

Package ‘henna’

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Type Package

Title A Versatile Visualization Suite

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Description A visualization suite primarily designed for single-cell RNA-sequencing data analysis applications, but adaptable to other purposes as well. It introduces novel plots to represent two-variable and frequency data and optimizes some commonly used plotting options (e.g., correlation, network, density and alluvial plots) for ease of usage and flexibility.

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centerTitle	<i>Add a centered title to a plot</i>
-------------	---------------------------------------

Description

This function adds a centered title to a ggplot object.

Usage

```
centerTitle(p, title, ...)
```

Arguments

- p A ggplot object.
- title Plot title.
- ... Other arguments passed to ggplot2::element_text.

Value

A ggplot object.

classPlot	<i>Plot item bars grouped by class</i>
-----------	--

Description

This function plots bars for each item while grouping them by class and ordering them.

Usage

```
classPlot(  
  df,  
  title = "Class plot",  
  xLab = "Value",  
  yLab = "Item",  
  legendLab = "Class",  
  palette = "Spectral",  
  labelSize = 2.5,  
  labelColor = "black",  
  decreasing = TRUE,  
  valueCutoff = 0,  
  ...  
)
```

Arguments

df	A data frame with at least three columns, with class, item and value as the first three columns. The latter must be numeric.
title	Plot title.
xLab	Label of x axis.
yLab	Label of y axis.
legendLab	Legend label.
palette	grDevices palette.
labelSize	Label size. Ignored if labelDF is NULL.
labelColor	Label color.
decreasing	Whether to display the bars in decreasing order of length.
valueCutoff	Cutoff used for filtering the input data frame based on the value column. Only values greater than this cutoff will be displayed on the plot.
...	Other arguments passed to centerTitle.

Value

An object of class gg.

Examples

```
df <- data.frame(Class = sample(paste0('C', seq(13))), 25, replace=TRUE),
Item = paste0('I', seq(25)),
Value = runif(25, 0.5, 1))
classPlot(df)

df <- data.frame(Class = sample(paste0('C', seq(13))), 25, replace=TRUE),
Item = sample(paste0('I', seq(21)), 25, replace=TRUE),
Value = runif(25, 0.5, 1))
classPlot(df)
```

connectedComponents *Find the connected components of a graph data frame*

Description

This function finds the connected components of a graph data frame.

Usage

```
connectedComponents(df, colName = "component")
```

Arguments

df	A data frame with two categorical columns representing the edges of a graph.
colName	Name of the connected components column to be added.

Value

A data frame with a column indicating the connected component of each edge.

Examples

```
df <- data.frame(
gene1 = paste0('G', c(1, 2, 6, 7, 8, 9,
11, 25, 32, 17, 18)),
gene2 = paste0('G', c(2, 8, 8, 8, 1, 25,
32, 24, 24, 26, 26))
)
connectedComponents(df)
```

convexHull	<i>Construct the convex hull of a set of points</i>
------------	---

Description

This function constructs the convex hull of a set of points.

Usage

```
convexHull(pointsDF, hullIndices = NULL)
```

Arguments

pointsDF	A data frame with the x and y coordinates of the points.
hullIndices	Precalculated hull indices. Default is NULL: hull indices are not provided, but they are calculated by convexHull.

Details

The points must be provided as a data frame with two columns.

Value

A data frame with two columns representing the points on the convex hull.

Examples

```
pointsDF <- data.frame(a = c(1, 2, 2, 3, 3, 4, 5, 6, 8, 6,  
7, 8, 6, 8, 10, 3, 1),  
b = c(2, 3, 4, 8, 5, 6, 5, 4, 8, 11, 13, 14, 2, 1, 2, 14, 9))  
hull <- convexHull(pointsDF)
```

correlationPlot	<i>Plot a correlation matrix</i>
-----------------	----------------------------------

Description

This function plots a correlation matrix.

Usage

```
correlationPlot(  
  mat,  
  title = "Correlation plot",  
  legendLab = "Correlation",  
  ...  
)
```

Arguments

<code>mat</code>	A numeric matrix or data frame.
<code>title</code>	Plot title.
<code>legendLab</code>	Legend label.
<code>...</code>	Additional parameters passed to <code>tilePlot</code> .

Details

A thin wrapper around `tilePlot`.

Value

An object of class `gg`.

Examples

```
mat <- matrix(runif(100, -1, 1), nrow=10)
colnames(mat) <- paste0('I', seq(10))
mat <- round(cor(mat), 2)
correlationPlot(mat)
```

<code>densityPlot</code>	<i>Create density plot</i>
--------------------------	----------------------------

Description

This function creates a density plot.

Usage

```
densityPlot(
  df,
  title = "Density plot",
  colorScheme = c("sea", "lava", "custom"),
  useSchemeDefaults = FALSE,
  drawNN = TRUE,
  drawScores = FALSE,
  palette = NULL,
  segColor = "plum1",
  pointSize = 0.8,
  pointColor = "red",
  segType = c("dashed", "solid", "dotted", "dotdash", "longdash", "twodash"),
  segWidth = 0.4,
  legendPos = c("right", "none"),
  nGridPoints = 300,
```

```

    expandPerc = 20,
    labelSize = 2.5,
    labelColor = "black",
    labelRepulsion = 1,
    labelPull = 1,
    maxOverlaps = Inf,
    verbose = FALSE,
    ...
)

```

Arguments

<code>df</code>	A data frame with at least two columns, representing the x and y coordinates of the points. A score column can also be provided as the third column. Nearest neighbor information can be provided in the last column as a character vector with elements selected from the rownames.
<code>title</code>	Plot title.
<code>colorScheme</code>	Color scheme.
<code>useSchemeDefaults</code>	Whether to use the default <code>segColor</code> , <code>pointColor</code> and <code>labelColor</code> for scheme. Ignored if <code>colorScheme</code> is set to 'custom'.
<code>drawNN</code>	Whether to draw segments linking each point to its nearest neighbor.
<code>drawScores</code>	Whether to render scores on the plot. If set to TRUE, the third column of the input data frame will be numeric and scores will be taken from there.
<code>palette</code>	Color palette. Used only if color scheme is set to 'custom'.
<code>segColor</code>	Nearest neighbor segment color. Ignored if <code>drawNN</code> is set to FALSE, or if <code>useSchemeDefaults</code> is TRUE and <code>colorScheme</code> is different from 'custom'.
<code>pointSize</code>	Point size.
<code>pointColor</code>	Point color. Ignored if <code>useSchemeDefaults</code> is TRUE and <code>colorScheme</code> is different from 'custom'.
<code>segType</code>	Nearest neighbor segment type. Must choose between 'solid', 'dashed', 'dotted', 'dotdash', 'longdash' and 'twodash'. Ignored if <code>drawNN</code> is set to FALSE.
<code>segWidth</code>	Nearest neighbor segment width. Ignored if <code>drawNN</code> is set to FALSE.
<code>legendPos</code>	Legend position. Choose between 'right' and 'none'.
<code>nGridPoints</code>	Number of grid points in each direction.
<code>expandPerc</code>	Percentage by which the grid will be expanded.
<code>labelSize</code>	Size of labels of strata elements.
<code>labelColor</code>	Label color. Ignored if <code>useSchemeDefaults</code> is TRUE and <code>colorScheme</code> is different from 'custom'.
<code>labelRepulsion</code>	Repulsion strength between labels.
<code>labelPull</code>	Attraction strength between a text label and its data point.
<code>maxOverlaps</code>	Maximum overlaps.
<code>verbose</code>	Whether output should be verbose.
<code>...</code>	Other arguments passed to <code>centerTitle</code> .

Value

An object of class gg.

Examples

```
x <- c(1, 2, 3, 4, 6, 7, 8, 10, 12, 11, 3, 6, 4, 1, 13, 13, 14, 18, 16)
y <- c(1, 3, 1, 4, 3, 2, 8, 2, 1, 11, 8, 8, 10, 14, 13, 11, 11, 12, 15)
z <- round(runif(19, 75, 100), 2)
df <- data.frame(x, y, z)
rownames(df) <- paste0('p', rownames(df))
densityPlot(df)
```

dpColors*Create a palette designed for densityPlot*

Description

This function returns a palette designed for densityPlot.

Usage

```
dpColors(palette = c("sea", "lava"))
```

Arguments

palette One of 'sea' and 'lava'.

Value

A character vector of colors.

hpColors*Create the default hullPlot palette*

Description

This function returns the default palette used by hullPlot.

Usage

```
hpColors()
```

Value

A character vector of colors.

hullPlot	<i>Plot the convex hull of a set of points</i>
----------	--

Description

This function plots the convex hull of a set of points. It can also draw a vertical or a horizontal line (or both), dividing the hull into areas of different colors.

Usage

```
hullPlot(
  pointsDF,
  title = "Hull plot",
  xInt = NULL,
  yInt = NULL,
  borderColor = NULL,
  palette = hpColors(),
  hullWidth = 0,
  xLab = "x",
  yLab = "y",
  legendLabs = paste0("Group ", seq(4)),
  legendPos = "bottom",
  pointShape = 4,
  alpha = 0.2,
  labelDF = NULL,
  labelSize = 2.5,
  labelColor = "black",
  labelRepulsion = 1,
  labelPull = 0,
  maxOverlaps = 10,
  ...
)
```

Arguments

pointsDF	A data frame with the x and y coordinates of the points.
title	Plot title.
xInt	The coordinate where the vertical line intersects the x axis.
yInt	The coordinate where the horizontal line intersects the y axis.
borderColor	The color of the horizontal and vertical dividing lines, if provided. If NULL, no dividing lines will be drawn, though the hull will still be split along these lines (if xInt and/or yInt are not NULL).
palette	Color palette.
hullWidth	Width of the convex hull. If 0 (as default), the convex hull will not be displayed.
xLab	Label of x axis.

yLab	Label of y axis.
legendLabs	Legend labels.
legendPos	Legend position.
pointShape	Point shape.
alpha	Opaqueness level for the colors of the alluvia.
labelDF	Label data frame.
labelSize	Label size. Ignored if labelDF is NULL.
labelColor	Label color. Ignored if labelDF is NULL.
labelRepulsion	Repulsion strength between labels.
labelPull	Attraction strength between a text label and its data point.
maxOverlaps	Maximum overlaps. Ignored if labelDF is NULL.
...	Other arguments passed to centerTitle.

Value

An object of class gg.

Examples

```
pointsDF <- data.frame(x = c(1, 2, 4, 7, 10,
12, 13, 15, 16),
y = c(1, 1, 2, 3, 3, 2,
1, 2, 1))
hullPlot(pointsDF, 'Hull plot', 7, 1.5)
```

isPointOnBoundary	<i>Check if a point is on a polygon boundary</i>
-------------------	--

Description

This function checks if a point P is on a polygon boundary.

Usage

```
isPointOnBoundary(xPoint, yPoint, boundary)
```

Arguments

xPoint	x coordinate of point P.
yPoint	y coordinate of point P.
boundary	A data frame with four columns representing segments comprising the boundary.

Value

Logical; whether the point is on the boundary.

Examples

```
pointsDF <- data.frame(x = c(1, 2, 4, 7, 10,
 12, 13, 15, 16),
y = c(1, 1, 2, 3, 3, 2,
1, 2, 1))

hullIndices <- grDevices::chull(pointsDF[, 1], pointsDF[, 2])
hull <- convexHull(pointsDF, hullIndices)
hullSegments <- pointsToSegments(hull)

isPointOnBoundary(2, 3, hullSegments)
```

isPointOnSeg	<i>Check if a point is on a segment</i>
--------------	---

Description

This function checks if a point P is on a segment AB.

Usage

```
isPointOnSeg(xPoint, yPoint, xStart, yStart, xEnd, yEnd)
```

Arguments

xPoint	x coordinate of point P.
yPoint	y coordinate of point P.
xStart	x coordinate of point A.
yStart	y coordinate of point A.
xEnd	x coordinate of point B.
yEnd	y coordinate of point B.

Value

Logical; whether the point is on the segment.

Examples

```
isPointOnSeg(2, 3, 1, 2, 3, 4)
isPointOnSeg(2, 3, 1, 2, 3, 8)
isPointOnSeg(4, 5, 1, 2, 3, 4)
```

networkPlot

*Plot graph with different colors for connected components***Description**

This function plots the graph of the data frame, using different colors for nodes belonging to different connected components.

Usage

```
networkPlot(
  df,
  title = "Network plot",
  rankCol = "rank",
  edgeScale = 2,
  nodePointSize = 10,
  nodeTextSize = 2.3,
  palette = "Pastel 1",
  ...
)
```

Arguments

df	Data frame.
title	Plot title.
rankCol	Name of the rank column.
edgeScale	Scaling factor used in generating edge weights.
nodePointSize	Point size of graph nodes.
nodeTextSize	Text size of graph nodes.
palette	grDevices palette.
...	Other arguments passed to centerTitle.

Value

An object of class ggraph.

Examples

```
df <- data.frame(gene1 = paste0('G', c(1, 2, 5, 6, 7, 17)),
  gene2 = paste0('G', c(2, 5, 8, 11, 11, 11)),
  rank = c(1, 1, 3, 3, 3, 3))
networkPlot(df)
```

pointsToSegments	<i>Construct a data frame of segments from a data frame of points</i>
------------------	---

Description

This function constructs a data frame of segments from a data frame of points.

Usage

```
pointsToSegments(pointsDF, joinEnds = TRUE)
```

Arguments

pointsDF	A data frame with the x and y coordinates of the points. Each point must appear only once.
joinEnds	Whether to join the last point with the first one.

Value

A data frame of segments represented using four columns (x, y, xEnd, yEnd).

Examples

```
pointsDF <- data.frame(x = c(1, 2, 4, 7, 10,
 12, 13, 15, 16),
y = c(1, 1, 2, 3, 3, 2, 1, 2, 1))

hullIndices <- grDevices::chull(pointsDF[, 1], pointsDF[, 2])
hull <- convexHull(pointsDF, hullIndices)
pointsToSegments(hull)
```

radialPlot	<i>Draw radial plot for a degrees data frame</i>
------------	--

Description

This function draws a radial plot for a degrees data frame, plotting positive integer-valued points over concentric circles, with points located more centrally representing higher values.

Usage

```
radialPlot(
  degreesDF,
  title = "Radial plot",
  degreeLegendTitle = "Degree",
  groupLegendTitle = "Group",
  extraCircles = 0,
  palette = rpColors(length(unique(degreesDF[, 3]))),
  labelSize = 3,
  pointSize = 0.8,
  labelRepulsion = 1,
  labelPull = 0,
  maxOverlaps = 10,
  ...
)
```

Arguments

<code>degreesDF</code>	A data frame with names on the first column and positive integers on the second column.
<code>title</code>	Plot title.
<code>degreeLegendTitle</code>	Legend title corresponding to the positive integer column.
<code>groupLegendTitle</code>	Legend title corresponding to the categorical column.
<code>extraCircles</code>	Number of circles drawn beyond those required to include the points representing the genes.
<code>palette</code>	Color palette.
<code>labelSize</code>	Label size.
<code>pointSize</code>	Point size.
<code>labelRepulsion</code>	Repulsion strength between labels.
<code>labelPull</code>	Attraction strength between a text label and its data point.
<code>maxOverlaps</code>	Maximum overlaps. Ignored if <code>labelDF</code> is NULL.
<code>...</code>	Other arguments passed to <code>centerTitle</code> .

Value

An object of class `gg`.

Examples

```
degreesDF <- data.frame(Protein = paste0('P', seq(20)),
  Degree = sample(10, 20, replace=TRUE),
  Group = sample(3, 20, replace=TRUE))
radialPlot(degreesDF)
```

rankPlot	<i>Create a rank plot</i>
----------	---------------------------

Description

This function creates a rank plot.

Usage

```
rankPlot(
  df,
  title = "Rank plot",
  summarize = TRUE,
  viridisPal = "turbo",
  xLab = "Item",
  yLab = "Rank count",
  legendLab = "Rank",
  sigDigits = NULL,
  labelSize = 2.5,
  labelColor = "black",
  labelFace = c("plain", "bold", "italic", "bold-italic"),
  xAngle = 45,
  vJust = 0.6,
  ...
)
```

Arguments

df	A data frame with ranks as columns and items as rows, or a summary data frame generated with rankSummary. If the latter, summarize must be set to FALSE.
title	Plot title.
summarize	Whether to summarize the ranks with rankSummary. Must be set to FALSE if the input data frame has been generated with rankSummary.
viridisPal	Viridis palette.
xLab	Label of x axis.
yLab	Label of y axis.
legendLab	Legend label.
sigDigits	Number of significant digits used when displaying mean ranks. If NULL, the mean ranks will not be displayed.
labelSize	Size of label marking average rank for each item. Ignored if showMeanRanks is FALSE.
labelColor	Color of label marking average rank for each item. Ignored if showMeanRanks is FALSE.

labelFace	Font face of label marking average rank for each item. Must be one among 'plain', 'bold', 'italic' and 'bold-italic'. Ignored if showMeanRanks is FALSE.
xAngle	Angle of x axis text.
vJust	Vertical justification in [0, 1].
...	Other arguments passed to centerTitle.

Value

An object of class gg.

Examples

```
df <- do.call(cbind, lapply(seq(30), function(i) sample(10, 10)))
rownames(df) <- paste0('M', seq(10))
colnames(df) <- paste0('R', seq(30))
rankPlot(df)
```

rankSummary

*Create a rank summary***Description**

This function creates a summary of multiple ranks provided for input items.

Usage

```
rankSummary(df)
```

Arguments

df A data frame with ranks as columns, items as rows.

Value

A rank summary data frame with three columns: 'Rank', 'Item' and 'Count'.

Examples

```
df <- do.call(cbind, lapply(seq(30), function(i) sample(10, 10)))
rownames(df) <- paste0('M', seq(10))
colnames(df) <- paste0('R', seq(30))
rankSummary(df)
```

riverPlot	Create an alluvial plot
-----------	-------------------------

Description

This function creates an alluvial plot.

Usage

```
riverPlot(  
  df,  
  title = "River plot",  
  fillColIndex = 2,  
  curveType = "sigmoid",  
  alpha = 0.8,  
  strataFill = "lightgoldenrod1",  
  labelSize = 3,  
  viridisPal = "turbo",  
  legendPos = "none",  
  margins = margin(0, -10, -10, -10),  
  ...  
)
```

Arguments

df	A data frame with two categorical columns and a numeric column.
title	Plot title.
fillColIndex	Index of column used for coloring the alluvia.
curveType	Curve type.
alpha	Opacity level for the colors of the alluvia.
strataFill	Color used for the strata.
labelSize	Size of labels of strata elements.
viridisPal	Viridis palette.
legendPos	Legend position.
margins	Plot margins. Must be a vector of size 4 listing the desired top, right, bottom and left margin, in that order.
...	Other arguments passed to centerTitle.

Value

An object of class gg.

Examples

```
df <- data.frame(x = sample(c('a','b', 'c', 'd', 'e', 'f'), 20,
  replace=TRUE),
  y = sample(c('p','q', 'r', 's', 't', 'u', 'v', 'w'), 20,
  replace=TRUE),
  z = runif(20, 1, 3))
riverPlot(df)
```

rpColors

*Create a palette designed to represent dots over a viridis background***Description**

This function returns a 10-color palette used as the default of radialPlot.

Usage

```
rpColors(nColors = 10)
```

Arguments

nColors Number of colors.

Value

A character vector of colors.

tilePlot

*Plot a numeric matrix or data frame***Description**

This function plots a numeric matrix or data frame.

Usage

```
tilePlot(
  mat,
  title = "Tile plot",
  xLab = "x",
  yLab = "y",
  legendLab = "Value",
  sigDigits = 2,
  isCor = FALSE,
  labelSize = 3,
```

```

    labelColor = "black",
    tileBoundaryColor = "white",
    tileBoundaryWidth = 0.2,
    palette = "Spectral",
    reverseColors = TRUE,
    xAngle = 45,
    vJust = 0.6,
    ...
)

```

Arguments

<code>mat</code>	A numeric matrix or data frame.
<code>title</code>	Plot title.
<code>xLab</code>	Label of x axis.
<code>yLab</code>	Label of y axis.
<code>legendLab</code>	Legend label.
<code>sigDigits</code>	Number of significant digits to be displayed for each matrix element.
<code>isCor</code>	Whether the matrix is a correlation matrix, in which case the limits of the color scale will be set to [-1, 1].
<code>labelSize</code>	Label size. Ignored if <code>labelDF</code> is NULL.
<code>labelColor</code>	Label color.
<code>tileBoundaryColor</code>	Tile boundary color.
<code>tileBoundaryWidth</code>	Tile boundary width.
<code>palette</code>	grDevices palette.
<code>reverseColors</code>	Whether to reverse the order of colors in the palette.
<code>xAngle</code>	Angle of x axis text.
<code>vJust</code>	Vertical justification in [0, 1].
<code>...</code>	Other arguments passed to <code>centerTitle</code> .

Value

An object of class `gg`.

Examples

```

mat <- matrix(round(runif(100, 0, 1), 2), nrow=10)
rownames(mat) <- paste0('R', seq(10))
colnames(mat) <- paste0('C', seq(10))
tilePlot(mat)

```

vertexComponents	<i>Return the connected components of vertices</i>
------------------	--

Description

This function returns the connected components of vertices from a graph data frame in which edges have been assigned connected components.

Usage

```
vertexComponents(df, colName = "component")
```

Arguments

df	A data frame with two categorical columns representing graph edges and a connected components column.
colName	Name of the connected components column.

Value

A factor vector representing the connected component of each vertex.

Examples

```
df <- data.frame(gene1 = c('A', 'B', 'C', 'A'),  
  gene2 = c('B', 'D', 'F', 'G'),  
  component = c(1, 1, 2, 1))  
vertexComponents(df)
```

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