Package ‘CCPlotR’

March 27, 2024

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, ggbump, stringr, ggtex, 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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Encoding UTF-8

LazyData false

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Suggests knitr, rmarkdown, BiocStyle, testthat (>= 3.0.0)

VignetteBuilder knitr

biocViews SingleCell, Network, Visualization, CellBiology, SystemsBiology

Config/testthat/edition 3

git_url https://git.bioconductor.org/packages/CCPlotR

git_branch RELEASE_3_18

git_last_commit 560c3de

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-03-27

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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.
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**

```r
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

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 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**

*Signoid 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 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**

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**Description**

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

**Usage**

```r
data(toy_exp)
```

**Format**

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

**Value**

```r
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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