

# Package ‘CCPlotR’

January 22, 2025

**Title** Plots For Visualising Cell-Cell Interactions

**Version** 1.5.0

**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, 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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**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** devel

**git\_last\_commit** c2f2f50

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2025-01-22

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## Contents

|                         |   |
|-------------------------|---|
| 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 |

|              |           |
|--------------|-----------|
| <b>Index</b> | <b>10</b> |
|--------------|-----------|

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|          |                                   |
|----------|-----------------------------------|
| cc_arrow | <i>Paired Arrow Plot Function</i> |
|----------|-----------------------------------|

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### 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"
)
```

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 cc\_circos

*Circos Plot Function*


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### 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")
```

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`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**

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

---

`paletteMartin`*Discrete palette generator*

---

**Description**

Generate a palette of up to 15 colours. The colours are from the `paletteMartin` palette in the `colorBlindness` 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))
```

---

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.  $-\log_{10}(\text{aggregate\_rank})$  returned by Liana

**Source**

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



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`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**

```
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](#)