Package ‘CCPlotR’

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Title Plots For Visualising Cell-Cell Interactions

Version 1.2.0

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, gg bump,
stringr, ggtext, ggh4x, patchwork, RColorBrewer, scales,
viridis, grDevices, graphics, stats, methods

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

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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"
)
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
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.
**cc_heatmap**

**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)

c

---

**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")
**Description**

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

**Usage**

```r
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**

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

*Sigmod Plot Function*

**Description**

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

**Usage**

```r
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**

```r
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)
```

---

**paletteMartin**

*Discrete palette generator*

**Description**

Generate a palette of up to 15 colours. The colours are from the `paletteMartin` palette in the color-Blindess R package.

**Usage**

```r
paletteMartin(n = 15)
```
Arguments

\( n \)  
Number of colours to return. Max = 15.

Value

Returns a vector of colours of length \( n \).

Examples

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

---

`toy_data`  
*Toy data for CCPlotR*

Description

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

Usage

```r
data(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. \(-\log_{10}(\text{aggregate} \_\text{rank})\) returned by Liana

Source

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

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

Usage

data(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 ligand/receptor gene in cell type
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