Package 'loon'

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Type Package

Title Interactive Statistical Data Visualization

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URL https://great-northern-diver.github.io/loon/

Description An extendable toolkit for interactive data visualization and exploration.

License GPL-2

Depends R (>= 3.5.0), methods, tcltk

Imports tools, graphics, grDevices, utils, stats, gridExtra

Suggests maps, sp, graph, scagnostics, PairViz, RColorBrewer, loon.data, rworldmap, mgcv, rgl, Rgraphviz, RDRToolbox, kernlab, scales, MASS, testthat, knitr, rmarkdown, png, formatR, covr

BugReports https://github.com/great-northern-diver/loon/issues

Encoding UTF-8

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R topics documented:

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/view=gR.

Usage

```
as.graph(loongraph)
```

Arguments

loongraph	object of class loongraph

Details

See https://www.bioconductor.org/packages/release/bioc/html/graph.html for more information 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

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

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

Value

graph object of class loongraph

Examples

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

---

color_loon *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

Examples

```
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)) {
  grid::grid.newpage()
  grid::pushViewport(grid::plotViewport())
  grid::grid.rect()
  n <- c(2,4,8,16, 21)
  # beyond this, colors are generated algorithmically
  # generating a warning
  grid::pushViewport(grid::dataViewport(xscale=c(0, max(n)+1),
                     yscale=c(0, length(n)+1)))
  grid::grid.yaxis(at=c(1:length(n)), label=paste("n =", n))
  for (i in rev(seq_along(n))) {
   cols <- pal(1:n[i])
   grid::grid.points(x = 1:n[i], y = rep(i, n[i]),
                     default.units = "native", pch=15,
                     gp=grid::gpar(col=cols))
  }
  grid::grid.text("note the first i colors are shared for each n",
                  y = grid::unit(1,"npc") + grid::unit(1, "line"))
}
```

---

complement *Create the Complement Graph of a Graph*

Description

Creates a complement graph of a graph

Usage

```
complement(x)
```

Arguments

x	graph or loongraph object

Value

graph object

---

complement.loongraph *Create the Complement Graph of a loon Graph*

Description

Creates a complement graph of a graph

Usage

```
## 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

```
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 wheter the returned object is a complete graph (undirected) or a complete digraph (directed).

Details

Note that this function masks the completegraph function of the graph package. Hence it is a good idead 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

```
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

```
condGrob(test = TRUE, grobFun = 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

```
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

```
facet_grid_layout(
  plots,
  subtitles,
  by = NULL,
  prop = 10,
  parent = NULL,
  title = "",
  xlabel = "",
  ylabel = "",
  labelLocation = c("top", "right"),
  byrow = FALSE,
  swapAxes = FALSE,
  labelBackground = "gray80",
  labelForeground = "black",
  labelBorderwidth = 2,
```

```
  labelRelief = "groove",
  sep = "*",
  maxCharInOneRow = 15,
  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
xlabel	The xlabel of the widget
ylabel	The ylabel of the widget
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
sep	The character string to separate or combine a vector
maxCharInOneRow	Max char in one row. If it exceeds the max, then a char will be displayed into two rows
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.

facet_separate_layout *layout separately*

Description

layout separately

Usage

```
facet_separate_layout(
  plots,
  subtitles,
  title = "",
  xlabel = "",
  ylabel = "",
  sep = "*",
  maxCharInOneRow = 15,
  ...
)
```

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	Max char in one row. If it exceeds the max, then a char will be displayed into two rows
...	named arguments to modify plot states. See l_info_states of any instantiated l_plot for examples of names and values.

facet_wrap_layout *Layout as a wrap*

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 = FALSE,
  swapAxes = FALSE,
  labelBackground = "gray80",
  labelForeground = "black",
  labelBorderwidth = 2,
  labelRelief = "groove",
  sep = "*",
  maxCharInOneRow = 15,
  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
sep	The character string to separate or combine a vector
maxCharInOneRow	Max char in one row. If it exceeds the max, then a char will be displayed into two rows
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.

`graphreduce` *Make each space in a node apprear only once*

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

```
G <- completegraph(nodes=LETTERS[1:4])
LG <- linegraph(G)

LLG <- linegraph(LG)

graphreduce(LLG)

if (requireNamespace("Rgraphviz", quietly = TRUE)) {
  plot(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. `'.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.
`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 hexidecimal 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

```
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

```
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
```

---

linegraph *Create a linegraph*

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

```
linegraph(x, ...)
```

Arguments

x	graph of class graph or loongraph
...	arguments passed on to method

Value

graph object

---

linegraph.loongraph *Create a linegraph of a graph*

Description

Create a lingraph of a loongraph

Usage

```
## S3 method for class 'loongraph'
linegraph(x, separator = ":", ...)
```

Arguments

x	loongraph object
separator	one character - node names in x get concatenated with this character
...	additional arguments are not used for this methiod

Details

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

Value

graph object of class loongraph

Examples

```
g <- loongraph(letters[1:4], letters[1:3], letters[2:4], FALSE)

linegraph(g)
```

---

loon *loon: A Toolkit for Interactive Data Visualization and Exploration*

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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See Also

Useful links:

- https://great-northern-diver.github.io/loon/
- Report bugs at https://github.com/great-northern-diver/loon/issues

---

`loongraph` *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

```
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)
```

---

loonGrob *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).

Value

a grid grob

See Also

grid.loon

Examples

```
## Not run:
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:

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:Petal.Length",
  to = "Sepal.Width: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)
lgrob <- 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)
```

`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` *Loon’s color generator for creating color palettes*

Description

Loon has a color sequence generator implemented creates a color palettes 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 on 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

Details

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

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

l_aspect(p)
l_aspect(p) <- 1

## End(Not run)
```

l_basePaths *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 base (non-compound) loon path types.

Usage

```
l_basePaths()
```

Value

character vector of the base path types.

See Also

l_compoundPaths l_getFromPath l_loonWidgets

l_binCut *Get labels for each observation according to bin cuts in the histogram.*

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

```
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

```
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
}
```

---

l_bind_canvas *Create a Canvas Binding*

Description

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

Usage

```
l_bind_canvas(widget, event, callback)
```

Arguments

widget	widget path as a string or as an object handle
event	event patterns as defined for Tk canvas widget https://www.tcl.tk/man/tcl8.6/TkCmd/bind.htm#M5.
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

Canvas bindings are used to evaluate callbacks at certain X events on the canvas widget (underlying widget for all of loon's plot widgets). Such X events include re-sizing of the canvas and entering the canvas with the mouse.

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

Value

canvas binding id

See Also

l_bind_canvas_ids, l_bind_canvas_get, l_bind_canvas_delete, l_bind_canvas_reorder

Examples

```
# 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

```
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

l_bind_canvas_get *Get the event pattern and callback Tcl code of a canvas 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_canvas_get(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")`

Value

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

See Also

l_bind_canvas, l_bind_canvas_ids, l_bind_canvas_delete, l_bind_canvas_reorder

Examples

```
# 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_ids *List canvas binding ids*

Description

List all user added canvas binding ids

Usage

```
l_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

l_bind_canvas, l_bind_canvas_get, l_bind_canvas_delete, l_bind_canvas_reorder

Examples

```
# 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

```
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

```
l_bind_context(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 evnets: `'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

context binding id

See Also

`l_bind_context_ids`, `l_bind_context_get`, `l_bind_context_delete`, `l_bind_context_reorder`

l_bind_context_delete *Delete a context binding*

Description

Remove a context binding

Usage

```
l_bind_context_delete(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")`

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

l_bind_glyph *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 as an object handle
event	a vector with one or more of the following evnets: '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

---

l_bind_glyph_delete *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

l_bind_glyph_get *Get the event pattern and callback Tcl code of a glyph 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_glyph_get(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")`

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

```
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

```
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 `l_help("learn_R_bind")`

Value

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

See Also

`l_bind_glyph`, `l_bind_glyph_ids`, `l_bind_glyph_get`, `l_bind_glyph_delete`

`l_bind_item` *Create a Canvas Binding*

Description

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

Usage

```
l_bind_item(widget, tags, event, callback)
```

Arguments

`widget`	widget path as a string or as an object handle
`tags`	item tags as as explained in `l_help("learn_R_bind.html#item-bindings")`
`event`	event patterns as defined for Tk canvas widget https://www.tcl.tk/man/tcl8.6/TkCmd/bind.htm#M5.
`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

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 `l_help("learn_R_bind")`

Value

item binding id

See Also

`l_bind_item_ids`, `l_bind_item_get`, `l_bind_item_delete`, `l_bind_item_reorder`

l_bind_item_delete *Delete a item binding*

Description

Remove a 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_ids` *List item binding ids*

Description

List all user added item binding ids

Usage

```
l_bind_item_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 item binding ids

See Also

l_bind_item, l_bind_item_get, 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 evnets: '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_R_bind")`

Value

layer binding id

See Also

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

---

l_bind_layer_delete *Delete a layer binding*

Description

Remove a layer binding

Usage

```
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_R_bind")`

See Also

`l_bind_layer`, `l_bind_layer_ids`, `l_bind_layer_get`, `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 a 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

```
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 evnets: '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

```
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 defines 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_navigator`, `l_bind_navigator_ids`, `l_bind_navigator_get`, `l_bind_navigator_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

```
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. `'.l0.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. '.l0.plot'), 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. '.l0.plot'), 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`

`l_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. '.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

---

l_cget *Query a Plot State*

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 refered to as plot states). This function queries a single plot state.

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. '.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']
}
```

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.
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_basePathsl_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 refered 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. `'.l0.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 slicind2d 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 hanlde
id	context id

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 *Query the label of a context*

Description

Context labels are eventually used in the context inspector. This function queries the label of a context.

Usage

```
l_context_getLabel(navigator, id)
```

Arguments

navigator	navigator hanlde
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_context_ids(navigator)
```

Arguments

navigator	navigator hanlde

Details

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

See Also

l_context_delete, l_context_add_context2d, l_context_add_geodesic2d, l_context_add_slicing2d, l_context_getLabel, 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_context_relabel(navigator, id, label)
```

Arguments

navigator	navigator hanlde
id	context id
label	context label shown

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_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 ‘sources‘ 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
                )

   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)
   l_copyStates(p, pp)  # makes no copy (not one to one)

   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

```
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. `".l0.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)))
nav_new['from']

# 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']

}
```

---

l_currentindex *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

```
l_currentindex(widget)
```

Arguments

widget	widget path as a string or as an object handle

Details

For more details see `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

l_bind_item, l_currenttags

Examples

```
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'))
}

l_bind_item(p, tags='model&&point', event='<Enter>',
            callback=function(W) {printEntered(W)})

l_bind_item(p, tags='model&&point', event='<Leave>',
            callback=function(W) {printLeave(W)})

}
```

---

l_currenttags *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	widget path as a string or as an object handle

Details

For more details see `l_help("learn_R_bind.html#item-bindings")`

Value

vector with item tags of visual

See Also

`l_bind_item`, `l_currentindex`

Examples

```
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))
}
```

---

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

```
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

```
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.

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"),
  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"),
  parent = NULL,
  ...
)
```

Arguments

widget	A loon widget
by	loon plot can be separated by some variables into mutiple 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 color

labelForeground
: Label foreground color

labelBorderwidth
: Label border width

labelRelief
: Label relief

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.

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

```
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$Species,
                  scaling = "observation")
fs <- l_facet(s, layout = "wrap", by = iris$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

```
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

```
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. `".l0.plot"`)

Details

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

See Also

`l_create_handle` `l_loonWidgets`

Examples

```
## 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

```
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

---

l_getLinkedStates *Query the States that are Linked with 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 in the documentation for l_setLinkedStates.

Usage

```
l_getLinkedStates(widget)
```

Arguments

widget	widget path as a string or as an object handle

Value

vector with state names that are linked states

See Also

l_setLinkedStates

`l_getLocations` *For the target compound loon plot, determines location (only and excluding the grobs) arguments to pass to 'gridExtra::arrangeGrob()'*

Description

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

Usage

```
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)
```

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 TODO
}
```

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

Examples

```
l_getOption("background")
```

l_getOptionNames *Get the names of all loon display options*

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)
```

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_getSavedStates` *Retrieve saved plot states from the named file.*

Description

`l_getSavedStates` reads a file created by `l_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 `l_getSavedStates` will return a list of the plots with each list item being the saved states of the corresponding plots.

Usage

```
l_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

`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$color
#
# The result is that p_new looks like p did
# (after your interactive exploration)
# and can now be plotted as part of the document
plot(p_new)
#
# For compound plots, the info_states are saved for each plot
pp <- l_pairs(iris)
myPairsFile <- tempfile("myPairsPlot", fileext = ".rds")
#
# Save the names states of pp
l_saveStates(pp,
             states = c("color", "active", "selected"),
             file = myPairsFile)
pairs_info <-  l_getSavedStates(myPairsFile)
#
# For compound plots, the info states for all constitutent
# plots are saved.  The result is a list of class "l_savedStates"
# whose elements are the named plots as "l_savedStates"
# themselves.
#
# The names of the plots which were saved
names(pairs_info)
#
# And the names of the info states whose values were saved for
# the first plot
names(pairs_info$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_getScaledData` *Data Scaling*

Description

Scaling the data set

Usage

```
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

---

l_get_arrangeGrobArgs *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.*

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

Inpectors 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()
}
```

l_glyphs_inspector_image

Create a 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()
}
```

l_glyphs_inspector_pointrange

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

Inpectors 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

```
if(interactive()){

i <- l_glyphs_inspector_serialaxes()
}
```

`l_glyphs_inspector_text` *Create a Text Glyph Inspector*

Description

Inpectors provide graphical user interfaces to oversee and modify plot states

Usage

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

Arguments

`parent`	parent widget path
`...`	state arguments

Value

widget handle

See Also

`l_create_handle`

Examples

```
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:

Type	R creator function
Text	`l_glyph_add_text`
Serialaxes	`l_glyph_add_serialaxes`
Pointranges	`l_glyph_add_pointrange`
Images	`l_glyph_add_image`
Polygon	`l_glyph_add_polygon`

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 observations. See in the examples.

Currently loon does not support compound glyphs. However, it is possible to cunstruct 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

```
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',
    rep(text_glyph, 3)
)
}
```

---

l_glyph_add.default *Default method for adding non-primitive glyphs*

Description

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

Usage

```
## 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 transparancy.

Usage

```
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(), l_primitiveGlyphs()

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.

showArea	boolean, show a filled point or just the outline point
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_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()

Examples

```
if(interactive()){

p <- l_plot(x = 1:3, color = c('red', 'blue', 'green'), showScales=TRUE)
g <- l_glyph_add_pointrange(p, ymin=(1:3)-(1:3)/5, ymax=(1:3)+(1:3)/5)
p['glyph'] <- g
}
```

---

l_glyph_add_polygon *Add a Polygon Glyph*

Description

Add one polygon per scatterplot point.

Usage

```
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), one list element for each scatterplot point.
y	nested list of y-coordinates of polygons, one list element for each scatterplot point.

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 l_glyphs 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,
      0.474503025064823, 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,
      0.259651397291847, 0.259651397291847, 0.948934024776722,
      0.948934024776722, 0.259651397291847, 0.259651397291847,
      -0.258931143762604, -0.258931143762604, -0.950374531835206)
x_hexagon <-
    c(0.773552290406223, 0, -0.773552290406223, -0.773552290406223,
      0, 0.773552290406223)
y_hexagon <-
    c(0.446917314894843, 0.894194756554307, 0.446917314894843,
      -0.447637568424085, -0.892754249495822, -0.447637568424085)

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

```
gl <- l_glyph_add_polygon(p, x = list(x_star, x_cross, x_hexagon),
                          y = list(y_star, y_cross, y_hexagon))

p['glyph'] <- gl

gl['showArea'] <- FALSE
}
```

`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)

axesColor	color of axes
showEnclosing	boolean, circle (axesLayout=radial) or sqaure (axesLayout=parallel) to show bounding box/circle of the glyph (or showing unit circle or rectangle with height 1 if scaling=none)
bboxColor	color of bounding box/circle
label	label of a glyph (currently shown only in the glyph inspector)
...	state arguments

See Also

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 <- with(olive, l_plot(oleic, stearic, color=Area))
gs <- l_glyph_add_serialaxes(p, data=olive[,-c(1,2)], showArea=FALSE)
p['glyph'] <- gs
}
```

---

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 observartion. 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_serialaxes(), 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

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(), l_glyph_getType(), l_glyph_ids(), l_glyph_relabel(), l_primitiveGlyphs()

---

l_glyph_getType *Get Glyph Type*

Description

Query the type of a glyph

Usage

```
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

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_ids(), l_glyph_relabel(), l_primitiveGlyphs()

---

l_glyph_ids *List glyphs ids*

Description

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

Usage

```
l_glyph_ids(widget)
```

Arguments

widget	widget path as a string or as an object handle

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(), l_primitiveGlyphs()

---

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(), 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_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_relabel(p, g, "Species")
}
```

`l_graph` *Generic funtction to create an interactive graph display*

Description

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

Usage

```
l_graph(nodes, ...)

## S3 method for class 'graph'
l_graph(nodes, ...)

## S3 method for class 'loongraph'
l_graph(nodes, ...)

## Default S3 method:
l_graph(nodes = "", from = "", to = "", isDirected = FALSE, parent = NULL, ...)
```

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

```
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

```
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

```
## 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 creat 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 methiod

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

```
## 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 methiod

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

```
## 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 methiod

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 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 oder 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 postion 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 the 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

l_graphswitch_reorder *Reorder the Positions of the Graphs in the Graph List*

Description

Define a new graph order in the graph list.

Usage

```
l_graphswitch_reorder(widget, ids)
```

Arguments

widget	graphswitch widget handle (or widget path)
ids	vector with all graph ids from the graph widget. Use l_graphswitch_ids to query the ids.

See Also

l_graphswitch

l_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

```
l_graphswitch_set(widget, id)
```

Arguments

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

See Also

l_graphswitch

l_graph_inspector *Create a Graph Inspector*

Description

Inpectors 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

Inpectors 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_analysis()
}
```

`l_graph_inspector_navigators` *Create a Graph Navigator Inspector*

Description

Inpectors provide graphical user interfaces to oversee and modify plot states

Usage

```
l_graph_inspector_navigators(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()
}
```

l_help — *Open a browser with loon's combined (TCL and R) documentation website*

Description

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

Usage

```
l_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, l_web for R manual or web R manual

Examples

```
## Not run:
l_help()
l_help("learn_R_intro")
l_help("learn_R_display_hist")
l_help("learn_R_bind")
# jump to a section
l_help("learn_R_bind.html#list-reorder-delete-bindings")

## End(Not run)
```

l_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

```
l_hexcolor(color)
```

Arguments

color	a vector with color names

Value

a character vector with the 12 digit hexadecimal color strings.

Examples

```
if(interactive()){

p <- l_plot(1:2)
p['color'] <- 'red'
p['color']

l_hexcolor('red')
}
```

---

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)) < 10L, ...)

## S3 method for class 'character'
l_hist(x, showFactors = length(unique(x)) < 10L, ...)

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

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

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

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

## S3 method for class 'array'
l_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.
yshows	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 minumum 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 draw the factor names

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

```
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

Inpectors provide graphical user interfaces to oversee and modify plot states

Usage

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

Arguments

`parent`	parent widget path
`...`	state arguments

Value

widget handle

See Also

`l_create_handle`

Examples

```
if(interactive()){

i <- l_hist_inspector()
}
```

`l_hist_inspector_analysis`
Create a Histogram Analysis Inspector

Description

Inpectors provide graphical user interfaces to oversee and modify plot states

Usage

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

Arguments

parent	parent widget path
...	state arguments

Value

widget handle

See Also

l_create_handle

Examples

```
if(interactive()){

i <- l_hist_inspector_analysis()
}
```

---

l_imageviewer *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

```
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)))

}
```

---

l_image_import_array *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=withe, 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("l_ng_images_frey_LLE")

## End(Not run)
```

`l_image_import_files` *Import Image Files as Tk Image Objects*

Description

Note that the supported image file formats depend on whether the `Img` Tk extension is installed.

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. `'.l0.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	object that should be layered
...	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.

Type	Description	Creator Function
group	a group can be a parent of other layers	l_layer_group
polygon	one polygon	l_layer_polygon
text	one text string	l_layer_text

line	one line (i.e. connected line segments)	l_layer_line
rectangle	one rectangle	l_layer_rectangle
oval	one oval	l_layer_oval
points	n points (filled) circle	l_layer_points
texts	n text strings	l_layer_text
polygons	n polygons	l_layer_polygons
rectangles	n rectangles	l_layer_rectangles
lines	n sets of connected line segments	l_layer_lines

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
l_layer_ids	List layer ids
l_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
l_layer_getParent	Get parent layer id of a layer
l_layer_getChildren	Get children of a group layer
l_layer_index	Get the order index of a layer among its siblings
l_layer_printTree	Print out the layer tree
l_layer_move	Move a layer
l_layer_lower	Switch the layer place with its sibling to the right
l_layer_raise	Switch the layer place with its sibling to the left
l_layer_demote	Moves the layer up to be a left sibling of its parent
l_layer_promote	Moves the layer to be a child of its right group layer sibling
l_layer_hide	Set the layers visibility flag to `FALSE`
l_layer_show	Set the layers visibility flag to `TRUE`
l_layer_isVisible	Return visibility flag of layer
l_layer_layerVisibility	Returns logical value for whether layer is actually seen
l_layer_groupVisibility	Returns `all`, `part` or `none` for expressing which part of the layers children are visible.
l_layer_delete	Delete a layer. If the layer is a group move all its children layers to the layers parent.
l_layer_expunge	Delete layer and all its children layer.
l_layer_getLabel	Get layer label.
l_layer_relabel	Change layer label.
l_layer_bbox	Get the bounding box 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

```
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.foo <- function(widget, x) {
    x$widget <- widget
    id <- do.call('l_layer_polygon', x)
    return(id)
}

p <- l_plot()

obj <- newFoo(x=c(1:6,6:2), y=c(3,1,0,0,1,3,3,5,6,6,5), color='yellow')

id <- l_layer(p, obj)

l_scaleto_world(p)

}
```

---

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

widget	widget path as a string or as an object handle
x	object from density of class "density"
...	additional arguments, often state definition for the basic layering function

Value

layer object handle, layer id

See Also

density, l_layer

Examples

```
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)

}
```

---

l_layer.Line *Layer line in Line object*

Description

Methods to plot map data defined in the sp package

Usage

```
## S3 method for class 'Line'
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

```
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

```
## 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

```
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

```
## S3 method for class 'map'
l_layer(
  widget,
  x,
  color = "",
  linecolor = "black",
```

```
  linewidth = 1,
  label,
  parent = "root",
  index = 0,
  asSingleLayer = TRUE,
  ...
)
```

Arguments

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	fill color, if empty string "", then the fill is transparant
linecolor	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 methiod

Value

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

Examples

```
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']
}

}
```

`l_layer.Polygon` *Layer polygon in Polygon object*

Description

Methods to plot map data defined in the sp package

Usage

```
## 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

```
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.Polygons` *Layer polygons in Polygons object*

Description

Methods to plot map data defined in the sp package

Usage

```
## 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-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

```
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

```
## 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-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

```
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.SpatialLinesDataFrame

Layer lines in SpatialLinesDataFrame object

Description

Methods to plot map data defined in the sp package

Usage

```
## 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

```
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.SpatialPoints *Layer points in SpatialPoints object*

Description

Methods to plot map data defined in the sp package

Usage

```
## 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

```
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.SpatialPointsDataFrame

Layer points in SpatialPointsDataFrame object

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	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

```
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

```
## 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

See Also

sp, l_layer

Examples

```
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.SpatialPolygonsDataFrame

Layer polygons in SpatialPolygonDataFrame

Description

Methods to plot map data defined in the sp package

Usage

```
## 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-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

```
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_layers_inspector *Create a Layers Inspector*

Description

Inpectors 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

```
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

```
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

```
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')

}
```

---

l_layer_contourLines *Layer Contour Lines*

Description

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

Usage

```
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 **iff** 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

```
if(interactive()){

p <- l_plot()
x <- 10*1:nrow(volcano)
y <- 10*1:ncol(volcano)
lcl <- l_layer_contourLines(p, x, y, volcano)
l_scaleto_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"))
  })
}

}
```

`l_layer_delete` *Delete a layer*

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

Examples

```
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)

l_layer_printTree(p)
l_layer_demote(p, l1)
l_layer_printTree(p)
l_layer_demote(p, l1)
l_layer_printTree(p)

}
```

`l_layer_expunge` *Delete a layer and all its descendants*

Description

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

Usage

```
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

```
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

```
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

```
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)

}
```

`l_layer_getLabel` *Get 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_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)

}
```

l_layer_getParent *Get parent layer id of a layer*

Description

The toplevel parent is the 'root' layer.

Usage

```
l_layer_getParent(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

See Also

l_layer, l_layer_getChildren

Examples

```
if(interactive()){

p <- with(iris, l_plot(Sepal.Length ~ Sepal.Width, color=Species))

l_layer_getParent(p, 'model')

}
```

l_layer_getType *Get layer type*

Description

To see the manual page of l_layer for all the primitive layer types.

Usage

```
l_layer_getType(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

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

```
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 decendants

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

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 ancesters visibile 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.
...	argumnets 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 rectangles layer

Examples

```
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

```
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

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 ancesters visibile 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

```
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_ids *List ids of layers in Plot*

Description

Every layer within a display has a unique id. This function returns a list of all the layer ids for a widget.

Usage

```
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

```
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=range(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

```
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

```
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 ancesters visibile 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

```
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

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 ancesters visibile 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

```
l_layer_line(
  widget,
  x,
  y = NULL,
  color = "black",
  linewidth = 1,
  dash = "",
  label = "line",
  parent = "root",
  index = 0,
  ...
)
```

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
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_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)

}
```

---

l_layer_lines *Layer lines*

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_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

Examples

```
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)

}
```

`l_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

```
l_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

```
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)

}
```

---

l_layer_move *Move a layer*

Description

The postition 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

```
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

```
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

```
l_layer_oval(
  widget,
  x,
  y,
  color = "gray80",
  linecolor = "black",
  linewidth = 1,
  label = "oval",
  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 transparant
`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_oval(p, c(1,5), c(2,12), color='steelblue')
l_configure(p, panX=0, panY=0, deltaX=20, deltaY=20)

}
```

---

l_layer_points *Layer points*

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

Usage

```
l_layer_points(
  widget,
  x,
  y = NULL,
  color = "gray60",
  size = 6,
  label = "points",
  parent = "root",
```

```
  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 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

---

l_layer_polygon *Layer a polygon*

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_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 transparant
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()){
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=range(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_polygons` *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,
```

```
  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

```
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

```
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

```
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

```
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

```
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)

}
```

`l_layer_rasterImage` *Layer a Raster Image*

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

```
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'
`...`	argumnets 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 rectangles layer

Examples

```
if(interactive()){

plot(1,1, xlim = c(0,1), ylim=c(0,1))
mat <- matrix(c(0,0,0,0, 1,1), ncol=2)
rasterImage(mat, 0,0,1,1, interpolate = FALSE)

p <- l_plot()
l_layer_rasterImage(p, mat, 0,0,1,1)
l_scaleto_world(p)

image <- as.raster(matrix(0:1, ncol = 5, nrow = 3))
p <- l_plot(showScales=TRUE, background="thistle", useLoonInspector=FALSE)
l_layer_rasterImage(p, image, 100, 300, 150, 350, interpolate = FALSE)
l_layer_rasterImage(p, image, 100, 400, 150, 450)
l_layer_rasterImage(p, image, 200, 300, 200 + 10, 300 + 10,
   interpolate = FALSE)
l_scaleto_world(p)

# from examples(rasterImage)

# set up the plot region:
op <- par(bg = "thistle")
plot(c(100, 250), c(300, 450), type = "n", xlab = "", ylab = "")
rasterImage(image, 100, 300, 150, 350, interpolate = FALSE)
rasterImage(image, 100, 400, 150, 450)
rasterImage(image, 200, 300, 200 + 10, 300 + 10,
           interpolate = FALSE)

}
```

---

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 transparant
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='steelblue')
l_scaleto_layer(l)

}
```

`l_layer_rectangles` *Layer rectangles*

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_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 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_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

```
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)

}
```

---

l_layer_show *Show or unhide a Layer*

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

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 ancesters visibile 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

```
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)

}
```

---

l_layer_smooth *Layer a smooth line for* loon

Description

Display a smooth line layer

Usage

```
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, eg. 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

```
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

```
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")

}
```

`l_layer_texts` *Layer texts*

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

```
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

```
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)
}
```

---

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

```
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_basePathsl_compoundPaths l_getFromPath

Examples

```
if(interactive()){
l_plot(iris)
l_hist(iris)
l_hist(mtcars)
l_pairs(iris)
# The following will not be loonWidgets (neither is the inspector)
tt <- 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)
              }
              )
}
```

---

l_loon_inspector *Create a loon inspector*

Description

The loon inspector is a singleton widget that provids 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.
...	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

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	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

```
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(1,1,1,1)*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,],
```

```
                                    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 periodicity
#
# First some itemlabels
elementLabels <- with(elements,
                      paste("   ", Number, Symbol, "\n",
                            "   ", Name, "\n",
                            "   ", Mass
                            )
                      )

periodicPlot  <- 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


}
```

`l_move_grid` *Arrange Points or Nodes on a Grid*

Description

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

Usage

```
l_move_grid(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 wile 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

---

`l_move_halign` *Horizontally Align Points or Nodes*

Description

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

Usage

```
l_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 wile 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

---

`l_move_hdist` *Horizontally Distribute Points or Nodes*

Description

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

Usage

```
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 wile 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

`l_move_jitter` *Jitter Points Or Nodes*

Description

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

Usage

```
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 wile 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`

`l_move_reset` *Reset Temporary Point or Node Locations to the x and y states*

Description

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

Usage

```
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 wile 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`

`l_move_valign` *Vertically Align Points or Nodes*

Description

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

Usage

```
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 wile 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`

`l_move_vdist` *Vertically Distribute Points or Nodes*

Description

Scatterplot and graph displays support interactive temporary relocation of single points (nodes for graphs).

Usage

```
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 wile 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`

`l_navgraph` *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)

}
```

`l_navigator_add` *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

```
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 descriptoin above for `from`
`proportion`	see descriptoin above for `from`
`color`	of navigator
`...`	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`

l_navigator_delete *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

l_navigator_getLabel *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

```
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

```
l_navigator_ids(widget)
```

Arguments

widget	graph widget

See Also

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.

See Also

l_navigator_add

`l_navigator_walk_forward` *Have the Navigator Walk Forward on the Current Path*

Description

Animate a navigator by having it walk on a path on the graph

Usage

```
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

l_navigator_add

`l_navigator_walk_path` *Have the Navigator Walk a Path on the Graph*

Description

Animate a navigator by having it walk on a path on the graph

Usage

```
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

See Also

l_navigator_add

---

l_nDimStateNames *N dimensional state names access*

Description

Get all n dimensional state names

Usage

```
l_nDimStateNames(loon_plot)
```

Arguments

loon_plot	A loon widget or the class name of a loon plot

Examples

```
if(interactive()){

p <- l_plot()
l_nDimStateNames(p)
l_nDimStateNames("l_plot")

}
```

---

l_nestedTclList2Rlist *Convert a Nested Tcl List to an R List*

Description

Helper function to work with R and Tcl

Usage

```
l_nestedTclList2Rlist(tclobj, transform = function(x) {
    as.numeric(x)
})
```

Arguments

tclobj	a tcl object as returned by tcl or .Tcl.
transform	a function to transfrom the string output to another data type

Value

a nested R list

See Also

l_Rlist2nestedTclList

Examples

```
tclobj <- .Tcl('set a {{1 2 3} {2 3 4 4} {3 5 3 3}}')
l_nestedTclList2Rlist(tclobj)
```

---

l_ng_plots *2d navigation graph setup with with dynamic node fitering using a scatterplot matrix*

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

```
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

`l_ng_plots.default` *Select 2d spaces with variable associated measures displayed in scatterplot matrix*

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

```
## Default S3 method:
l_ng_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#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

`l_ng_plots`, `l_ng_plots.measures`, `l_ng_plots.scagnostics`, `measures1d`, `measures2d`, `scagnostics2d`, `l_ng_ranges`

Examples

```
if(interactive()){

## Not run:
n <- 100
dat <- 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)

}
```

`l_ng_plots.measures` *2d Navigation Graph Setup with dynamic node fitering using a scatterplot matrix*

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

```
## S3 method for class 'measures'
l_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, l_ng_plots, l_ng_ranges

Examples

```
if(interactive()){

## Not run:
# 2d measures
scags <- scagnostics2d(oliveAcids, separator='**')
scags()
ng <- l_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 <- l_ng_plots(m1d, color=iris$Species)

# with only one measure
nav <- l_ng_plots(measures1d(oliveAcids, sd))

# with two measures
nav <- l_ng_plots(measures1d(oliveAcids, sd=sd, mean=mean))
```

```
## End(Not run)

}
```

`l_ng_plots.scagnostics` *2d Navigation Graph Setup with dynamic node fitering based on scagnostic measures and by using a scatterplot matrix*

Description

This method is useful when working with objects from the `scagnostics` function from the scagnostics R package. In order to dynamically re-calcultate the scagnostic measures for a subset of the data use the `scagnostics2d` measures creature function.

Usage

```
## S3 method for class 'scagnostics'
l_ng_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

`l_ng_plots`, `l_ng_plots.default`, `l_ng_plots.measures`, `measures1d`, `measures2d`, `scagnostics2d`, `l_ng_ranges`

Examples

```
if(interactive()){

## Not run:
library(scagnostics)
  scags <- scagnostics::scagnostics(oliveAcids)
  l_ng_plots(scags, oliveAcids, color=olive$Area)
```

```
## End(Not run)

}
```

`l_ng_ranges` *2d navigation graph setup with with dynamic node fitering 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

```
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`

`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

```
## 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

```
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)
)
```

```
nav <- l_ng_ranges(m1d, dat)

}
```

`l_ng_ranges.measures` *2d Navigation Graph Setup with dynamic node fitering using a slider*

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

```
## S3 method for class 'measures'
l_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#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

`measures1d`, `measures2d`, `scagnostics2d`, `l_ng_ranges`, `l_ng_plots`

Examples

```
if (interactive()){

# 2d measures
# s <- scagnostics2d(oliveAcids)
# nav <- l_ng_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 fitering 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-calcultate the scagnostic measures for a subset of the data use the `scagnostics2d` measures creature function.

Usage

```
## S3 method for class 'scagnostics'
l_ng_ranges(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

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`

Examples

```
## Not run:
if (requireNamespace("scagnostics", quietly = TRUE)) {
  s <- scagnostics::scagnostics(oliveAcids)
  ng <- l_ng_ranges(s, oliveAcids, color=olive$Area)
}

## End(Not run)
```

`l_pairs` *An interactive scatterplot matrix*

Description

Function creates a scatterplot matrix using loon's scatterplot widgets

Usage

```
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,
  span = 10L,
  ...
)
```

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.
span	How many column/row occupies for each widget
...	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"),
  parent = NULL,
  ...
)

## 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"),
  linecolor = 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"),
  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 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 l_primitiveGlyphs().
- the string names of constructed glyphs:
  - text as glyphs: see l_glyph_add_text()
  - point ranges: see l_glyph_add_pointrange()
  - polygons: see l_glyph_add_polygon()
  - parallel coordinates: see l_glyph_add_serialaxes()
  - star or radial axes: see l_glyph_add_serialaxes()
  - 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.

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.

tk_title — provides an alternative window name to Tk's wm title. If NULL, stl will be used.

linecolor — 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_navgraph).

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 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 loonGrob, grid.loon, plot.loon.

Density layer l_layer.density

Map layer l_layer, l_layer.map, map

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

Examples

```
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 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
# 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 <- 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()
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.)
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 `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 `l_primitiveGlyphs()`.
- the string names of constructed glyphs:
  - `text` as `glyphs`: see `l_glyph_add_text()`
  - `point ranges`: see `l_glyph_add_pointrange()`
  - `polygons`: see `l_glyph_add_polygon()`
  - `parallel coordinates`: see `l_glyph_add_serialaxes()`
  - `star` or `radial axes`: see `l_glyph_add_serialaxes()`
  - 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.

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")
)

# 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 desribed 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.
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.
linkingGroup	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()).
linkingKey	an n-dimensional character vector of unique entries. The entries identify which points match other points in other plots. Default is c("0","1",...,"n-1") (for numerical n).
itemLabel	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 "tool tip". Note that all objects drawn in any layer of a plot (e.g. maps) will have an itemLabel.
showItemLabels	a logical (default FALSE) which indicates whether the "tool tip" itemLabel is to be displayed whenever the mouse hovers over it.
color	colours of points (default "grey60"); colours are repeated until matching the number points,

`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 `l_primitiveGlyphs()`.

the string names of constructed glyphs text as glyphs see `l_glyph_add_text()`

point ranges see `l_glyph_add_pointrange()`

polygons see `l_glyph_add_polygon()`

parallel coordinates see `l_glyph_add_serialaxes()`

star or radial axes see `l_glyph_add_serialaxes()`

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)

`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.

`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 `l_plot` for more details about the interaction gestures.

See Also

the demos `demo(l_glyph_sizes,package = "loon")`, `demo(l_glyphs,package = "loon")`, and `demo(l_make_glyphs,package = "loon")`.

Examples

```
## 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")
 p1["size"] <- 10
 p1["glyph"][versicolor]<- "csquare"
 p1["minimumMargins"][1] <- 100

## End(Not run)
```

`l_plot_inspector` *Create a Scatterplot Inspector*

Description

Inpectors 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

Inpectors 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 component, and the remainder. If `NULL`, the default, `ylabel` will be `c("data","trend","seasonality","rema` 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 l_plot() which constructs each loon scatterplot 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

l_plot.stl, l_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

```
l_predict(model, ...)

## Default S3 method:
l_predict(model, ...)

## S3 method for class 'lm'
l_predict(
  model,
  newdata = NULL,
  interval = c("none", "confidence", "prediction"),
  level = 0.95,
  ...
)
```

```
## S3 method for class 'nls'
l_predict(
  model,
  newdata = NULL,
  interval = c("none", "confidence", "prediction"),
  level = 0.95,
  ...
)

## 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
...	arguments passed in predict
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

```
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).

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).

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

Value

A character vector of the names of all primitive glyphs in loon.

See Also

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_ids(), l_glyph_relabel()

---

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

```
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

```
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

```
l_Rlist2nestedTclList(x)
```

Arguments

x	a list of vectors

Value

a string that represents the tcl nested list

See Also

l_nestedTclList2Rlist

Examples

```
x <- list(c(1,3,4), c(4,3,2,1), c(4,3,2,5,6))
l_Rlist2nestedTclList(x)
```

---

l_saveStates *Save the info states of a loon plot widget in a file*

Description

l_saveStates uses saveRDS() to save the info states of a loon plot as an 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

```
l_saveStates(
  p,
  states = c("color", "active", "selected", "linkingKey", "linkingGroup"),
  file = stop("missing name of file"),
  ...
)
```

Arguments

p	the 'l_plot' object whose info states are to be saved.
states	either the logical 'TRUE' or a character vector of info states to be saved. Default value 'c("color", "active", "selected", "linkingKey", "linkingGroup")' consists of 'n' dimensional states that are common to many 'l_plot's and which are most important to reconstruct the plot's display in any summary. If 'states' is the logical 'TRUE', by 'names(p)' are saved.
file	is a string giving the file name where the saved information' will be written (custom suggests this file name end in the suffix '.rds'.
...	further arguments passed to saveRDS().

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

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 constitutent
# 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

```
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 `NA`s, 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

```
##### Iris data
#
# All variables (including Species as a factor)
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)})

# 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-NAs in each column
apply(result_sphere, 2, FUN = function(x) {mean(x, na.rm = TRUE)})
```

---

l_scaleto_active *Change Plot Region to Display All Active Data*

Description

The function modifies the zoomX, zoomY, panX, and panY so that all active data points are displayed.

Usage

```
l_scaleto_active(widget)
```

Arguments

widget	widget path as a string or as an object handle

---

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

```
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. '.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

```
l_scaleto_plot(widget)
```

Arguments

widget	widget path as a string or as an object handle

l_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

```
l_scaleto_selected(widget)
```

Arguments

widget	widget path as a string or as an object handle

l_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

```
l_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.

layout	layout facets as 'grid', 'wrap' or 'separate'
andrews	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 (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).
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

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

- 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 date 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).
```

```
#        Then scaling can always be changed via the inspector.

}
```

`l_serialaxes_inspector` *Create a Serialaxes Inspector*

Description

Inpectors 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, 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 aspect argument is missing then x and y can be specified and the aspect ratio is calculted usding y/x.
y	see description for x argument above

Examples

```
## 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 pallettes 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

l_setColorList, 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()
l_setColorList(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
l_setColorList(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)) {
  p_custom <- 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.

Usage

```
l_setColorList_baseR()
```

See Also

l_setColorList, l_setColorList_loon, l_setColorList_ColorBrewer, l_setColorList_hcl, l_setColorList_baseR, l_setColorList_ggplot2

---

l_setColorList_ColorBrewer

Set loon's color mapping list to the colors from ColorBrewer

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

l_setColorList, l_setColorList_loon, l_setColorList_ColorBrewer, l_setColorList_hcl, l_setColorList_baseR, l_setColorList_ggplot2

Examples

```
if (interactive()){

## Not run:
if (requireNamespace("RColorBrewer", quietly = TRUE)) {
  RColorBrewer::display.brewer.all()
}
```

```
## End(Not run)

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

```
l_setColorList_ggplot2()
```

See Also

`l_setColorList`, `l_setColorList_loon`, `l_setColorList_ColorBrewer`, `l_setColorList_hcl`, `l_setColorList_baseR`, `l_setColorList_ggplot2`

`l_setColorList_hcl` *Set loon's color mapping list to the colors from hcl color wheen*

Description

Loon's color list is used to map nominal values to colors. See the documentation for `l_setColorList`.

Usage

```
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.

Details

Samples equally distant colors from the hcl color wheel. See the documentation for `hcl` for more information.

See Also

`l_setColorList`, `l_setColorList_loon`, `l_setColorList_ColorBrewer`, `l_setColorList_hcl`, `l_setColorList_baseR`, `l_setColorList_ggplot2`

---

l_setColorList_loon *Set loon's color mapping list to the colors from loon defaults*

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_setColorList`, `l_setColorList_loon`, `l_setColorList_ColorBrewer`, `l_setColorList_hcl`, `l_setColorList_baseR`, `l_setColorList_ggplot2`

---

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

Display	Default *used linkable* states
scatterplot	`selected`, `color`, `active`, `size`
histogram	`selected`, `color`, `active`
serialaxes	`selected`, `color`, `active`
graph	`selected`, `color`, `active`, `size`

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

`option`	the name of the option being set
`value`	the value to be assigned to the option. If value == "default", then the option is set to loon's default value for it.

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

l_size *Query Size of a Plot Display*

Description

Get the width and height of a plot in pixels

Usage

```
l_size(widget)
```

Arguments

widget	widget path as a string or as an object handle

Value

Vector width width and height in pixels

See Also

l_resize, l_size<-

l_size<- *Resize Plot Widget*

Description

Resizes the toplevel widget to a specific size. This setter function uses l_resize.

Usage

```
l_size(widget) <- value
```

Arguments

widget	widget path as a string or as an object handle
value	numeric vector of length 2 with width and height in pixels

See Also

l_resize, l_size

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

```
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()`

l_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

```
l_subwin(parent, name = "w")
```

Arguments

`parent`	parent widget path
`name`	child name

Value

widget path name as a string

l_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

```
l_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` *loon tk top level*

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,
```

```
                row = 10,
                column = 0,
                rowspan = 1,
                columnspan = 1,
                sticky="nesw")
  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=200, height=200)

  # 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 conver 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 at https://great-northern-diver.github.io/loon/.

Usage

```
l_web(page = "index", directory = c("home", "reference", "articles"), ...)
```

Arguments

page	relative path to a page, the .html part may be omitted
directory	if "home" then page is ignored and the browser will open at the home page of the official loon documentation website at https://great-northern-diver.github.io/loon/. If page refers to a loon manual reference, then directory must be "reference"; if page refers to the name of a vignette file, then directory should be "articles"
...	arguments forwarded to browseURL, e.g. to specify a browser

See Also

l_help,help, vignette

Examples

```
## Not run:
l_web()
#
vignette("introduction", package = "loon")
# or
l_web(page = "introduction", directory = "articles")
#
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

```
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

Inpectors provide graphical user interfaces to oversee and modify plot states

Usage

```
l_worldview(parent = NULL, ...)
```

Arguments

parent	parent widget path
...	state arguments

Value

widget handle

See Also

l_create_handle

Examples

```
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

```
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')
```

`measures2d` *Closure of Two Dimensional Measures*

Description

Function creates a 2d measures object that can be used with `l_ng_plots` and `l_ng_ranges`.

Usage

```
measures2d(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

```
m <- measures2d(oliveAcids, separator='*', cov=cov, cor=cor)
m
m()
m(keep=olive$palmitic>1360)
m('data')
m('grid')
m('measures')
```

`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

https://www.statcan.gc.ca/

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

```
## 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

```
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=':')
```

`olive` *Fatty Acid Composition of Italian Olive Oils*

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:

Region	Area
North	North-Apulia, South-Apulia, Calabria, Sicily
South	East-Liguria, West-Liguria, Umbria
Sardinia	Coastal-Sardinia, Inland-Sardinia

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

Forina, M., Armanino, C., Lanteri, S., and Tiscornia, E. (1983) "Classification of Olive Oils from their Fatty Acid Composition", in Food Research and Data Analysis (Martens, H., Russwurm, H., eds.), p. 189, Applied Science Publ., Barking.

Wikipedia https://en.wikipedia.org/

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)
  loonPlot['showGuides'] <- TRUE
  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

```
if (requireNamespace("Rgraphviz", quietly = TRUE)) {
  g <- loongraph(letters[1:4], letters[1:3], letters[2:4], FALSE)
  plot(g)
}
```

print.l_layer *Print a summary of a loon layer object*

Description

Prints the layer label and layer type

Usage

```
## S3 method for class 'l_layer'
print(x, ...)
```

Arguments

x	an l_layer object
...	additional arguments are not used for this methiod

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

```
## S3 method for class 'measures1d'
print(x, ...)
```

Arguments

x	measures1d 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

```
## 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

```
scagnostics2d(
  data,
 scagnostics = c("Clumpy", "Monotonic", "Convex", "Stringy", "Skinny", "Outlying",
    "Sparse", "Striated", "Skewed"),
  separator = ":"
)
```

Arguments

`data`	a data.frame with the data used to calculate the measures
`scagnostics`	vector with valid scanostics meausure 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

```
## Not run:
m <- scagnostics2d(oliveAcids, separator='**')
m
m()
m(olive$palmitoleic > 80)
m('data')
m('grid')
m('measures')

## End(Not run)
```

---

tkcolors *List the valid Tk color names*

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

```
tkcolors()
```

Examples

```
# 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
tohex <- 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")

  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/ 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/

Index