Package 'scRNAtools'

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Description We integrated the common analysis methods utilized in single cell RNA sequencing data, which included cluster method, principal components analysis (PCA), the filter of differentially expressed genes, pathway enrichment analysis and correlated analysis methods.

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Depends R (>= 2.10), foreach, base

Imports ALL, ConsensusClusterPlus, scatterplot3d, ggplot2, Rtsne, limma, edgeR, TPEA, Rmisc, lattice, plyr, ggthemes, reshape2, PerformanceAnalytics, corrplot, Hmisc, igraph, survival

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`scRNAtools-package` *Single Cell RNA Sequencing Data Analysis Tools*

Description

We integrated the common analysis methods utilized in single cell RNA sequencing data, which included cluster method, PCA, the filter of differentially expressed genes, pathway enrichment analysis and correlated analysis methods.

Author(s)

Qian Yang Maintainer: Qian Yang <bioqianyang@163.com>

Examples

```
####Here list three main function, cluster, PCA and t-SNE####
####cluster####
data(example1);##Example data in this package.
k<-6;##set K based on your own requirement.
scRNAtools_cluster(example1,k)
####PCA####
data(example1)
data(types)
pdf(file=file.path(tempdir(), "PCA_result-R.pdf"))##Save the figures of PCA results.
scRNAtools_pca(example1,types)
dev.off()
####t-SNE#####
data(exam)
scRNAtools_tsne(exam)

####Gene expression###
data(example)
types<-"1"
```

```
num<-0.8
scRNAtools_Geneexp(example,types,num)
```

`corr_re` *correlation index*

Description

The correlation index of the genes in the section of correlated analysis.

`DEGs` *Users interested genes or differentially expressed genes*

Description

Gene list with two columns. The first column is Entrez ID of genes and the second column is gene symbol

---

`exam` *exam*

Description

Example data in t-SNE method

`exam1` *exam1*

Description

Example data in correlated analysis

`example` *example*

Description

scRNA sequencing data in 50 cells and 1000 genes

example1 *example1*

Description

scRNA sequencing data

scRNAtools_cluster *Cluster section*

Description

Do consistent clustering analysis use clusterProfiler method

Usage

```
scRNAtools_cluster(example1, k)
```

Arguments

example1	scRNA sequencing data with header.
k	The number of class. If you set k is 6, you will obtain 6 results of cluster.

Details

The results are presented in your occurrent path.

Author(s)

Qian Yang

References

Guangchuang Yu, Li-Gen Wang, Yanyan Han and Qing-Yu He. clusterProfiler: an R package for comparing biological themes among gene clusters. OMICS: A Journal of Integrative Biology 2012, 16(5):284-287.

Examples

```
##setwd("")###Set the path your data in.
data(example1)##Example data in this package.
k<-6##set K based on your own requirement.
scRNAtools_cluster(example1,k)
```

scRNAtools_cor_map *Correlation analysis*

Description

Correlation analysis of interested gene set or differentially expressed gene set.

Usage

```
scRNAtools_cor_map(exam1, types_all, type, methods)
```

Arguments

exam1	scRNA sequencing data of several genes and cells.
types_all	Cell names of each type.
type	Cell type.
methods	correlation methods including "pearson", "kendall" and "spearman".

Details

Return the correlation index of each two genes.

Author(s)

Qian Yang

Examples

```
data(exam1)
data(types_all)
type<-"Malignant";
methods<-"pearson";##methods = c("pearson", "kendall", "spearman").
pdf(file=file.path(tempdir(), "correlation_color.pdf"))
scRNAtools_cor_map(exam1,types_all,type,methods)
dev.off()
```

scRNAtools_cor_map_r *Present correlation index in figure*

Description

Correlation analysis with correlation index of interested gene set or differentially expressed gene set.

Usage

```
scRNAtools_cor_map_r(exam1, types_all, type, methods)
```

Arguments

exam1	scRNA sequencing data of several genes and cells.
types_all	Cell names of each type.
type	Cell type.
methods	correlation methods including "pearson", "kendall" and "spearman".

Details

Return the correlation index of each two genes.

Author(s)

Qian Yang

Examples

```
data(exam1)
data(types_all)
type<-"Malignant";
methods<-"pearson";##methods = c("pearson", "kendall", "spearman").
pdf(file=file.path(tempdir(), "correlation_num.pdf"))
scRNAtools_cor_map_r(exam1,types_all,type,methods)
dev.off()
```

scRNAtools_DEGsA *Identification of differentially expressed genes*

Description

Users can identify differentially expressed genes between two type of cells based on fold change value.

Usage

```
scRNAtools_DEGsA(example, types_all, type1, type2, num)
```

Arguments

example	scRNA sequencing data with header.
types_all	Cell types in the example data.
type1	Cell type one.
type2	Cell type two.
num	Threshold value of expressed genes in appointed cell types. For example, we set 0.8 in example section.

Details

The output data is the fold change value of differentially expressed genes.

Author(s)

Qian Yang

Examples

```
data(example)
data(types)
type1<-"No malignant"
type2<-"Malignant"
num<-0.8;###type1 Vs type2
pdf(file=file.path(tempdir(), "DEGs.pdf"))
scRNAtools_DEGsA(example,types_all,type1,type2,num)
dev.off()
```

scRNAtools_Gene2exp_1 *Present the expression of two genes*

Description

This function can present the expression of two gene in appointed cell type.

Usage

```
scRNAtools_Gene2exp_1(example, types_all, gene1, gene2, n, col_1, col_2, pch, lwd)
```

Arguments

example	scRNA sequencing data without header.
types_all	Cell names of each type.
gene1	Gene one you are interested in.
gene2	Gene two you are interested in.
n	Number of cell names in scRNA sequening data.
col_1	The color of line of gene one in the figure.
col_2	The color of line of gene two in the figure.
pch	The shape of nodes in figure.
lwd	The width of lines in figure.

Author(s)

Qian Yang

Examples

```
data(example)
data(types_all)
gene1<-"CHD1"
gene2<-"CD82"
col_1="red"
col_2="blue"
pch=19
lwd=1
n<-2
scRNAtools_Gene2exp_1(example,types_all,gene1,gene2,n,col_1,col_2,pch,lwd)
```

scRNAtools_Gene3exp_1 *Present gene expression*

Description

This function can present the expression of two gene in appointed cell type.

Usage

```
scRNAtools_Gene3exp_1(example,types_all,gene1,gene2,gene3,n,col_1,col_2,col_3,pch,lwd)
```

Arguments

example	scRNA sequencing data without header.
types_all	Cell names of each type.
gene1	Gene one you are interested in.
gene2	Gene two you are interested in.
gene3	Gene three you are interested in.
n	Number of cell names in scRNA sequening data.
col_1	The color of line of gene one in the figure.
col_2	The color of line of gene two in the figure.
col_3	The color of line of gene three in the figure.
pch	The shape of nodes in figure.
lwd	The width of lines in figure.

Author(s)

Qian Yang

Examples

```
data(example)
data(types_all)
gene1<-"CHD1"
gene2<-"CD82"
gene3<-"ASS1"
col_1="red"
col_2="blue"
col_3="green"
pch=19
lwd=2
n<-3
scRNAtools_Gene3exp_1(example,types_all,gene1,gene2,gene3,n,col_1,col_2,col_3,pch,lwd)
```

scRNAtools_Geneexp *Expressed genes in scRNA sequencing data*

Description

Extracted the genes expressed in cells. Users can set the threshold value.

Usage

```
scRNAtools_Geneexp(example, types, num)
```

Arguments

example	scRNA sequencing data without header.
types	Cell types in the example data.
num	Threshold value of expressed genes in appointed cell types. For example, we set 0.8 in example section.

Value

zset	Gene expression data required the threshold value.

Author(s)

Qian Yang

Examples

```
data(example)
types<-"1"
num<-0.8
scRNAtools_Geneexp(example,types,num)
```

scRNAtools_Geneexp_1 *Present gene expression*

Description

This function can present the expression of one gene in appointed cell type.

Usage

```
scRNAtools_Geneexp_1(example, gene, types_all, n, col, pch, lwd)
```

Arguments

example	scRNA sequencing data without header.
gene	One gene you are interested in.
types_all	Cell names of each type.
n	Number of cell names in scRNA sequening data.
col	The color of line in the figure.
pch	The shape of nodes in figure.
lwd	The width of lines in figure.

Author(s)

Qian Yang

Examples

```
data(example)
data(types_all)
gene<-"CHD1";###Set the gene you are interested in.
n<-3;###Set the type of cells you are interested in.
col<-"red";###Set the color of line in the figure.
pch<-19;###Set the shape of nodes in figure.
lwd<-2;###Set the width of lines in figure.
scRNAtools_Geneexp_1(example,gene,types_all,n,col,pch,lwd)
```

---

scRNAtools_inter_net *Construction of interactive network in scRNA sequencing data*

Description

Construction of interactive network based on scRNa sequencing data.

Usage

```
scRNAtools_inter_net(corr_re, p, r, size, color)
```

Arguments

corr_re	The results of correlation analysis, which including four columns, the first two columns are genes and the last two columns are correlation index and p-value,respectively.
p	The p-value of correlation index.
r	Correlation index
size	The size of nodes in the network.
color	The color of nodes in the network.

Author(s)

Qian Yang

Examples

```
data(corr_re)
p<-0.05
r<-0.9
size<-5 #nodes size
color<-"#00B2EE" ##Color of nodes.
pdf(file=file.path(tempdir(), "interact_net.pdf"))
scRNAtools_inter_net(corr_re,p,r,size,color)
dev.off()
```

---

scRNAtools_pca *PCA analysis*

Description

PCA analysis for scRNA sequencing data

Usage

```
scRNAtools_pca(example1, types)
```

Arguments

example1	scRNA sequencing data with header.
types	Cell types in the example data.

Author(s)

Qian Yang

Examples

```
data(example1)
data(types)
pdf(file=file.path(tempdir(), "PCA_result-R.pdf"))##Save the figures of PCA results.
scRNAtools_pca(example1,types)
dev.off()
```

scRNAtools_pca_3D *3D PCA analysis*

Description

PCA analysis for scRNA sequencing data and present 3D figure.

Usage

```
scRNAtools_pca_3D(example1, types)
```

Arguments

example1	scRNA sequencing data with header.
types	Cell types in the example data.

Author(s)

Qian Yang

Examples

```
##3D PCA analysis
data(example1)
data(types)
scRNAtools_pca_3D(example1,types)##3D figure of PCA results.
```

scRNAtools_PEA *Pathway enrichment analysis*

Description

Pathway enrichment analysis using the interested gene set or differentially expressed gene set provided by users. This data contains two column (Enterz ID and gene sybmols)

Usage

```
scRNAtools_PEA(DEGs,number)
```

Arguments

DEGs	Interested gene set of differentially expressed gene set.
number	The number of random, for example, users can set 1000, 5000 or more.

Details

This function integrated method to do the pathway enrichment analysis, TPEA.

Value

The significant pathways are wrote in the occurrent path.

Author(s)

Qian Yang

References

Wei Jiang (2017). TPEA: A Novel Topology-Based Pathway Enrichment Analysis Approach.

Examples

```
data(DEGs)
number<-10
pdf(file=file.path(tempdir(), "enrichment analysis.pdf"))
scRNAtools_PEA(DEGs,number)
dev.off()
```

`scRNAtools_tsne` *t-SNE analysis*

Description

t-SNE analysis for scRNA sequencing data

Usage

```
scRNAtools_tsne(exam)
```

Arguments

`exam`	scRNA sequencing data with four genes. Users can reference the format and input their own data.

Author(s)

Qian Yang

References

L.J.P. van der Maaten and G.E. Hinton. Visualizing High-Dimensional Data Using t-SNE. Journal of Machine Learning Research 9(Nov):2579-2605, 2008.

Examples

```
data(exam)
scRNAtools_tsne(exam)
```

types *types*

Description

Cell types in the example data

types_all *types_all*

Description

Cell names of each type

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