Package ‘CCPlotR’

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Title Plots For Visualising Cell-Cell Interactions

Version 1.11.0

Description CCPlotR is an R package for visualising results from tools that predict cell-cell interactions from single-cell RNA-seq data. These plots are generic and can be used to visualise results from multiple tools such as Liana, CellPhoneDB, NATMI etc.

Imports plyr, tidyr, dplyr, ggplot2, forcats, ggraph, igraph, scatterpie, circlize, ComplexHeatmap, tibble, grid, stringr, ggtext, ggh4x, patchwork, RColorBrewer, scales, viridis, grDevices, graphics, stats, methods

URL `https://github.com/Sarah145/CCPlotR`

BugReports `https://github.com/Sarah145/CCPlotR/issues`

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Contents

`cc_arrow` *Paired Arrow Plot Function*

Description

This function plots interactions between a pair of cell types

Usage

```
cc_arrow(
  cc_df,
  cell_types = NULL,
  option = "A",
  n_top_ints = 15,
  exp_df = NULL,
  colours = setNames(paletteMartin(n = 2), cell_types),
  palette = "BuPu"
)
```

Arguments

`cc_df`	A dataframe with columns 'source', 'target', 'ligand', 'receptor' and 'score'. See `toy_data` for example.
`cell_types`	A vector of which two cell types to plot.
`option`	Either 'A' or 'B'. Option A will plot the top `n_top_ints` interactions between `cell_types` and their scores. Option B will plot the top `n_top_ints` interactions between `cell_types`, their scores and the expression of the ligand/receptor genes in the sender/receiver cell types.
`n_top_ints`	The number of top interactions to plot.
`exp_df`	A dataframe containing the mean expression values for each ligand/receptor in each cell type. See `toy_exp` for an example. Only required for option B.
`colours`	A named vector of colours for each cell type. Default is `paletteMartin()`, a colourblind-friendly palette. Only used for option A.
`palette`	Which colour palette to use to show the mean expression. Should be one of the RColorBrewer sequential palettes. Only used for option B.

Value

Returns a plot generated with the ggplot2 package

Examples

```
data(toy_data, toy_exp, package = 'CCPlotR')
cc_arrow(toy_data, cell_types = c("B", "CD8 T"), colours = c(`B` = "hotpink", `CD8 T` = "orange"))
cc_arrow(toy_data,
    cell_types = c("NK", "CD8 T"), option = "B", exp_df = toy_exp,
    n_top_ints = 10, palette = "OrRd"
)
```

`cc_circos` *Circos Plot Function*

Description

This function creates a circos plot

Usage

```
cc_circos(
  cc_df,
  option = "A",
  n_top_ints = 15,
  exp_df = NULL,
  cell_cols = NULL,
  palette = "BuPu",
  cex = 1,
  show_legend = TRUE,
  scale = FALSE,
  ...
)
```

Arguments

`cc_df`	A dataframe with columns 'source', 'target', 'ligand', 'receptor' and 'score'. See `toy_data` for example.
`option`	Either 'A' , 'B' or 'C'. Option A will plot the number of interactions between pairs of cell types, option B will plot the top `n_top_ints` interactions and their scores. Option C will plot the top `n_top_ints` interactions, their scores and the mean expression of the ligands/receptors in the sending/receiver cell types.
`n_top_ints`	The number of top interactions to plot. Only required for options B and C.
`exp_df`	A dataframe containing the mean expression values for each ligand/receptor in each cell type. See `toy_exp` for an example. Only required for option C.
`cell_cols`	A named vector of colours for each cell type. Default uses `paletteMartin()`, a colourblind-friendly palette.
`palette`	Which colour palette to use to show the mean expression. Should be one of the RColorBrewer sequential palettes.

`cex`	Determines text size
`show_legend`	TRUE or FALSE - whether to add legend or not. Only required for options B and C.
`scale`	TRUE or FALSE - whether to scale each sector to same width. Only required for options B and C.
`...`	Additional parameters passed to `chordDiagram` function.

Value

Returns a chord diagram generated by the circlize R package

Examples

```
data(toy_data, toy_exp, package = 'CCPlotR')
cc_circos(toy_data)
cc_circos(toy_data, option = "B", n_top_ints = 10, cex = 0.5)
cc_circos(toy_data,
    option = "C", n_top_ints = 15, exp_df = toy_exp,
    cell_cols = c(`B` = "hotpink", `NK` = "orange", `CD8 T` = "cornflowerblue"),
    palette = "PuRd", cex = 0.5
)
```

`cc_dotplot` *Dotplot Function*

Description

This function plots a dotplot

Usage

```
cc_dotplot(cc_df, option = "A", n_top_ints = 30)
```

Arguments

`cc_df`	A dataframe with columns ’source’, ’target’, ’ligand’, ’receptor’ and ’score’. See `toy_data` for example.
`option`	Either ’A’, ’B’, ’CellPhoneDB’ or ’Liana’. Option A will plot the number of interactions between pairs of cell types, option B will plot the top `n_top_ints` interactions and their scores. The ’CellPhoneDB’ and ’Liana’ options will generate a dotplot in the style of these popular tools.
`n_top_ints`	The number of top interactions to plot. Only required for option B.

Value

Returns a plot generated with the ggplot2 package

Examples

```
data(toy_data, package = 'CCPlotR')
cc_dotplot(toy_data)
cc_dotplot(toy_data, option = "B", n_top_ints = 10)
cc_dotplot(toy_data, option = "Liana", n_top_ints = 15)
```

`cc_heatmap` *Heatmap Function*

Description

This plots a heatmap

Usage

```
cc_heatmap(cc_df, option = "A", n_top_ints = 30)
```

Arguments

`cc_df`	A dataframe with columns 'source', 'target', 'ligand', 'receptor' and 'score'. See `toy_data` for example.
`option`	Either 'A', 'B', 'CellPhoneDB' or 'Liana'. Option A will plot the number of interactions between pairs of cell types, option B will plot the top `n_top_ints` interactions and their scores. The 'CellPhoneDB' and 'Liana' options will generate a heatmap in the style of these popular tools.
`n_top_ints`	The number of top interactions to plot. Only required for option B.

Value

Returns a plot generated with the ggplot2 package

Examples

```
data(toy_data, package = 'CCPlotR')
cc_heatmap(toy_data)
cc_heatmap(toy_data, option = "B", n_top_ints = 10)
cc_heatmap(toy_data, option = "CellPhoneDB")
```

`cc_network` *Network Plot Function*

Description

This function plots a network of representing the number of interactions between cell types

Usage

```
cc_network(
  cc_df,
  colours = paletteMartin(),
  option = "A",
  n_top_ints = 20,
  node_size = 2.75,
  label_size = 4,
  layout = "kk"
)
```

Arguments

`cc_df`	A dataframe with columns 'source', 'target', 'ligand', 'receptor' and 'score'. See `toy_data` for example.
`colours`	A vector of colours for each cell type. Default is `paletteMartin()`, a colourblind-friendly palette.
`option`	Either 'A' or 'B'. Option A will plot the number of interactions between pairs of cell types, option B will plot the top `n_top_ints` interactions and their scores.
`n_top_ints`	The number of top interactions to plot. Only required for option B.
`node_size`	Point size for nodes in option B.
`label_size`	Size for labels in option B.
`layout`	Algorithm for determining layout in option B. One of 'dh', 'drl', 'fr', 'gem', 'graphopt', 'kk', 'lgl', 'mds', 'nicely'. See iGraph layouts for more details.

Value

Returns a plot generated with the ggplot2 package

Examples

```
data(toy_data, package = 'CCPlotR')
cc_network(toy_data)
cc_network(toy_data, colours = c("orange", "cornflowerblue", "hotpink"), option = "B")
```

`cc_sigmoid` *Sigmoid Plot Function*

Description

This function plots interactions using the `geom_sigmoid` function from the ggbump R package

Usage

```
cc_sigmoid(cc_df, n_top_ints = 20, colours = paletteMartin())
```

Arguments

`cc_df`	A dataframe with columns 'source', 'target', 'ligand', 'receptor' and 'score'. See `toy_data` for example.
`n_top_ints`	The number of top interactions to plot.
`colours`	A named vector of colours for each cell type. Default is `paletteMartin()`, a colourblind-friendly palette.

Value

Returns a plot generated with the ggplot2 package

Examples

```
data(toy_data, package = 'CCPlotR')
cc_sigmoid(toy_data)
cc_sigmoid(toy_data, colours = c(
    `B` = "hotpink", `CD8 T` = "orange",
    `NK` = "cornflowerblue"
), n_top_ints = 25)
```

`geom_sigmoid` *geom_sigmoid This function is copied from the ggbump package*

Description

Creates a ggplot that makes a smooth rank over time. To change the `smooth` argument you need to put it outside of the `aes` of the geom. Uses the x, xend, y and yend aestethics. Make sure each sigmoid curve is its own group.

Usage

```
geom_sigmoid(
  mapping = NULL,
  data = NULL,
  geom = "line",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  smooth = 8,
  direction = "x",
  inherit.aes = TRUE,
  ...
)
```

Arguments

`mapping`	provide you own mapping. both x, xend, y and yend need to be numeric.
`data`	provide you own data
`geom`	xhange geom
`position`	change position
`na.rm`	remove missing values
`show.legend`	show legend in plot
`smooth`	how much smooth should the curve have? More means steeper curve.
`direction`	the character x or y depending of smoothing direction
`inherit.aes`	should the geom inherits aestethics
`...`	other arguments to be passed to the geom

Value

ggplot layer

Examples

```
library(ggplot2)
df <- data.frame(x = 1:6,
       y = 5:10,
       xend = 7,
       yend = -3:2)

ggplot(df, aes(x = x, xend = xend, y = y, yend = yend, color = factor(x))) +
  geom_sigmoid()
```

`paletteMartin` *Discrete palette generator*

Description

Generate a palette of up to 15 colours. The colours are from the paletteMartin palette in the colorBlindess R package.

Usage

```
paletteMartin(n = 15)
```

Arguments

`n`	Number of colours to return. Max = 15.

Value

Returns a vector of colours of length n.

Examples

```
scales::show_col(paletteMartin(n = 9))
```

`StatSigmoid` *This function is copied from the ggbump package*

Description

This function is copied from the ggbump package

`toy_data` *Toy data for CCPlotR*

Description

A toy dataset of ligand-receptor interactions to demonstrate cell-cell interaction plots.

Usage

```
toy_data
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 735 rows and 5 columns.

Value

`toy_data`**:**

A data frame with 735 rows and 5 columns:

source	Cell type expressing the ligand
target	Cell type expressing the receptor
ligand	Ligand
receptor	Receptor
score	A score for each interaction e.g. -log10(aggregate_rank) returned by Liana

Source

This is a modified version of the toy dataset that comes with the Liana R package.

`toy_exp` *Toy expression data for CCPlotR*

Description

A dataframe showing the mean expression values for each ligand and receptor in each cell type.

Usage

```
toy_exp
```

Format

An object of class `grouped_df` (inherits from `tbl_df`, `tbl`, `data.frame`) with 477 rows and 3 columns.

Value

`toy_exp`**:**

A data frame with 477 rows and 3 columns:

cell_type Cell type

gene Ligand/receptor gene

mean_exp Mean (normalised) expression of lignad/receptor gene in cell type

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