Package 'sccca'

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Type Package

Title Single-Cell Correlation Based Cell Type Annotation

Version 0.1.1

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Description Performing cell type annotation based on cell markers from a unified database. The approach utilizes correlation-based approach combined with association analysis using Fisher-exact and phyper statistical tests (Upton, Graham JG. (1992) <DOI:10.2307/2982890>).

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Encoding UTF-8

Imports Seurat, dplyr, plyr, scales, HGNChelper, openxlsx

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Contents

`calculate_cor_mat` *Performs aggregation based on cell clusters and condition. Then, it calculates correlation matrix of genes*

Description

This Function is used to perform cell aggregation by averaging the expression of scRNA-seq matrix and then perform correlation matrix

Usage

```
calculate_cor_mat(expression_mat, condition  = NULL, clusters, assay = "RNA")
```

Arguments

`expression_mat`	Seurat object that contains the expression matrix.
`condition`	column name of the condition in th meta data of the Seurat object.
`clusters`	column name of the cluster numbers in the meta data of the Seurat object.
`assay`	the assay to be used default is set to RNA

Value

correlation matrix of genes.

Author(s)

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`calculate_normalized_ratio` *Calculate cell scores based on number of genes*

Description

This Function is used to calculate cell scores based on number of genes

Usage

```
calculate_normalized_ratio(vec)
```

Arguments

vec	list of genes of cell types.

Value

vector of cell scores based on the number of overlapped genes with the input matrix.

Author(s)

Mohmed Soudy <Mohamed.soudy@uni.lu> and Sohpie LE BARS <sophie.lebars@uni.lu> and Enrico Glaab <enrico.glaab@uni.lu>

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correct_gene_symbols *Process the cell markers names*

Description

This Function is used to return the cell markers names processed for the sctype approach

Usage

```
correct_gene_symbols(markers)
```

Arguments

markers	list of unique cell markers.

Value

vector of genes names which overlap with the correlation matrix.

Author(s)

Mohmed Soudy <Mohamed.soudy@uni.lu> and Sohpie LE BARS <sophie.lebars@uni.lu> and Enrico Glaab <enrico.glaab@uni.lu>

enrich_genes *Performs parallel function on two lists*

Description

This Function is used to perform parallel function on two lists

Usage

```
enrich_genes(ref_list, overlap_list, func)
```

Arguments

ref_list	reference list.
overlap_list	overlap list.
func	function to be applied.

Value

list where each element is the result of applying the function 'func' to the corresponding elements of 'ref_list' and 'overlap_list'.

Author(s)

Mohmed Soudy <Mohamed.soudy@uni.lu> and Sohpie LE BARS <sophie.lebars@uni.lu> and Enrico Glaab <enrico.glaab@uni.lu>

filter_correlation *Filter the genes based on specific correlation threshold*

Description

This Function is used to filter the gene correlation matrix based on user-defined threshold

Usage

```
filter_correlation(cor_mat, gene_list, threshold = 0.7)
```

Arguments

cor_mat	correlation matrix generated from calculate_cor_mat function.
gene_list	cell markers that passed threshold.
threshold	absolute correlation threshold.

Value

vector of gene names that pass user-defined correlation threshold.

Author(s)

Mohmed Soudy <Mohamed.soudy@uni.lu> and Sohpie LE BARS <sophie.lebars@uni.lu> and Enrico Glaab <enrico.glaab@uni.lu>

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filter_list *Process the cell markers that overlap between the cell markers and scRNA matrix*

Description

This Function is used to return the cell markers that overlap between the cell markers and scRNA matrix

Usage

```
filter_list(gene_list, passed_cells)
```

Arguments

gene_list	list of unique genes of cell types.
passed_cells	cells types that pass the specified threshold.

Value

list of cell types which genes are found in the input matrix.

Author(s)

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`fisher_test` *Performs fisher exact test to get the significant overlap between genes for cell type assignment*

Description

This Function is used to perform fisher exact test to get cell types

Usage

```
fisher_test(ref, gene_overlap)
```

Arguments

`ref`	reference gene set.
`gene_overlap`	genes that pass the correlation threshold.

Value

vector of p-value and overlap.

Author(s)

Mohmed Soudy <Mohamed.soudy@uni.lu> and Sohpie LE BARS <sophie.lebars@uni.lu> and Enrico Glaab <enrico.glaab@uni.lu>

Examples

```
fisher_test(c("PAX8","PAX6","TP53","AOC3","LIPF"), c("LIPF","PAX8","PAX6","TP53","TSHB","AOC3"))
```

`match_characters` *Process the cell markers that pass specific threshold in the gene correlation matrix*

Description

This Function is used to return the cell markers that pass specific threshold in the gene correlation matrix

Usage

```
match_characters(genes, gene_mat)
```

Arguments

genes	list of unique genes of cell types.
gene_mat	correlation matrix of genes.

Value

vector of genes names which overlap with the correlation matrix.

Author(s)

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phyper_test *Performs phyper test to get the significant overlap between genes for cell type assignment*

Description

This Function is used to perform phyper test to get cell types

Usage

```
phyper_test(ref, overlap)
```

Arguments

ref	reference gene set.
overlap	genes that pass the correlation threshold.

Value

vector of p-value and overlap.

Author(s)

Mohmed Soudy <Mohamed.soudy@uni.lu> and Sohpie LE BARS <sophie.lebars@uni.lu> and Enrico Glaab <enrico.glaab@uni.lu>

Examples

```
phyper_test(c("PAX8","PAX6","TP53","AOC3","LIPF"), c("LIPF","PAX8","PAX6","TP53","TSHB","AOC3"))
```

process_clus *Gets the associated cell types using correlation-based approach*

Description

This Function is used to get the associated cell clusters using correlation-based approach

Usage

```
process_clus(cluster,sobj,assay="RNA",clus,markers,cor_m,m_t=0.9,c_t=0.7,test="p")
```

Arguments

cluster	associated cluster name.
sobj	Seurat object.
assay	assay to be used default is set to RNA.
clus	cell clusters.
markers	cell markers database.
cor_m	gene correlation matrix.
m_t	overlap threshold between cell markers and expression matrix.
c_t	correlation threshold between genes.
test	statistical test that check if overlap is significant could be "p" for phyper or "f" for fisher.

Value

data frame of proposed cell types.

Author(s)

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process_database *Process the database for the sctype approach*

Description

This Function is used to process the database that will be used for sctype approach

Usage

```
process_database(database_name = "sctype", org = 'a', tissue, tissue_type = 'n')
```

Arguments

database_name	name of the database to be used that can be 'sctype' or 'UMD'.
org	name of organism to be used that can be 'h' for human, 'm' for mouse, and 'a' for all markers.
tissue	specified tissue from which the data comes.
tissue_type	tissue type whether 'a' for all types 'n' for normal tissues only or "c" for cancer tissues.

Value

vector of genes names which overlap with the correlation matrix.

Author(s)

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process_markers *Process the cell markers database and return the processed list*

Description

This Function is used to process the cell markers database and return the processed list

Usage

```
process_markers(markers_df)
```

Arguments

markers_df	data frame with markers named as gene_original and cell names as cell type.

Value

list of lists of the processed markers

Author(s)

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sccca *Run the pipeline for the cell type assignment*

Description

This Function is used to run the main pipeline that does the cell type assignment

Usage

```
sccca(sobj,assay="RNA",cluster,marker,tissue,tt="a",cond,m_t=0.9,c_t=0.7,test="p",org="a")
```

Arguments

sobj	Seurat object.
assay	assay to be used default is set to RNA.
cluster	colname in the mata.data that have the cell cluster numbers.
marker	cell markers database path.
tissue	specified tissue from which the data comes.
tt	tissue type whether 'a' for all types 'n' for normal tissues only or "c" for cancer tissues.
cond	colname in the meta.data that have the condition names.
m_t	overlap threshold between cell markers and expression matrix.
c_t	correlation threshold between genes.
test	statistical test that check if overlap is significant could be "p" for phyper or "f" for fisher.
org	organism to be used that can be 'h' for human, 'm' for mouse, and 'a' for all markers.

Value

list of Seurat object that have the assigned clusters, and top 3 proposed cell types.

Author(s)

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`sctype` *Run the sctype approach as it's implemented by Ianevski, A., Giri, A.K. and Aittokallio, T.*

Description

This Function is used to run the sctype approach with faster implementation

Usage

```
sctype(sobj,assay="RNA",tissue,tt="a",clus,org="a",scaled=T,database="sctype")
```

Arguments

`sobj`	Seurat object.
`assay`	assay to be used default is set to RNA.
`tissue`	specified tissue from which the data comes.
`tt`	tissue type whether 'a' for all types 'n' for normal tissues only or "c" for cancer tissues.
`clus`	colname in the mata.data that have the cell cluster numbers.
`org`	organism to be used that can be 'h' for human, 'm' for mouse, and 'a' for all markers.
`scaled`	indicates whether the matrix is scaled (TRUE by default)
`database`	name of the database to be used that can be 'sctype' or 'UMD'

Value

vector of genes names which overlap with the correlation matrix.

Author(s)

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