for l_savedStates for compound plots and so may have unintentional consequences if the user is not careful.

# Generally, one does not want/need to change the value of saved states. Instead, the states would be saved again from the interactive plot if change is necessary.
# Alternatively, more nuanced and careful control is maintained using
# the $ selectors for lists.

---

## l_scale3D

### Scale for 3d plotting

**Description**

`l_scale3D` scales its argument in a variety of ways used for 3D visualization.

**Usage**

```r
l_scale3D(x, center = TRUE, method = c("box", "sphere"))
```

**Arguments**

- `x` the matrix or data.frame whose columns are to be scaled. Any NA entries will be preserved but ignored in calculations. `x` must have exactly 3 columns for `method = "sphere"`.
- `center` either a logical value or numeric-alike vector of length equal to the number of columns of `x`, where 'numeric-alike' means that `as.numeric(.)` will be applied successfully if `is.numeric(.)` is not true.
- `method` the scaling method to use. If `method = "box"` (the default) then the columns are scaled to have equal ranges and, when `center = TRUE`, to be centred by the average of the min and max; If `method = "sphere"` then `x` must be three dimensional. For sphering, on each of the original 3 dimensions `x` is first centred (mean centred when `center = TRUE`) and scaled to equal standard deviation on. The V matrix of the singular value decomposition (svd) is applied to the right resulting in uncorrelated variables. Coordinates are then divided by (non-zero as tested by `!all.equal(0,.)`) singular values. If `x` contains no NAs, the resulting coordinates are simply the U matrix of the svd.

**Value**

a data.frame whose columns are centred and scaled according to the given arguments. For `method = "sphere"), the three variable names are x1, x2, and x3.

**See Also**

- `l_plot3D`, `scale`, and `prcomp`.
- Other three-dimensional plotting functions: `l_plot3D()`
Examples

```r
# Examples

# Iris data
result_box <- l_scale3D(iris)
head(result_box, n = 3)
apply(result_box, 2, FUN = range)
# Note mean is not zero.
apply(result_box, 2, FUN = mean)

# Sphering only on 3D data.
result_sphere <- l_scale3D(iris[, 1:3], method = "sphere")
head(result_sphere, n = 3)
apply(result_sphere, 2, FUN = range)
# Note mean is numerically zero.
apply(result_sphere, 2, FUN = mean)

# With NAs
x <- iris
x[c(1, 3), 1] <- NA
x[2, 3] <- NA
result_box <- l_scale3D(x)
head(result_box, n = 5)
apply(result_box, 2, FUN = function(x) {range(x, na.rm = TRUE),class(x)})

# Sphering only on 3D data.
result_sphere <- l_scale3D(x[, 1:3], method = "sphere")
# Rows having had any NA are all NA after sphering.
head(result_sphere, n = 5)
# Note with NAs mean is no longer numerically zero.
# because centring was based on all non-NA in each column
apply(result_sphere, 2, FUN = function(x) {mean(x, na.rm = TRUE)})
```

Description

The function modifies the `zoomX`, `zoomY`, `panX`, and `panY` so that all active data points are displayed.

Usage

```r
l_scaleto_active(widget)
```
`l_scaleto_layer`  
*Change Plot Region to Display All Elements of a Particular Layer*

**Description**

The function modifies the `zoomX`, `zoomY`, `panX`, and `panY` so that all elements of a particular layer are displayed.

**Usage**

```r
l_scaleto_layer(target, layer)
```

**Arguments**

- **target**: either an object of class `loon` or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. `'/quotesingle.Var.l0.plot'`), the remaining objects by their ids.
- **layer**: layer id

**See Also**

`l_layer_ids`

---

`l_scaleto_plot`  
*Change Plot Region to Display the All Data of the Model Layer*

**Description**

The function modifies the `zoomX`, `zoomY`, `panX`, and `panY` so that all elements in the model layer of the plot are displayed.

**Usage**

```r
l_scaleto_plot(widget)
```

**Arguments**

- **widget**: widget path as a string or as an object handle
1_scaleto_selected  
**Change Plot Region to Display All Selected Data**

**Description**

The function modifies the zoomX, zoomY, panX, and panY so that all selected data points are displayed.

**Usage**

```javascript
1_scaleto_selected(widget)
```

**Arguments**

- **widget**: widget path as a string or as an object handle

---

1_scaleto_world  
**Change Plot Region to Display All Plot Data**

**Description**

The function modifies the zoomX, zoomY, panX, and panY so that all elements in the plot are displayed.

**Usage**

```javascript
1_scaleto_world(widget)
```

**Arguments**

- **widget**: widget path as a string or as an object handle
l_serialaxes

Create an interactive serialaxes (parallel axes or radial axes) plot

Description

l_serialaxes is a generic function for displaying multivariate data either as a stacked star glyph plot, or as a parallel coordinate plot.

Usage

l_serialaxes(data, ...)

## Default S3 method:
l_serialaxes(
  data,
  sequence,
  scaling = "variable",
  axesLayout = "radial",
  by = NULL,
  on,
  layout = c("grid", "wrap", "separate"),
  andrews = FALSE,
  showAxes = TRUE,
  color = l_getOption("color"),
  active = TRUE,
  selected = FALSE,
  linewidth = l_getOption("linewidth"),
  parent = NULL,
  ...
)

Arguments

data a data frame with numerical data only
...

named arguments to modify the serialaxes states or layouts, see details.

sequence vector with variable names that defines the axes sequence

scaling one of ‘variable’, ‘data’, ‘observation’ or ‘none’ to specify how the data is scaled. See Details and Examples for more information.

axesLayout either "radial" or "parallel"

by loon plot can be separated by some variables into multiple panels. This argument can take a formula, \( n \) dimensional state names (see \( l_nDimStateNames \)) an \( n \)-dimensional vector and data.frame or a list of same lengths \( n \) as input.

on if the x or by is a formula, an optional data frame containing the variables in the x or by. If the variables are not found in data, they are taken from environment, typically the environment from which the function is called.
l_serialaxes

layout
Andrew's plot (a 'Fourier' transformation)
showAxes
boolean to indicate whether axes should be shown or not
color
vector with line colors. Default is given by l_getOption("color").
active
a logical determining whether points appear or not. If a logical vector is given of length equal to the number of points, then it identifies which points appear (TRUE) and which do not (FALSE).
selected
a logical determining whether points appear selected at first (default is FALSE for all points). If a logical vector is given of length equal to the number of points, then it identifies which points are (TRUE) and which are not (FALSE).
linewidth
vector with line widths. Default is given by l_getOption("linewidth").
parent
a valid Tk parent widget path. When the parent widget is specified (i.e. not NULL) then the plot widget needs to be placed using some geometry manager like tkpack or tkplace in order to be displayed. See the examples below.

Details
For more information run: l_help("learn_R_display_hist")

• The scaling state defines how the data is scaled. The axes display 0 at one end and 1 at the other. For the following explanation assume that the data is in a nxp dimensional matrix. The scaling options are then

<table>
<thead>
<tr>
<th>variable</th>
<th>per column scaling</th>
</tr>
</thead>
<tbody>
<tr>
<td>observation</td>
<td>per row scaling</td>
</tr>
<tr>
<td>data</td>
<td>whole matrix scaling</td>
</tr>
<tr>
<td>none</td>
<td>do not scale</td>
</tr>
</tbody>
</table>

• Some arguments to modify layouts can be passed through, e.g. "separate", "byrow", etc. Check l_facet to see how these arguments work.

Value
if the argument by is not set, a loon widget will be returned; else an l_facet object (a list) will be returned and each element is a loon widget displaying a subset of interest.

See Also
Turn interactive loon plot static loonGrob, grid.loon, plot.loon.
Other loon interactive states: l_hist(), l_info_states(), l_plot(), l_state_names(), names.loon()

Examples
if(interactive()){

    #######
    #
}
# Effect of the choice of the argument "scaling"
#
# To illustrate we will look at the four measurements of
# 150 iris flowers from the iris data of Edgar Anderson made
# famous by R.A. Fisher.
#
# First separate the measurements
irisFlowers <- iris[, 1:4]
# from their species
species <- iris[,5]
# and get some identifiers for the individual flowers
flowerIDs <- paste(species, 1:50)
#
# Now create parallel axes plots of the measurements
# using different scaling values.
#
# # scaling = "variable"
#
# This is the standard scaling of most serial axes plots,
# scaling each axis from the minimum to the maximum of that variable.
# Hence it is the default scaling.
#
# More precisely, it maps the minimum value in each column (variable) to
# zero and the maximum to one. The result is every parallel
# axis will have a point at 0 and a point at 1.
#
# This scaling highlights the relationships (e.g. correlations)
# between the variables (removes the effect of the location and scale of
# each variable).
#
# For the iris data, ignoring species we see for example that
# Sepal.Length and Sepal.Width are negatively correlated (lots of
# crossings) across species but more positively correlated (mostly
# parallel lines) within each species (colour).
#
# sa_var <- l_serialaxes(irisFlowers,
#     scaling = "variable", # scale within column
#     axesLayout = "parallel",
#     color = species,
#     linewidth = 2,
#     itemLabel = flowerIDs,
#     showItemLabels = TRUE,
#     title = "scaling = variable (initially)",
#     linkingGroup = "irisFlowers data")
#
# # scaling = "observation"
#
# This maps the minimum value in each row (observation) to
# zero and the maximum value in each row to one.
#
# The result is that every observation (curve in the parallel
# coordinate plot) will touch 0 on at least one axis and touch 1 on another.
# This scaling highlights the differences between observations (rows)
# in terms of the relative measurements across the variables for each observation.
# For example, for the iris data we can see that for every flower (row) the Sepal.Length is the largest measurement and the Petal.Width is the smallest. Each curve gives some sense of the *shape* of each flower without regard to its size. Two species (versicolor and virginica) have similar shaped flowers (relatively long but narrow sepals and petals), whereas the third (setosa) has relatively large sepals compared to small petals.

sa_obs <- l_serialaxes(irisFlowers,
  scaling = "observation", # scale within row
  axesLayout = "parallel",
  color = species,
  linewidth = 2,
  itemLabel = flowerIDs,
  showItemLabels = TRUE,
  title = "scaling = observation (initially)",
  linkingGroup = "irisFlowers data")

# scaling = "data"
# This maps the minimum value in the whole dataset (over all elements)
# to zero and the maximum value in the whole dataset to one.
# The result is that every measurement is on the same numeric (if not measurement) scale. Highlighting the relative magnitudes of all numerical values in the data set, each curve shows the relative magnitudes without rescaling by variable.
# This is most sensible data such as the iris flower where all four measurements appear to have been taken on the same measuring scale.
# For example, for the iris data full data scaling preserves the size and shape of each flower. Again virginica is of roughly the same shape as versicolor but has distinctly larger petals.
# Setosa in contrast is quite differently shaped in both sepals and petals but with sepals more similar in size to the two other flowers and with significantly smaller petals.

sa_dat <- l_serialaxes(irisFlowers,
  scaling = "data",  # scale using all data
  axesLayout = "parallel",
  color = species,
  linewidth = 2,
  itemLabel = flowerIDs,
  showItemLabels = TRUE,
  title = "scaling = data (initially)"
linkingGroup = "irisFlowers data")

# scaling = "none"
#
# Sometimes we might wish to choose a min and max to use
# for the whole data set; or perhaps a separate min and max
# for each variable.
#
# This would be done outside of the construction of the plot
# and displayed by having scaling = "none" in the plot.
#
# For example, for the iris data, we might choose scales so that
# the minimum and the maximum values within the data set do not
# appear at the end points 0 and 1 of the axes but instead inside.
#
# Suppose we choose the following limits for all variables
lower_lim <- -3; upper_lim <- max(irisFlowers) + 1

# These are the limits we want to use to define the end points of
# the axes for all variables.
# We need only scale the data as
irisFlowers_0_1 <- (irisFlowers - lower_lim)/(upper_lim - lower_lim)
# Or alternatively using the built-in scale function
# (which allows different scaling for each variable)
irisFlowers_0_1 <- scale(irisFlowers,
    center = rep(lower_lim, 4),
    scale = rep((upper_lim - lower_lim), 4))

# Different scales for different
# And instruct the plot to not scale the data but plot it on the 0-1 scale
# for all axes. (Note any rescaled data outside of [0,1] will not appear.)
# sa_none <- l_serialaxes(irisFlowers_0_1,
#     scaling = "none", # do not scale
#     axesLayout = "parallel",
#     color = species,
#     linewidth = 2,
#     itemLabel = flowerIDs,
#     showItemLabels = TRUE,
#     title = "scaling = none (initially)",
#     linkingGroup = "irisFlowers data")

# This is particularly useful for "radial" axes to keep the polygons away from
# the centre of the display.
# For example
sa_none["axesLayout"] <- "radial"
# now displays each flower as a polygon where shapes and sizes are easily
# compared.
#
# NOTE: rescaling the data so that all values are within [0,1] is perhaps
# the best way to proceed (especially if there are natural lower and
# upper limits for each variable).
l_serialaxes_inspector

Create a Serialaxes Inspector

Description

Inspectors provide graphical user interfaces to oversee and modify plot states.

Usage

l_serialaxes_inspector(parent = NULL, ...)

Arguments

parent parent widget path
...
state arguments

Value

widget handle

See Also

l_create_handle

Examples

if(interactive()){
  i <- l_serialaxes_inspector()
}
l_setAspect  

Set the aspect ratio of a plot

**Description**

The aspect ratio is defined by the ratio of the number of pixels for one data unit on the y axis and the number of pixels for one data unit on the x axes.

**Usage**

\[ l\_setAspect(widget, \text{aspect}, x, y) \]

**Arguments**

- **widget**  
  widget path as a string or as an object handle
- **aspect**  
  aspect ratio, optional, if omitted then the \( x \) and \( y \) arguments have to be specified.
- **x**  
  optional, if the \( \text{aspect} \) argument is missing then \( x \) and \( y \) can be specified and the aspect ratio is calculated using \( y/x \).
- **y**  
  see description for \( x \) argument above

**Examples**

```r
## Not run:
p <- with(iris, l_plot(Sepal.Length ~ Sepal.Width, color=Species))

l_aspect(p)

l_setAspect(p, x = 1, y = 2)

## End(Not run)
```

l_setColorList  

Use custom colors for mapping nominal values to distinct colors

**Description**

Modify loon’s color mapping list to a set of custom colors.

**Usage**

\[ l\_setColorList(colors) \]

**Arguments**

- **colors**  
  vector with valid color names or hex-encoded colors
Details

There are two commonly used mapping schemes of data values to colors: one scheme maps numeric values to colors on a color gradient and the other maps nominal data to colors that can be well differentiated visually (e.g. to highlight the different groups). Presently, loon always uses the latter approach for its color mappings. You can use specialized color palettes to map continuous values to color gradients as shown in the examples below.

When assigning values to a display state of type color then loon maps those values using the following rules:

1. If all values already represent valid Tk colors (see `tkcolors`) then those colors are taken.
2. If the number of distinct values are less than number of values in loon’s color mapping list then they get mapped according to the color list, see `l_setColorList` and `l_getColorList`.
3. If there are more distinct values as there are colors in loon’s color mapping list then loon’s own color mapping algorithm is used. See `loon_palette` and for more details about the algorithm below in this documentation.

Loon’s default color list is composed of the first 11 colors from the hcl color wheel (displayed below in the html version of the documentation). The letters in hcl stand for hue, chroma and luminance, and the hcl wheel is useful for finding "balanced colors" with the same chroma (radius) and luminance but with different hues (angles), see Ross Ihaka (2003) “Colour for presentation graphics”, Proceedings of DSC, p. 2 (https://www.stat.auckland.ac.nz/~ihaka/courses/787/color.pdf).

The colors in loon’s internal color list are also the default ones listed as the "modify color actions" in the analysis inspectors. To query and modify loon’s color list use `l_getColorList` and `l_setColorList`.

In the case where there are more unique data values than colors in loon’s color list then the colors for the mapping are taken from different locations distributed on the hcl color wheel (see above).

One of the advantages of using the hcl color wheel is that one can obtain any number of "balanced colors" with distinct hues. This is useful in encoding data with colors for a large number of groups; however, it should be noted that the more groups we have the closer the colors sampled from the wheel become and, therefore, the more similar in appearance.

A common way to sample distinct "balanced colors" on the hcl wheel is to choose evenly spaced hues distributed on the wheel (i.e. angles on the wheel). However, this approach leads to color sets where most colors change when the sample size (i.e. the number of sampled colors from the wheel) increases by one. For loon, it is desirable to have the first $m$ colors of a color sample of size $m+1$ to be the same as the colors in a color sample of size $m$, for all positive natural numbers $m$. Hence, we prefer to have a sequence of colors. This way, the colors on the inspectors stay relevant (i.e. they match with the colors of the data points) when creating plots that encode with color a data variable with different number of groups.

We implemented such a color sampling scheme (or color sequence generator) that also makes sure that neighboring colors in the sequence have different hues. In you can access this color sequence generator with `loon_palette`. The color wheels below show the color generating sequence twice, once for 16 colors and once for 32 colors.

Note, for the inspector: If there are more unique colors in the data points than there are on the inspectors then it is possible to add the next five colors in the sequence of the colors with the +5
button. Alternatively, the + button on the modify color part of the analysis inspectors allows the user to pick any additional color with a color menu. Also, if you change the color mapping list and close and re-open the loon inspector these new colors show up in the modify color list.

When other color mappings of data values are required (e.g. numerical data to a color gradient) then the functions in the scales R package provide various mappings including mappings for qualitative, diverging and sequential values.

See Also

lSetColorList, l_getColorList, l_setColorList_ColorBrewer, l_setColorList_hcl, l_setColorList_baseR

Examples

if(interactive()){

l_plot(1:3, color=1:3) # loon's default mapping

cols <- l_getColorList()
lSetColorList(c("red", "blue", "green", "orange")

## close and reopen inspector
l_plot(1:3, color=1:3)  # use the new color mapping
l_plot(1:10, color=1:10) # use loons default color mapping as color list is too small

# reset to default
lSetColorList(cols)
}

## Not run:
# you can also perform the color mapping yourself, for example with
# the col_numeric function provided in the scales package
if (requireNamespace("scales", quietly = TRUE)) {
  pcustom <- with(olive, l_plot(stearic ~ oleic,
                               color = scales::col_numeric("Greens", domain = NULL)(palmitic))
}

## End(Not run)

l_setColorList_baseR  
Set loon’s color mapping list to the colors from base R

Description

Loon’s color list is used to map nominal values to colors. See the documentation for l_setColorList.
l_setColorList_ColorBrewer

Usage

l_setColorList_baseR()

See Also


Description

Loon’s color list is used to map nominal values to colors. See the documentation for l_setColorList.

Usage

l_setColorList_ColorBrewer(
  palette = c("Set1", "Set2", "Set3", "Pastel1", "Pastel2", "Paired", "Dark2", "Accent")
)

Arguments

palette one of the following RColorBrewer palette name: Set1, Set2, Set3, Pastel1, Pastel2, Paired, Dark2, or Accent

Details

Only the following palettes in ColorBrewer are available: Set1, Set2, Set3, Pastel1, Pastel2, Paired, Dark2, and Accent. See the examples below.

See Also


Examples

if (interactive()){

## Not run:
if (requireNamespace("RColorBrewer", quietly = TRUE)) {
  RColorBrewer::display.brewer.all()
}
## End(Not run)

```r
l_setColorList_ColorBrewer("Set1")
p <- l_plot(iris)
}
```

---

### l_setColorList_ggplot2

*Set loon's color mapping list to the colors from ggplot2*

---

**Description**

Loon’s color list is used to map nominal values to colors. See the documentation for `l_setColorList`.

**Usage**

```r
l_setColorList_ggplot2()
```

**See Also**


---

### l_setColorList_hcl

*Set loon's color mapping list to the colors from hcl color wheel*

---

**Description**

Loon’s color list is used to map nominal values to colors. See the documentation for `l_setColorList`.

**Usage**

```r
l_setColorList_hcl(chroma = 56, luminance = 51, hue_start = 231)
```

**Arguments**

- `chroma` The chroma of the color. The upper bound for chroma depends on hue and luminance.
- `luminance` A value in the range [0,100] giving the luminance of the colour. For a given combination of hue and chroma, only a subset of this range is possible.
- `hue_start` The start hue for sampling. The hue of the color specified as an angle in the range [0,360]. 0 yields red, 120 yields green 240 yields blue, etc.
l_setColorList_loon

Details

Samples equally distant colors from the hcl color wheel. See the documentation for hcl for more information.

See Also


Description

Loon’s color list is used to map nominal values to colors. See the documentation for l_setColorList.

Usage

l_setColorList_loon()

See Also


l_setLinkedStates

Modify States of a Plot that are Linked in Loon’s Standard Linking Model

Description

Loon’s standard linking model is based on three levels, the linkingGroup and linkingKey states and the used linkable states. See the details below.

Usage

l_setLinkedStates(widget, states)

Arguments

widget

widget path as a string or as an object handle

states

used linkable state names, see in details below
Details

Loon’s standard linking model is based on two states, linkingGroup and linkingKey. The full capabilities of the standard linking model are described here. However, setting the linkingGroup states for two or more displays to the same string is generally all that is needed for linking displays that plot data from the same data frame. Changing the linking group of a display is also the only linking-related action available on the analysis inspectors.

The first linking level is as follows: loon’s displays are linked if they share the same string in their linkingGroup state. The default linking group 'none' is a keyword and leaves a display un-linked.

The second linking level is as follows. All n-dimensional states can be linked between displays. We call these states linkable. Further, only linkable states with the same name can be linked between displays. One consequence of this shared state name rule is that, with the standard linking model, the linewidth state of a serialaxes display cannot be linked with the size state of a scatterplot display. Also, each display maintains a list that defines which of its linkable states should be used for linking; we call these states the used linkable states. The default used linkable states are as follows

<table>
<thead>
<tr>
<th>Display</th>
<th>Default used linkable states</th>
</tr>
</thead>
<tbody>
<tr>
<td>scatterplot</td>
<td>selected, color, active, size</td>
</tr>
<tr>
<td>histogram</td>
<td>selected, color, active</td>
</tr>
<tr>
<td>serialaxes</td>
<td>selected, color, active</td>
</tr>
<tr>
<td>graph</td>
<td>selected, color, active, size</td>
</tr>
</tbody>
</table>

If any two displays are set to be linked (i.e. they share the same linking group) then the intersection of their used linkable states are actually linked.

The third linking level is as follows. Every display has a n-dimensional linkingKey state. Hence, every data point has an associated linking key. Data points between linked plots are linked if they share the same linking key.

---

l_setOption

Set the value of a loon display option

Description

All of loon’s displays access a set of common options. This function assigns the value to the named option.

Usage

l_setOption(option, value)

Arguments

<table>
<thead>
<tr>
<th>option</th>
<th>the name of the option being set</th>
</tr>
</thead>
<tbody>
<tr>
<td>value</td>
<td>the value to be assigned to the option. If value == &quot;default&quot;, then the option is set to loon’s default value for it.</td>
</tr>
</tbody>
</table>
l_setTitleFont

Value
the new value

See Also
l_getOption, l_getOptionNames, l_userOptions, l_userOptionDefault

Examples
l_setOption("select-color", "red")
l_setOption("select-color", "default")

---

l_setTitleFont Set the title font of all loon displays

Description
All of loon’s displays access a set of common options. This function sets the font for the title bar of
the displays.

Usage
l_setTitleFont(size = "16", weight = "bold", family = "Helvetica")

Arguments
size the font size.
weight the font size.
family the font family.

Value
the value of the named option.

See Also
l_getOptionNames, l_userOptions, l_userOptionDefault, l_setOption
\section*{\texttt{l_size}} \textit{Query Size of a Plot Display}

\subsection*{Description}
Get the width and height of a plot in pixels

\subsection*{Usage}
\begin{verbatim}
l_size(widget)
\end{verbatim}

\subsection*{Arguments}
\begin{verbatim}
widget widget path as a string or as an object handle
\end{verbatim}

\subsection*{Value}
Vector width width and height in pixels

\subsection*{See Also}
\begin{verbatim}
l_resize, l_size<-
\end{verbatim}

\section*{\texttt{l_size<-}} \textit{Resize Plot Widget}

\subsection*{Description}
Resizes the toplevel widget to a specific size. This setter function uses \texttt{l_resize}.

\subsection*{Usage}
\begin{verbatim}
l_size(widget) <- value
\end{verbatim}

\subsection*{Arguments}
\begin{verbatim}
widget widget path as a string or as an object handle
value numeric vector of length 2 with width and height in pixels
\end{verbatim}

\subsection*{See Also}
\begin{verbatim}
l_resize, l_size
\end{verbatim}
Examples

```
if(interactive()){
  p <- l_plot(iris)
  l_resize(p, 300, 300)
  l_size(p) <- c(500, 500)
}
```

---

l_state_names

### Get State Names of Loon Object

#### Description

States of loon objects can be accessed `[]` and `l_cget` and modified with `l_configure`.

#### Usage

```r
l_state_names(target)
```

#### Arguments

- **target**: either an object of class loon or a vector that specifies the widget, layer, glyph, navigator or context completely. The widget is specified by the widget path name (e.g. `'.l0.plot'`), the remaining objects by their ids.

#### Details

In order to access values of a states use `l_info_states`.

#### Value

state names

#### See Also

- `l_info_states`, `l_cget`, `l_configure`

Other loon interactive states: `l_hist()`, `l_info_states()`, `l_plot()`, `l_serialaxes()`, `names.loon()`
1_subwin

Create a child widget path

Description

This function is similar to .Tk.subwin except that does not the environment of the "tkwin" object to keep track of numbering the subwidgets. Instead it creates a widget path (parent).looni, where i is the smallest integer for which no widget exists yet.

Usage

1_subwin(parent, name = "w")

Arguments

parent parent widget path
name  child name

Value

widget path name as a string

1_throwErrorIfNotLoonWidget

Throw an error if string is not associated with a loon widget

Description

Helper function to ensure that a widget path is associated with a loon widget.

Usage

1_throwErrorIfNotLoonWidget(widget)

Arguments

widget widget path name as a string

Value

TRUE if the string is associated with a loon widget, otherwise an error is thrown.
l_toplevel

Description

Create a loon tk top-level window

Usage

l_toplevel(path)

Arguments

path

A valid path name (character); if missing, a valid path will be generated automatically

Value

a tk top level widget

Examples

if(interactive()) {

    tt <- l_toplevel(".test")
    subwin <- l_subwin(tt, 'ts')
    tktitle(tt) <- paste("path:", subwin)
    parent <- as.character(tcl('frame', subwin))

    # a loon widget
    p <- l_plot(rnorm(100), rnorm(100), parent = parent)

    # pack a refresh button (generate new data set)
    refresh_button <- as.character(
        tcltk::tcl('button',
            as.character(l_subwin(parent, 'refresh button')),
            text = "refresh",
            bg = "grey80",
            fg = "black",
            borderwidth = 2,
            relief = "raised")
    )

    # layout
    tcltk::tkgrid(p,
        row = 0,
        column = 0,
        rowspan = 10,
        columnspan = 10,
        sticky="nesw")

    tcltk::tkgrid(refresh_button,

```
for(i in 0:10) {
    tcltk::tkgrid.rowconfigure(parent, i, weight=1)
}
for(i in 0:9) {
    tcltk::tkgrid.columnconfigure(parent, i, weight=1)
}

update <- function(...) {
    l_configure(p,
        x = rnorm(100),
        y = rnorm(100))
    l_scaleto_world(p)
}

# configure button (callback function)
tcltk::tkconfigure(refresh_button,
    command = update)

# configure canvas size
tcltk::tkconfigure(paste(p,".canvas", sep=''), width=500, height=500)

# pack widgets
tkpack(parent, fill="both", expand=TRUE)
}

---

**l_toR**

*Convert a Tcl Object to some other R object*

**Description**

Return values from `.Tcl` and `tcl` are of class `tclObj` and often need to be mapped to a different data structure in `R`. This function is a helper class to do this mapping.

**Usage**

`l_toR(x, cast = as.character)`

**Arguments**

- `x` a `tclObj` object
- `cast` a function to convert the object to some other `R` object

**Value**

A object that is returned by the function specified with the `cast` argument.
**l_userOptionDefault**

*Get loon’s system default value for the named display option.*

### Description

All of loon’s displays access a set of common options. This function accesses and returns the default value for the named option.

### Usage

```
l_userOptionDefault(option)
```

### Arguments

- **option**: the name of the user changeable loon display option whose default value is to be determined.

### Value

the default value for the named option

### See Also

- `l_getOptionNames`, `l_getOption`, `l_userOptionDefault`, `l_userOptions`

### Examples

```
l_userOptionDefault("background")
```

---

**l_userOptions**

*Get the names of all loon display options that can be set by the user.*

### Description

All of loon’s displays access a set of common options. This function accesses and returns the names of the subset of loon options which can be changed by the user.

### Usage

```
l_userOptions()
```

### Value

a vector of all user settable option names.
See Also

l_getOptionNames, l_getOption, l_userOptionDefault, l_setOption

Examples

l_userOptions()

---

l_web

Open a browser with loon’s R documentation webpage

Description

l_web opens a browser with the relevant page on the official loon documentation website. This is constructed by joining together the information provided by the arguments site/package/directory/page. Default would be the documentation found at https://great-northern-diver.github.io/loon/.

Usage

l_web(
  page = "index",
  directory = c("home", "reference", "articles"),
  package = c("loon", "loon.data", "loon.ggplot", "loon.tourr", "ggmulti", "zenplots",
              "loon.shiny", "diveR"),
  site = "https://great-northern-diver.github.io",
  ...
)

Arguments

page relative path to a page (the ".html" part may be omitted)
directory if "home" (the default) then page is ignored and the browser will open at the home page of the official documentation website. If page refers to a package manual reference, then directory must be "reference"; if page refers to the name of a vignette file, then directory should be "articles"
package a string identifying the package name having an online documentation (default "loon")
site the URL of the site (default "https://great-northern-diver.github.io") prefixing the path to the requested documentation.
...

See Also

l_help, help, vignette
Examples

```r
## Not run:
l_widget()
#
vignette("introduction", package = "loon")
# or
l_web(page = "introduction", directory = "articles")
# or
l_web(package = "loon.data", directory = "reference")
#
help(l_hist)
l_web(page = "l_hist", directory = "reference")

## End(Not run)
```

---

**l_widget**

*Dummy function to be used in the Roxygen documentation*

**Description**

Dummy function to be used in the Roxygen documentation

**Usage**

```r
l_widget(widget)
```

**Arguments**

- `widget` widget path name as a string

**Value**

widget path name as a string

---

**l_worldview**

*Create a Worldview Inspector*

**Description**

Inspectors provide graphical user interfaces to oversee and modify plot states

**Usage**

```r
l_worldview(parent = NULL, ...)
```
Arguments

parent          parent widget path
...
...          state arguments

Value

widget handle

See Also

l_create_handle

Examples

```r
if(interactive()){
  i <- l_worldview()
}
```

---

**l_zoom**

*Zoom from and towards the center*

Description

This function changes the plot states `panX`, `panY`, `zoomX`, and `zoomY` to zoom towards or away from the center of the current view.

Usage

```r
l_zoom(widget, factor = 1.1)
```

Arguments

- **widget**
  - widget path as a string or as an object handle
- **factor**
  - a zoom factor
measures1d

Closure of One Dimensional Measures

Description

Function creates a 1d measures object that can be used with l_ng_plots and l_ng_ranges.

Usage

measures1d(data, ...)

Arguments

data

a data.frame with the data used to calculate the measures

...

named arguments, name is the function name and argument is the function to calculate the measure for each variable.

Details

For more information run: l_help("learn_R_display_graph.html#measures")

Value

a measures object

See Also

l_ng_plots, l_ng_ranges, measures2d

Examples

m1 <- measures1d(oliveAcids, mean=mean, median=median,
                 sd=sd, q1=function(x)as.vector(quantile(x, probs=0.25)),
                 q3=function(x)as.vector(quantile(x, probs=0.75)))

m1
m1()
m1(olive$palmitoleic>100)
m1('data')
m1('measures')
Description

Function creates a 2d measures object that can be used with \texttt{l\_ng\_plots} and \texttt{l\_ng\_ranges}.

Usage

\begin{verbatim}
measures2d(data, ...)
\end{verbatim}

Arguments

- \texttt{data} a data.frame with the data used to calculate the measures
- \texttt{...} named arguments, name is the function name and argument is the function to calculate the measure for each variable.

Details

For more information run: \texttt{l\_help("learn\_R\_display\_graph.html\#measures")}

Value

a measures object

See Also

\texttt{l\_ng\_plots, l\_ng\_ranges, measures2d}

Examples

\begin{verbatim}
m <- measures2d(oliveAcids, separator='*', cov=cov, cor=cor)
m
m()
m(keep=olive$palmitic>1360)
m('data')
m('grid')
m('measures')
\end{verbatim}
minority

Canadian Visible Minority Data 2006

Description

Population census count of various named visible minority groups in each of 33 major census metropolitan areas of Canada in 2006.

These data are from the 2006 Canadian census, publicly available from Statistics Canada.

Usage

minority

Format

A data frame with 33 rows and 18 variates

Arab Number identifying as ‘Arab’.
Black Number identifying as ‘Black’.
Chinese Number identifying as ‘Chinese’.
Filipino Number identifying as ‘Filipino’.
Japanese Number identifying as ‘Japanese’.
Korean Number identifying as ‘Korean’.
Latin.American Number identifying as ‘Latin American’.
Multiple.visible.minority Number identifying as being a member of more than one visible minority.
South.Asian Number identifying as ‘South Asian’.
Southeast.Asian Number identifying as ‘Southeast Asian’.
Total.population Total population of the metropolitan census area.
Visible.minority.not.included.elsewhere Number identifying as a member of a visible minority that was not included elsewhere.
Visible.minority.population Total number identifying as a member of some visible minority.
West.Asian Number identifying as ‘West Asian’.
lat, long Latitude and longitude (in degrees) of the metropolitan census area.
googleLat, googleLong Latitude and longitude in degrees determined using the Google Maps Geocoding API.

rownames(minority) are the names of the metropolitan areas or cities.

Source

Statistics Canada
names.loon  

Get State Names of Loon Object

Description
States of loon objects can be accessed `\[\]` and `l_cget` and modified with `l_configure`.

Usage
```r
## S3 method for class 'loon'
names(x)
```

Arguments
- `x` loon object

Value
state names

See Also
Other loon interactive states: `l_hist()`, `l_info_states()`, `l_plot()`, `l_serialaxes()`, `l_state_names()`

ndtransitiongraph  

Create a n-d transition graph

Description
A n-d transition graph has k-d nodes and all edges that connect two nodes that from a n-d subspace

Usage
```r
ndtransitiongraph(nodes, n, separator = ":")
```

Arguments
- `nodes` node names of graph
- `n` integer, dimension an edge should represent
- `separator` character that separates spaces in node names

Details
For more information run: `l_help("learn_R_display_graph.html.html#graph-utilities")`
Value

graph object of class loongraph

Examples

g <- ndtransitiongraph(nodes=c('A:B', 'A:F', 'B:C', 'B:F'), n=3, separator=': ')

Description

This data set records the percentage composition of 8 fatty acids found in the lipid fraction of 572 Italian olive oils. The oils are samples taken from three Italian regions varying number of areas within each region. The regions and their areas are recorded as shown in the following table:

<table>
<thead>
<tr>
<th>Region</th>
<th>Area</th>
</tr>
</thead>
<tbody>
<tr>
<td>North</td>
<td>North-Apulia, South-Apulia, Calabria, Sicily</td>
</tr>
<tr>
<td>South</td>
<td>East-Liguria, West-Liguria, Umbria</td>
</tr>
<tr>
<td>Sardinia</td>
<td>Coastal-Sardinia, Inland-Sardinia</td>
</tr>
</tbody>
</table>

Usage

olive

Format

A data frame containing 572 cases and 10 variates.

- **Region**: Italian olive oil general growing region: North, South, or Sardinia
- **Area**: These are "Administrative Regions" of Italy (e.g. Sicily, or Umbria), or parts of such a region like "Coastal-Sardinia" and "Inland-Sardinia" or "North-Apulia" and "South-Apulia". Administrative regions are larger than, and contain, Italian provinces.

- **palmitic**: Percentage (in hundredths of a percent) of Palmitic acid, or hexadecanoic acid in the olive oil. It is the most common saturated fatty acid found in animals, plants and micro-organisms.

- **palmitoleic**: Percentage (in hundredths of a percent) of Palmitoleic acid, an omega-7 monounsaturated fatty acid.

- **stearic**: Percentage (in hundredths of a percent) of Stearic acid, a saturated fatty acid. It is a waxy solid and its name comes from the Greek word for tallow. Like palmitic acid, it is one of the most common saturated fatty acids found in nature.

- **oleic**: Percentage (in hundredths of a percent) of Oleic acid, the most common fatty acid occurring in nature found in various animal and vegetable fats and oils.

- **linoleic**: Percentage (in hundredths of a percent) of Linoleic acid, a polyunsaturated omega-6 fatty acid. It is one of two essential fatty acids for humans.
linolenic  Percentage (in hundredths of a percent) of Linolenic acid, a type of fatty acid. It can refer to one of two types of fatty acids or a mixture of both. One is an omega-3 essential fatty acid; the other an omega-6.

arachidic  Percentage (in hundredths of a percent) of Arachidic acid, also known as eicosanoic acid, a saturated fatty acid that is used for the production of detergents, photographic materials and lubricants.

eicosenoic  Percentage (in hundredths of a percent) of Eicosenoic acid, which may refer to one of three closely related fatty acids: gadoleic acid (omega-11), gondoic acid (omega-9), or paullinic acid (omega-7).

Note that the percentages (in hundredths of a percent) should sum to approximately 10,000 for each oil (row).

References


See Also

oliveLocations

---

| oliveAcids | Just the Fatty Acid Composition of Italian Olive Oils |

Description

This is the olive data set minus the Region and Area variables.

Usage

oliveAcids

Format

A data frame containing 572 cases and 8 variates.

See Also

olive
oliveLocations

Geographic location of each Italian olive growing area named in the olive data.

Description

A longitude and latitude for each Area named in the olive data set.

Usage

oliveLocations

Format

A data frame containing 9 cases and 3 variates.

Area name of the Italian growing area of the olive oil.

lat, long latitude and longitude in degrees of the approximate centre of the named growing area

Source

https://www.latlong.net

See Also

olive

plot.loon

Plot the current view of any loon plot in the current device.

Description

This is a wrapper for grid.loon() to simplify the plotting of loon plots on any device. Frequent users are recommended to use grid.loon() for more control.

Usage

## S3 method for class 'loon'
plot(x, y = NULL, ...)

Arguments

x the loon plot to be plotted on the current device

y NULL, will be ignored.

... parameters passed to loonGrob
Value

invisible()

See Also

loonGrob, grid.loon, l_export

Examples

if(interactive()) {
  loonPlot <- with(iris, l_plot(Sepal.Length, Sepal.Width))
  loonPlot['color'] <- iris$Species
  loonPlot['selected'] <- iris$Species == "versicolor"
  l_scaleto_selected(loonPlot)
  plot(loonPlot)
}

---

plot.loongraph  

Plot a loon graph object with base R graphics

Description

This function converts the loongraph object to one of class graph and the plots it with its respective plot method.

Usage

## S3 method for class 'loongraph'
plot(x, ...)

Arguments

x  
object of class loongraph

...  
arguments forwarded to method

Examples

g <- loongraph(letters[1:4], letters[1:3], letters[2:4], FALSE)
**print.l_layer**

Print a summary of a loon layer object

**Description**

Prints the layer label and layer type

**Usage**

```r
## S3 method for class 'l_layer'
print(x, ...)
```

**Arguments**

- `x`:
  - an `l_layer` object
- `...`:
  - additional arguments are not used for this method

**See Also**

- `l_layer`

---

**print.measures1d**

Print function names from measure1d object

**Description**

Prints the function names of a measure1d object using `print.default`.

**Usage**

```r
## S3 method for class 'measure1d'
print(x, ...)
```

**Arguments**

- `x`:
  - a `measure1d` object
- `...`:
  - arguments passed on to `print.default`
print.measures2d  
*Print function names from measure2d object*

**Description**

Prints the function names of a measure2d object using print.default.

**Usage**

```r
## S3 method for class 'measures2d'
print(x, ...)  
```

**Arguments**

- `x`  
  measures2d object
- `...`  
  arguments passed on to print.default

---

**scagnostics2d**  
*Closure of Two Dimensional Scagnostic Measures*

**Description**

Function creates a 2d measures object that can be used with `l_ng_plots` and `l_ng_ranges`.

**Usage**

```r
cagnostics2d(
  data,
  separator = ":"
)
```

**Arguments**

- `data`  
  a data.frame with the data used to calculate the measures
- `scagnostics`  
  vector with valid scanostics measure names, i.e "Clumpy", "Monotonic", "Convex", "Stringy", "Skinny", "Outlying", "Sparse", "Striated", "Skewed". Also the prefix "Not" can be added to each measure which equals 1-measure.
- `separator`  
  string the separates variable names in 2d graph nodes

**Details**

For more information run: `l_help("learn_R_display_graph.html#measures")`
Value

A measures object

See Also

`l_ng_plots`, `l_ng_ranges`, `measures2d`

Examples

```r
## Not run:
m <- scagnostics2d(oliveAcids, separator='**')
m
m(olive$palmitoleic > 80)
m('data')
m('grid')
m('measures')
## End(Not run)
```

---

`tcl_img_2_r_raster`  
**A tk Image Object to a Raster Object**

Description

Turn a tk image object to an R raster object

Usage

`tcl_img_2_r_raster(img)`

Arguments

`img`  
a tk image object

Examples

```r
if(requireNamespace("grid")) {
puglia <- list.files(file.path(find.package(package = 'loon'), "images"),
  full.names = TRUE)[1L]
# `img` is a tk image object
img <- setNames(l_image_import_files(puglia),
  tools::file_path_sans_ext(basename(puglia)))
raster <- tcl_img_2_r_raster(img)
grid::grid.newpage()
grid::grid.raster(raster)
}
## tkcolors

### Description

The core of Loon is implemented in Tcl and Tk. Hence, when defining colors using color names, Loon uses the Tcl color representation and not those of R. The colors are taken from the Tk sources: `doc/colors.n`.

If you want to make sure that the color names are represented exactly as they are in R then you can convert the color names to hexencoded color strings, see the examples below.

### Usage

```r
tkcolors()
```

### Examples

```r
# check if R colors names and TK color names are the same
setdiff(tolower(colors()), tolower(tkcolors()))
setdiff(tolower(tkcolors()), tolower(colors()))

# hence there are currently more valid color names in Tk
# than there are in R

# Let's compare the colors of the R color names in R and Tk
thex <- function(x) {
  sapply(x, function(xi) {
    crgb <- as.vector(col2rgb(xi))
    rgb(crgb[1], crgb[2], crgb[3], maxColorValue = 255)
  })
}

df <- data.frame(
  R_col = tohex(colors()),
  Tcl_col = hex12tohex6(l_hexcolor(colors())),
  row.names = colors(),
  stringsAsFactors = FALSE
)

df_diff <- df[df$R_col != df$Tcl_col,]

if (requireNamespace("grid", quietly = TRUE)) {
  grid::grid.newpage()
  grid::pushViewport(grid::plotViewport())
  
  x_col <- grid::unit(0, "npc")
  x_R <- grid::unit(6, "lines")
  x_Tcl <- grid::unit(10, "lines")
```
UsAndThem

```
grid::grid.text('color', x=x_col, y=grid::unit(1, "npc"),
                just='left', gp=grid::gpar(fontface='bold'))
grid::grid.text('R', x=x_R, y=grid::unit(1, "npc"), just='center',
                 gp=grid::gpar(fontface='bold'))
grid::grid.text('Tcl', x=x_Tcl, y=grid::unit(1, "npc"), just='center',
             gp=grid::gpar(fontface='bold'))
for (i in 1:nrow(df_diff)) {
  y <- grid::unit(1, "npc") - grid::unit(i*1.2, "lines")
  grid::grid.text(rownames(df_diff)[i], x=x_col, y=y, just='left')
  grid::grid.rect(x=x_R, y=y, width=grid::unit(3, "line"),
                 height=grid::unit(1, "line"), gp=grid::gpar(fill=df_diff[i,1]))
  grid::grid.rect(x=x_Tcl, y=y, width=grid::unit(3, "line"),
                 height=grid::unit(1, "line"), gp=grid::gpar(fill=df_diff[i,2]))
}
```

**UsAndThem**

Data to re-create Hans Rosling’s famous "Us and Them" animation

**Description**

This data was sourced from [https://www.gapminder.org/](https://www.gapminder.org/) and contains Population, Life Expectancy, Fertility, Income, and Geographic.Region information between 1962 and 2013 for 198 countries.

**Usage**

UsAndThem

**Format**

A data frame with 9855 rows and 8 variables

- **Country**  country name
- **Year**  year of recorded measurements
- **Population**  country’s population
- **LifeExpectancy**  average life expectancy in years at birth
- **Fertility**  in number of babies per woman
- **Income**  Gross domestic product per person adjusted for inflation and purchasing power (in international dollars)
- **Geographic.Region**  one of six large global regions
- **Geographic.Region.ID**  two letter identification of country

**Source**

[https://www.gapminder.org/](https://www.gapminder.org/)
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