

# Package ‘InterCellar’

December 19, 2024

**Title** InterCellar: an R-Shiny app for interactive analysis and exploration of cell-cell communication in single-cell transcriptomics

**Version** 2.13.0

**Description** InterCellar is implemented as an R/Bioconductor Package containing a Shiny app that allows users to interactively analyze cell-cell communication from scRNA-seq data. Starting from precomputed ligand-receptor interactions, InterCellar provides filtering options, annotations and multiple visualizations to explore clusters, genes and functions. Finally, based on functional annotation from Gene Ontology and pathway databases, InterCellar implements data-driven analyses to investigate cell-cell communication in one or multiple conditions.

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**Imports** config, golem, shiny, DT, shinydashboard, shinyFiles, shinycssloaders, data.table, fs, dplyr, tidyr, circlize, colourpicker, dendextend, factoextra, ggplot2, plotly, plyr, shinyFeedback, shinyalert, tibble, umap, visNetwork, wordcloud2, readxl, htmlwidgets, colorspace, signal, scales, htmltools, ComplexHeatmap, grDevices, stats, tools, utils, biomaRt, rlang, fmsb, igraph

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annotateGO	<i>Perform GO annotation of input data</i>
------------	--

---

**Description**

Perform GO annotation of input data

**Usage**

```

annotateGO(
  input_select_ensembl,
  input_go_evidence_exclude,
  input_go_sources_checkbox,
  input.data
)
    
```

**Arguments**

input_select_ensembl	ensembl version selected by user
input_go_evidence_exclude	evidence codes to exclude by user
input_go_sources_checkbox	GO sources to use by user
input.data	preprocessed input data

**Value**

GO\_annotation

---

annotatePathways      *Annotate pathways for input data*

---

**Description**

Annotate pathways for input data

**Usage**

```
annotatePathways(selected.db, input.data)
```

**Arguments**

selected.db	pathways sources to use
input.data	filtered input data

**Value**

pathways\_annotation

---

buildPairsbyFunctionMatrix  
*Build binary matrix with int-pairs in rows, functions in cols*

---

**Description**

Build binary matrix with int-pairs in rows, functions in cols

**Usage**

```
buildPairsbyFunctionMatrix(functions_df)
```

**Arguments**

functions_df	annotated df (GO/path/combined)
--------------	---------------------------------

**Value**

binary matrix

---

checkLL_RR	<i>Manually change the annotation of L-L and R-R pairs</i>
------------	--

---

**Description**

Manually change the annotation of L-L and R-R pairs

**Usage**

```
checkLL_RR(input.data)
```

**Arguments**

input.data      preprocessed table

**Value**

input.data

**Examples**

```
data(input.data)
checked.input.data <- checkLL_RR(input.data)
```

---

circlePlot	<i>Plot circle plot</i>
------------	-------------------------

---

**Description**

Plot circle plot

**Usage**

```
circlePlot(data, cluster_colors, ipm_color, int_flow, link.color)
```

**Arguments**

data              subset of input data by flow / intpair module  
cluster\_colors    global  
ipm\_color        single color for chosen int-pair module  
int\_flow         string specifying the flow  
link.color        string specifying variable by which to color links

**Value**

circle plot

---

combineAnnotations      *Combine GO annotation and pathways in a unique object*

---

### Description

Combine GO annotation and pathways in a unique object

### Usage

```
combineAnnotations(GO_annotation, pathways_annotation)
```

### Arguments

```
GO_annotation  data
pathways_annotation
               data
```

### Value

combined annotation dataframe

---

createBarPlot1\_ggplot      *Create ggplot barplot to be saved in tiff*

---

### Description

Create ggplot barplot to be saved in tiff

### Usage

```
createBarPlot1_ggplot(
  barplotDF,
  input_cluster_selected_checkbox,
  input_num_or_weight_bar1
)
```

### Arguments

```
barplotDF      dataframe with N interactions per cluster (auto/para)
input_cluster_selected_checkbox
               checkbox input
input_num_or_weight_bar1
               number of int or weighted number by score
```

### Value

ggplot barplot

---

createBarPlot2\_CV      *Create barplot of number of interaction for selected cluster*

---

### Description

Create barplot of number of interaction for selected cluster

### Usage

```
createBarPlot2_CV(  
  barplotDF2,  
  input_cluster_selected_checkbox,  
  input_clust_barplot2  
)
```

### Arguments

barplotDF2      dataframe with barplot data  
input\_cluster\_selected\_checkbox  
                  selected clusters to keep  
input\_clust\_barplot2  
                  selected cluster to plot

### Value

plotly fig

---

createBarPlot2\_ggplot      *Create ggplot barplot of Nint per cluster selected*

---

### Description

Create ggplot barplot of Nint per cluster selected

### Usage

```
createBarPlot2_ggplot(  
  barplotDF2,  
  input_cluster_selected_checkbox,  
  input_clust_barplot2  
)
```

**Arguments**

barplotDF2      dataframe with barplot data  
input\_cluster\_selected\_checkbox  
                    selected clusters to keep  
input\_clust\_barplot2  
                    selected cluster to plot

**Value**

ggplot barplot

---

createBarPlot_CV	<i>Create Barplot cluster-verse</i>
------------------	-------------------------------------

---

**Description**

Create Barplot cluster-verse

**Usage**

```
createBarPlot_CV(
  barplotDF,
  input_cluster_selected_checkbox,
  input_num_or_weight_bar1
)
```

**Arguments**

barplotDF      dataframe with N interactions per cluster (auto/para)  
input\_cluster\_selected\_checkbox  
                    checkbox input  
input\_num\_or\_weight\_bar1  
                    number of int or weighted number by score

**Value**

plotly barplot



---

createNetwork	<i>Create Network of clusters</i>
---------------	-----------------------------------

---

**Description**

Create Network of clusters

**Usage**

```
createNetwork(data.filt.cluster, input_num_or_weight_ratio, input_edge_weight)
```

**Arguments**

data.filt.cluster  
filtered input data (by clusters)

input\_num\_or\_weight\_ratio  
either number of interactions or weighted by score

input\_edge\_weight  
small,medium or large from user input

**Value**

list containing nodes and edges for network

---

dendroIntPairModules	<i>Get dendrogram of int pair modules</i>
----------------------	---

---

**Description**

Get dendrogram of int pair modules

**Usage**

```
dendroIntPairModules(pairs_func_matrix)
```

**Arguments**

pairs\_func\_matrix  
binary matrix pairs x functions

**Value**

list with dendrogram, hclust and umap

**elbowPoint***Determine the elbow point on a curve (from package akmedoids)*

---

**Description**

Given a list of x, y coordinates on a curve, function determines the elbow point of the curve.

**Usage**

```
elbowPoint(x, y)
```

**Arguments**

x                    vector of x coordinates of points on the curve  
y                    vector of y coordinates of points on the curve

**Details**

highlight the maximum curvature to identify the elbow point (credit: 'github.com/agentlans')

**Value**

an x, y coordinates of the elbow point.

---

**ensemblLink***Get html link to ensembl*

---

**Description**

Get html link to ensembl

**Usage**

```
ensemblLink(ensembl)
```

**Arguments**

ensembl            symbol

**Value**

html link to website

---

getBack2BackBarplot     *Get back-to-back barplot for 2 conditions comparison*

---

**Description**

Get back-to-back barplot for 2 conditions comparison

**Usage**

```
getBack2BackBarplot(tab_c1, tab_c2, lab_c1, lab_c2)
```

**Arguments**

tab_c1	barplot dataframe generated by getBarplotDF() for condition 1
tab_c2	barplot dataframe generated by getBarplotDF() for condition 1
lab_c1	label for condition 1
lab_c2	label for condition 2

**Value**

ggplot object

---

getBarplotDF     *Get dataframe for plotting barplot (all clusters)*

---

**Description**

Get dataframe for plotting barplot (all clusters)

**Usage**

```
getBarplotDF(  
  data.filt.bar,  
  input_cluster_selected_checkbox,  
  input_num_or_weight_bar1  
)
```

**Arguments**

data.filt.bar	filtered object (checkbox auto/para)
input_cluster_selected_checkbox	checkbox input
input_num_or_weight_bar1	number of int or weighted number by score

**Value**

dataframe with number of interactions per cluster auto/para

---

<code>getBarplotDF2</code>	<i>Get dataframe for barplot (by cluster)</i>
----------------------------	---

---

**Description**

Get dataframe for barplot (by cluster)

**Usage**

```
getBarplotDF2(filt.data, input_cluster_selected_checkbox, input_clust_barplot2)
```

**Arguments**

<code>filt.data</code>	input data filtered in cluster-verse
<code>input_cluster_selected_checkbox</code>	selected clusters to keep
<code>input_clust_barplot2</code>	selected cluster to plot

**Value**

dataframe with num int per cluster

---

<code>getClusterA_Names</code>	<i>Get cluster names only from sender cluster A</i>
--------------------------------	---

---

**Description**

Get cluster names only from sender cluster A

**Usage**

```
getClusterA_Names(input.data)
```

**Arguments**

<code>input.data</code>	preprocessed input data
-------------------------	-------------------------

**Value**

named list of clusters

---

getClusterColors	<i>Get colors for clusters</i>
------------------	--------------------------------

---

**Description**

Get colors for clusters

**Usage**

```
getClusterColors(input.data)
```

**Arguments**

input.data      preprocessed input data

**Value**

named vector with colors per cluster

---

getClusterNames	<i>Get clusters names from initial input data</i>
-----------------	---

---

**Description**

Get clusters names from initial input data

**Usage**

```
getClusterNames(input.data)
```

**Arguments**

input.data      preprocessed input data

**Value**

named list of clusters

**Examples**

```
data(input.data)
cluster_list <- getClusterNames(input.data)
```

---

getClusterNetwork      *Creating edges dataframe for network of clusters*

---

**Description**

Creating edges dataframe for network of clusters

**Usage**

```
getClusterNetwork(input.data, input_num_or_weight_ratio, input_edge_weight)
```

**Arguments**

input.data      preprocessed input data  
input\_num\_or\_weight\_ratio  
                 either num of interactions or weighted by score  
input\_edge\_weight  
                 small,medium or large from user input

**Value**

edges dataframe

---

getClusterSize      *Get Clusters size*

---

**Description**

Get Clusters size

**Usage**

```
getClusterSize(c1, edges.df, input_num_or_weight_ratio)
```

**Arguments**

c1              cluster name  
edges.df      dataframe with edges for network  
input\_num\_or\_weight\_ratio  
                 either num of interactions or weighted by score

**Value**

sum of n interactions or weighted num for that cluster

---

getDistinctCouplets     *Get table of unique int-pairs/clust-pairs couplets*

---

**Description**

Get table of unique int-pairs/clust-pairs couplets

**Usage**

```
getDistinctCouplets(  
  data_cond1,  
  data_cond2,  
  data_cond3 = NULL,  
  lab_c1,  
  lab_c2,  
  lab_c3 = NULL  
)
```

**Arguments**

data_cond1	filt.data() corresponding to chosen condition 1
data_cond2	filt.data() corresponding to chosen condition 2
data_cond3	filt.data() corresponding to chosen condition 3
lab_c1	data label for condition 1
lab_c2	data label for condition 2
lab_c3	data label for condition 3

**Value**

modified filt.data containing only unique couplets

---

getDotPlot\_selInt     *Functions to plot DotPlots*

---

**Description**

Functions to plot DotPlots

**Usage**

```
getDotPlot_selInt(  
  selected_tab,  
  clust.order,  
  low_color = "aquamarine",  
  high_color = "#131780"  
)
```

**Arguments**

selected_tab	selected rows of filt.data by selection from gene table
clust.order	how to order clusters
low_color	of dotplot
high_color	of dotplot

**Value**

list with modified selected data and ggplot2 dotplot

---

getGeneTable	<i>Get table for gene-verse</i>
--------------	---------------------------------

---

**Description**

Get table for gene-verse

**Usage**

```
getGeneTable(input.data)
```

**Arguments**

input.data	preprocessed input data
------------	-------------------------

**Value**

gene table with unique intpairs (no connection to clusters)

**Examples**

```
data(input.data)
gene_table <- getGeneTable(input.data)
```



---

getGObiomaRt	<i>Connection to Ensembl via biomaRt to get GO terms</i>
--------------	--

---

**Description**

Connection to Ensembl via biomaRt to get GO terms

**Usage**

```
getGObiomaRt(input_select_ensembl, input.data)
```

**Arguments**

input_select_ensembl	chosen version of Ensembl
input.data	filtered input data

**Value**

dataframe with GO annotation

---

getHitsf	<i>Subfunction to calculate significant functions by permutation test</i>
----------	---

---

**Description**

Subfunction to calculate significant functions by permutation test

**Usage**

```
getHitsf(mat, gpModules_assign)
```

**Arguments**

mat	binary matrix of functional terms by int-pairs
gpModules_assign	assignment of intpairs to modules

**Value**

matrix with hits

Example

---

getIntFlow	<i>Get subset of interactions corresponding to a certain viewpoint and flow</i>
------------	---

---

**Description**

Get subset of interactions corresponding to a certain viewpoint and flow

**Usage**

```
getIntFlow(vp, input.data, flow)
```

**Arguments**

vp	viewpoint cluster
input.data	preprocessed/filtered input data
flow	one among directed_out, directed_in or undirected

**Value**

subset of data

**Examples**

```
data(input.data)
caf_out <- getIntFlow(vp = "CAF", input.data, flow = "directed_out")
```

---

getNtermsBYdb	<i>Calculate number of terms of a database</i>
---------------	--

---

**Description**

Calculate number of terms of a database

**Usage**

```
getNtermsBYdb(annotation)
```

**Arguments**

annotation	data from either pathways, GO or combined
------------	---

**Value**

number of terms by dataset

---

getNumLR	<i>Get number of unique ligands and receptors</i>
----------	---

---

**Description**

Get number of unique ligands and receptors

**Usage**

```
getNumLR(gene.table, type)
```

**Arguments**

gene.table	gene table of unique int-pairs
type	either L or R

**Value**

number of L or R genes

---

getPieChart	<i>Get Pie Chart of unique couplets</i>
-------------	---

---

**Description**

Get Pie Chart of unique couplets

**Usage**

```
getPieChart(data_dotplot)
```

**Arguments**

data_dotplot	same data used to generate dotplot
--------------	------------------------------------

**Value**

pie chart

getRadar\_df

---

```

#' Get radar plot of relative numbers of interactions for a certain
cell type #' #' @param tab_c1 barplot dataframe from Viewpoint
generated by getBarplotDF2() containing data for condition 1 #'
@param tab_c2 barplot dataframe from Viewpoint generated by get-
BarplotDF2() containing data for condition 2 #' @param tab_c3
barplot dataframe from Viewpoint generated by getBarplotDF2() con-
taining data for condition 3 #' @param lab_c1 label for condition
1 #' @param lab_c2 label for condition 2 #' @param lab_c3 label
for condition 3 #' @param cell_name label of cell type of interest
#' #' @return plot #' @importFrom fmsb radarchart #' @import-
From data.table transpose getRadarPlot <- function(tab_c1, tab_c2,
tab_c3, lab_c1, lab_c2, lab_c3, cell_name) if(is.null(tab_c3)) df <-
merge(tab_c1, tab_c2, by = "Clusters", all = TRUE) colnames(df)
<- c("Clusters", "nint_c1", "nint_c2") else df <- merge(tab_c1,
tab_c2, by = "Clusters", all = TRUE) df <- merge(df, tab_c3, by
= "Clusters", all = TRUE) colnames(df) <- c("Clusters", "nint_c1",
"nint_c2", "nint_c3") df[is.na(df)] <- 0 cluster_names <- df$Clusters
# add max and min max_nint <- max(df[, -1]) df <- add_column(df,
max_nint, .after = "Clusters") df <- add_column(df, "min_nint" =
0, .after = "max_nint") radar_df <- data.table::transpose(df[, -1])
if(is.null(lab_c3)) rownames(radar_df) <- c("max", "min", lab_c1,
lab_c2) else rownames(radar_df) <- c("max", "min", lab_c1, lab_c2,
lab_c3) colnames(radar_df) <- cluster_names color <- c("#438ECC",
"#E97778", "#00BA38") fmsb::radarchart( radar_df, axistype = 1, #
Customize the polygon pcol = color, pfc0l = scales::alpha(color, 0.5),
plwd = 2, pty = 1, # Customize the grid cglcol = "grey", cglty =
1, cglwd = 0.8, # Customize the axis axislabcol = "grey30", # Vari-
able labels vlcex = 1.2, vlabels = colnames(radar_df), caxislabels =
round(seq(from = 0, to = radar_df["max",1], length.out = 5)), title =
cell_name ) legend( x = "bottomleft", legend = rownames(radar_df[
c(1,2),]), horiz = FALSE, bty = "n", pch = 20 , col = color, text.col
= "black", cex = 1, pt.cex = 1.5 ) Get radar df of relative numbers of
interactions for a certain cell type

```

---

## Description

```

#' Get radar plot of relative numbers of interactions for a certain cell type #' #' @param tab_c1
barplot dataframe from Viewpoint generated by getBarplotDF2() containing data for condition 1 #'
@param tab_c2 barplot dataframe from Viewpoint generated by getBarplotDF2() containing data
for condition 2 #' @param tab_c3 barplot dataframe from Viewpoint generated by getBarplotDF2()
containing data for condition 3 #' @param lab_c1 label for condition 1 #' @param lab_c2 label
for condition 2 #' @param lab_c3 label for condition 3 #' @param cell_name label of cell
type of interest #' #' @return plot #' @importFrom fmsb radarchart #' @importFrom data.table
transpose getRadarPlot <- function(tab_c1, tab_c2, tab_c3, lab_c1, lab_c2, lab_c3, cell_name)
if(is.null(tab_c3)) df <- merge(tab_c1, tab_c2, by = "Clusters", all = TRUE) colnames(df) <- c("Clusters",

```

```

"nint_c1", "nint_c2") else df <- merge(tab_c1, tab_c2, by = "Clusters", all = TRUE) df <- merge(df,
tab_c3, by = "Clusters", all = TRUE) colnames(df) <- c("Clusters", "nint_c1", "nint_c2", "nint_c3")
df[is.na(df)] <- 0

cluster_names <- df$Clusters # add max and min max_nint <- max(df[, -1]) df <- add_column(df,
max_nint, .after = "Clusters") df <- add_column(df, "min_nint" = 0, .after = "max_nint")

radar_df <- data.table::transpose(df[, -1])

if(is.null(lab_c3)) rownames(radar_df) <- c("max", "min", lab_c1, lab_c2) else rownames(radar_df)
<- c("max", "min", lab_c1, lab_c2, lab_c3)

colnames(radar_df) <- cluster_names

color <- c("#438ECC", "#E97778", "#00BA38")

fmsb::radarchart( radar_df, axistype = 1, # Customize the polygon pcol = color, pfcoll = scales::alpha(color,
0.5), plwd = 2, plty = 1, # Customize the grid cglcol = "grey", cglty = 1, cglwd = 0.8, # Customize
the axis axislabcol = "grey30", # Variable labels vlce = 1.2, vlabels = colnames(radar_df), caxis-
labels = round(seq(from = 0, to = radar_df["max",1], length.out = 5)), title = cell_name ) legend( x
= "bottomleft", legend = rownames(radar_df[-c(1,2),]), horiz = FALSE, bty = "n", pch = 20 , col =
color, text.col = "black", cex = 1, pt.cex = 1.5 )

```

Get radar df of relative numbers of interactions for a certain cell type

## Usage

```
getRadar_df(tab_c1, tab_c2, tab_c3, lab_c1, lab_c2, lab_c3)
```

## Arguments

tab_c1	barplot dataframe from Viewpoint generated by getBarplotDF2() containing data for condition 1
tab_c2	barplot dataframe from Viewpoint generated by getBarplotDF2() containing data for condition 2
tab_c3	barplot dataframe from Viewpoint generated by getBarplotDF2() containing data for condition 3
lab_c1	label for condition 1
lab_c2	label for condition 2
lab_c3	label for condition 3

## Value

df to be then used with fmsb radarchart

---

getRankedTerms	<i>Get table with ranked functional terms</i>
----------------	---

---

**Description**

Get table with ranked functional terms

**Usage**

```
getRankedTerms(data.fun.annot)
```

**Arguments**

data.fun.annot annotated df (GO/path/combined)

**Value**

table with ranking

---

getSignificantFunctions	<i>Calculate significant function per intpair module</i>
-------------------------	--

---

**Description**

Calculate significant function per intpair module

**Usage**

```
getSignificantFunctions(
  subGenePairs_func_mat,
  gpModules_assign,
  rank.terms,
  input_maxPval
)
```

**Arguments**

subGenePairs_func_mat	subset of binary mat
gpModules_assign	assignment of intpairs to modules
rank.terms	table of ranked functions
input_maxPval	threshold of significance

**Value**

table with significant functions

---

getSignificantFunctions\_multiCond

*Get significance of functional terms related to unique int-pairs per condition*

---

**Description**

Get significance of functional terms related to unique int-pairs per condition

**Usage**

```
getSignificantFunctions_multiCond(sub_annot, unique_intpairs)
```

**Arguments**

sub\_annot            annotation matrix subset to unique int-pairs  
unique\_intpairs      data.frame with unique int-pairs by condition

**Value**

data.frame with calculated pvalue of significance

---

getSignif\_table

*Wrapper for other functions to get significant table of func terms*

---

**Description**

Wrapper for other functions to get significant table of func terms

**Usage**

```
getSignif_table(  
  data_cond1,  
  data_cond2,  
  data_cond3,  
  lab_c1,  
  lab_c2,  
  lab_c3,  
  annot_cond1,  
  annot_cond2,  
  annot_cond3  
)
```

**Arguments**

data_cond1	filt.data() corresponding to chosen condition 1
data_cond2	filt.data() corresponding to chosen condition 2
data_cond3	filt.data() corresponding to chosen condition 3
lab_c1	data label for condition 1
lab_c2	data label for condition 2
lab_c3	data label for condition 3
annot_cond1	binary matrix int-pair by functions for cond1
annot_cond2	binary matrix int-pair by functions for cond2
annot_cond3	binary matrix int-pair by functions for cond3

**Value**

list containing pvalue\_df and unique\_intpairs df

---

getSunburst	<i>Get Sunburst plot of selected functional terms</i>
-------------	---

---

**Description**

Get Sunburst plot of selected functional terms

**Usage**

```
getSunburst(
  sel.data,
  func_selected,
  int_p_fun,
  cluster.colors,
  input_num_or_weight_radio
)
```

**Arguments**

sel.data	dataframe of selected functions
func_selected	the selected functional term
int_p_fun	dataframe with int pairs annotated to this function
cluster.colors	for plotting
input_num_or_weight_radio	either num of interactions or weighted by score

**Value**

plotly figure



---

getUMAPipModules	<i>Get UMAP for IP modules</i>
------------------	--------------------------------

---

**Description**

Get UMAP for IP modules

**Usage**

```
getUMAPipModules(intPairs.dendro, gpModules_assign, ipm_colors)
```

**Arguments**

intPairs.dendro	list output of dendrogram
gpModules_assign	named vector of module assignment
ipm_colors	for intpair modules

**Value**

plotly umap

---

getUniqueDotplot	<i>Plot dotplot containing only unique int-pair/cluster pairs with many conditions</i>
------------------	--

---

**Description**

Plot dotplot containing only unique int-pair/cluster pairs with many conditions

**Usage**

```
getUniqueDotplot(data_dotplot, clust.order)
```

**Arguments**

data_dotplot	table with selected int_pairs for multiple conditions
clust.order	how to order clusters

**Value**

ggplot object

getUniqueIntpairs\_byCond

*Get table of unique int-pairs by condition*

---

### **Description**

Get table of unique int-pairs by condition

### **Usage**

```
getUniqueIntpairs_byCond(  
  data_cond1,  
  data_cond2,  
  data_cond3 = NULL,  
  lab_c1,  
  lab_c2,  
  lab_c3 = NULL  
)
```

### **Arguments**

data_cond1	filt.data() corresponding to chosen condition 1
data_cond2	filt.data() corresponding to chosen condition 2
data_cond3	filt.data() corresponding to chosen condition 3
lab_c1	data label for condition 1
lab_c2	data label for condition 2
lab_c3	data label for condition 3

### **Value**

modified merged filt.data containing only unique intpairs

---

goLink

*Get GO link*

---

### **Description**

Get GO link

### **Usage**

```
goLink(go_id)
```

**Arguments**

go\_id            string

**Value**

html link to website

---

input.data	<i>Input Data example</i>
------------	---------------------------

---

**Description**

A dataset obtained from Tirosh et al melanoma dataset, running CellPhoneDBv2. This data is generated by InterCellar running read.CPDBv2()

**Usage**

input.data

**Format**

A data frame with 5638 rows and 11 variables:

**int\_pair** interaction pair name, geneA & geneB

**geneA** name, hgnc\_symbol

**geneB** name, hgnc\_symbol

**typeA** molecular type of geneA, either L (ligand) or R (receptor)

**typeB** molecular type of geneB, either L (ligand) or R (receptor)

**clustA** name of first cluster, either character or number

**clustB** name of second cluster, either character or number

**score** int-pair score as avg expression of geneA and geneB over clustA and clustB, decimal

**p\_value** int-pair pvalue, decimal

**annotation\_strategy** database from which the int-pair was retrieved

**int.type** either autocrine or paracrine

---

read.cellchat	<i>Read dataframe of cell-cell communication from CellChat (ligand/receptor)</i>
---------------	--

---

**Description**

Read dataframe of cell-cell communication from CellChat (ligand/receptor)

**Usage**

```
read.cellchat(file_tab)
```

**Arguments**

file_tab	dataframe from cellchat
----------	-------------------------

**Value**

input.data formatted for InterCellar

---

read.CPDBv2	<i>Read output from CellPhoneDB v2.</i>
-------------	---

---

**Description**

Output is a folder containing 4 .txt files - deconvoluted.txt: containing list of single genes and their mean expression in each cluster (not considered); - means.txt: containing list of interacting pairs with info regarding L/R, annotation strategy and mean value of all pairs over cluster couples. - pvalues.txt: same as means, but containing pvalue of each pair, for each cluster couple. - significant\_means.txt: only means of those pairs that have pvalue < 0.05. Has one more column:rank. If the statistical analysis is not run, the folder would contain only deconvoluted and means

**Usage**

```
read.CPDBv2(folder)
```

**Arguments**

folder	folder containing output
--------	--------------------------

**Value**

input.data which is the pre-processed object with annotated L-R pairs

---

read.customInput	<i>Read custom input file and re-structure it with InterCellar format</i>
------------------	---

---

**Description**

Read custom input file and re-structure it with InterCellar format

**Usage**

```
read.customInput(tab, separator)
```

**Arguments**

tab	custom input table
separator	character that separates two elements of an interaction pair

**Value**

preprocessed table

---

read.icellnet	<i>Read ICELLNET dataframe</i>
---------------	--------------------------------

---

**Description**

Read ICELLNET dataframe

**Usage**

```
read.icellnet(tab, input_icellnet_CC, input_icellnet_dir)
```

**Arguments**

tab	dataframe with int-pairs in "X" column, other columns as cell types
input_icellnet_CC	central cell name
input_icellnet_dir	direction of interaction either out or in

**Value**

pre-processed input data

---

read.SCSignalR	<i>Read output from SingleCellSignalR</i>
----------------	---

---

### Description

SCSR description: the output folder is a collection of txt files, one for each clusters pair considered. The "paracrine" option looks for ligands expressed in cluster A and their associated receptors according to LRdb that are expressed in any other cluster but A. These interactions are labelled "paracrine". The interactions that involve a ligand and a receptor, both differentially expressed in their respective cell clusters according to the **edgeR** analysis performed by the **cluster\_analysis()** function, are labelled "specific". The "autocrine" option searches for ligands expressed in cell cluster A and their associated receptors also expressed in A. These interactions are labelled "autocrine". Additionally, it searches for those associated receptors in the other cell clusters (not A) to cover the part of the signaling that is "autocrine" and "paracrine" simultaneously. These interactions are labelled "autocrine/paracrine". This file is a 4-column table: ligands, receptors, interaction types ("paracrine", "autocrine", "autocrine/paracrine" and "specific"), and the associated LRscore. InterCellar: rename autocrinelparacrine to paracrine

### Usage

```
read.SCSignalR(folder)
```

### Arguments

folder            containing output from SingleCellSignalR, named cell-signaling

### Value

input.data: preprocessed object with annotated L-R pairs

---

run_app	<i>Run the Shiny Application</i>
---------	----------------------------------

---

### Description

Run the Shiny Application

### Usage

```
run_app(reproducible = TRUE)
```

### Arguments

reproducible    boolean for setting a seed, making plots reproducible

**Value**

a running instance of InterCellar

**Examples**

```
## Not run:
run_app()

## End(Not run)
```

---

subsetAnnot\_multiCond *Subset int-pair by function matrices to unique int-pairs by condition*

---

**Description**

Subset int-pair by function matrices to unique int-pairs by condition

**Usage**

```
subsetAnnot_multiCond(
  annot_cond1,
  annot_cond2,
  annot_cond3,
  unique_intpairs,
  lab_c1,
  lab_c2,
  lab_c3
)
```

**Arguments**

annot_cond1	binary matrix int-pair by functions for cond1
annot_cond2	binary matrix int-pair by functions for cond2
annot_cond3	binary matrix int-pair by functions for cond3
unique_intpairs	table of unique int-pairs by condition
lab_c1	label cond1
lab_c2	label cond2
lab_c3	label cond3

**Value**

subset merged matrix

---

subsetFuncMatBYFlow     *Subset pairs-function matrix by selected flow*

---

**Description**

Subset pairs-function matrix by selected flow

**Usage**

```
subsetFuncMatBYFlow(pairs_func_matrix, flow_df)
```

**Arguments**

pairs\_func\_matrix     binary  
flow\_df                subset of input data by flow

**Value**

subset of binary mat

---

swap.RLint                *Swaps interaction pairs that are R-L to L-R*

---

**Description**

Swaps interaction pairs that are R-L to L-R

**Usage**

```
swap.RLint(RLint)
```

**Arguments**

RLint                    subset of R-L interactions

**Value**

input data with ordered L-R pairs and L-L/R-R



---

uniprotLink	<i>Get html link to uniprot</i>
-------------	---------------------------------

---

**Description**

Get html link to uniprot

**Usage**

```
uniprotLink(uniprot)
```

**Arguments**

uniprot            symbol

**Value**

html link to website

---

updateInputLR	<i>Function that orders all interaction pairs as L-R. Leaves unchanged the R-R and L-L</i>
---------------	--

---

**Description**

Function that orders all interaction pairs as L-R. Leaves unchanged the R-R and L-L

**Usage**

```
updateInputLR(input.data)
```

**Arguments**

input.data        uploaded data

**Value**

ordered input data

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