Package ‘CCPlotR’

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Title  Plots For Visualising Cell-Cell Interactions
Version 1.0.0
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 bumped,
stringr, ggtex, ggh4x, patchwork, RColorBrewer, scales,
viridis, grDevices, graphics, stats, methods

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BugReports  https://github.com/Sarah145/CCPlotR/issues
License  MIT + file LICENSE

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**Description**

This function plots interactions between a pair of cell types

**Usage**

```r
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.
cc_circos

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.
cc_dotplot

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.
**cc_heatmap**

**Value**

Returns a plot generated with the ggplot2 package

**Examples**

```r
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**

```r
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**

```r
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**

```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**  
*Sigmoid 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)
```

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**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**

```r
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))

toy_data  Toy data for CCPlotR

Description

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

Usage

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. -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
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
Index

* datasets
  toy_data, 8
  toy_exp, 9

cc_arrow, 2
cc_circos, 3
cc_dotplot, 4
cc_heatmap, 5
cc_network, 6
cc_sigmoid, 7

paletteMartin, 7

toy_data, 8
toy_exp, 9