

# Package ‘CCPlotR’

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

**Version** 1.6.0

**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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|          |                                   |
|----------|-----------------------------------|
| 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 | <i>Circos Plot Function</i> |
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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
)
```

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cc\_dotplot

*Dotplot Function*


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### 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)
```

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|            |                         |
|------------|-------------------------|
| cc_heatmap | <i>Heatmap Function</i> |
|------------|-------------------------|

---

**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**

|                         |                                                                                                                         |
|-------------------------|-------------------------------------------------------------------------------------------------------------------------|
| <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))
```

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|          |                             |
|----------|-----------------------------|
| toy_data | <i>Toy data for CCPlotR</i> |
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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.

---

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

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