Package 'scMAGeCK'

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Type Package

Title Identify genes associated with multiple expression phenotypes in single-cell CRISPR screening data

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Description
scMAGeCK is a computational model to identify genes associated with multiple expression phenotypes from CRISPR screening coupled with single-cell RNA sequencing data (CROP-seq)

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biocViews CRISPR, SingleCell, RNASeq, PooledScreens, Transcriptomics, GeneExpression, Regression

NeedsCompilation yes

Imports Seurat, stats, utils

Suggests knitr, rmarkdown

VignetteBuilder knitr

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scMAGeCK-package *Identify genes associated with multiple expression phenotypes in single-cell CRISPR screening data*

Description

scMAGeCK is a computational model to identify genes associated with multiple expression phenotypes from CRISPR screening coupled with single-cell RNA sequencing data (CROP-seq)

Details

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Index: This package was not yet installed at build time.
scMAGeCK is a computational model to identify genes associated with multiple expression phenotypes from CRISPR screening coupled with single-cell RNA sequencing data (CROP-seq).scMAGeCK is based on our previous MAGeCK and MAGeCK-VISPR models for pooled CRISPR screens.

The scMAGeCK manuscript can be found at bioRxiv(https://www.biorxiv.org/content/10.1101/658146v1/).

Author(s)

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Examples

```
### BARCODE file contains cell identity information, generated from
### the cell identity collection step
BARCODE <- system.file("extdata","barcode_rec.txt",package = "scMAGeCK")
### RDS can be a Seurat object or local RDS file path that contains
### the scRNA-seq dataset
RDS <- system.file("extdata","singles_dox_mki67_v3.RDS",package = "scMAGeCK")

### Set RRA executable file path.
###   You can generate RRA executable file by following commands:
###   wget https://bitbucket.org/weililab/scmageck/downloads/RRA_0.5.9.zip
###   unzip RRA_0.5.9.zip
###   cd RRA_0.5.9
###   make
RRAPATH <- "/Library/RRA_0.5.9/bin/RRA"

target_gene <- "MKI67"

rra_result <- scmageck_rra(BARCODE=BARCODE, RDS=RDS, GENE=target_gene,
                           RRAPATH=RRAPATH, LABEL='dox_mki67',
                           NEGCTRL=NULL, KEEPTMP=FALSE,
                           PATHWAY=FALSE, SAVEPATH=NULL)
head(rra_result)

lr_result <- scmageck_lr(BARCODE=BARCODE, RDS=RDS, LABEL='dox_scmageck_lr',
        NEGCTRL = 'NonTargetingControlGuideForHuman', PERMUTATION = 1000,
        SAVEPATH=NULL, LAMBDA=0.01)
```

```
lr_score <- lr_result[1]
lr_score_pval <- lr_result[2]
head(lr_score_pval)
```

---

scmageck_lr *Use linear regression to test the association of gene knockout with all possible genes*

Description

echo "Use linear regression to test the association of gene knockout with all possible genes"

Usage

```
scmageck_lr(BARCODE, RDS, NEGCTRL, SELECT_GENE=NULL, LABEL = NULL,
PERMUTATION = NULL, SAVEPATH = "./",LAMBDA=0.01,GENE_FRAC=0.01)
```

Arguments

BARCODE	A txt file to include cell identity information, generated from the cell identity collection step.
RDS	A Seurat object or local RDS file path that contains the scRNA-seq dataset. Note that the dataset has to be normalized and scaled.
NEGCTRL	The name of the genes (separated by ",") served as negative controls.
SELECT_GENE	The list of genes for regression. By default, all genes in the table are subject to regression.
LABEL	The label of the output file.
PERMUTATION	The number of permutations for p value calculation.
SAVEPATH	The save path of result. Default save path is the current working directory. If you don't need save the result, set SAVEPATH as NULL.
LAMBDA	A paramter for the LR model for ridge regression. Default: 0.01.
GENE_FRAC	A paramter for filtering low expressed genes. By default, only genes that have expressions in at least that fractions of cells are kept. Default: 0.01.

Value

The result for object RDS

Examples

```
### BARCODE file contains cell identity information, generated from the cell identity collection step
 BARCODE <- system.file("extdata","barcode_rec.txt",package = "scMAGeCK")

### RDS can be a Seurat object or local RDS file path that contains the scRNA-seq dataset
 RDS <- system.file("extdata","singles_dox_mki67_v3.RDS",package = "scMAGeCK")

 lr_result <- scmageck_lr(BARCODE=BARCODE, RDS=RDS, LABEL='dox_scmageck_lr',
     NEGCTRL = 'NonTargetingControlGuideForHuman', PERMUTATION = 1000, SAVEPATH=NULL, LAMBDA=0.01)
 lr_score <- lr_result[1]
 lr_score_pval <- lr_result[2]
 head(lr_score_pval)
```

scmageck_rra *Use RRA to test the association of gene knockout with certain marker expression*

Description

echo "Use RRA to test the association of gene knockout with certain marker expression"

Usage

```
scmageck_rra(BARCODE, RDS, GENE, RRAPATH = NULL, LABEL = NULL, NEGCTRL = NULL,
KEEPTMP = FALSE, PATHWAY = FALSE, SAVEPATH = "./")
```

Arguments

BARCODE	A txt file to include cell identity information, generated from the cell identity collection step.
RDS	A Seurat object or local RDS file path that contains the scRNA-seq dataset. Note that the dataset has to be normalized and scaled.
GENE	Genes whose expressions are to be tested. Multiple genes can be provided, separated by ",". For example, "MKI67,TP53"
RRAPATH	The path to the RRA program, if RRA cannot be found in the PATH environment variable.
LABEL	The label of the output file.
NEGCTRL	The name of the negative control gene. For example, "NonTargetingControlGuideForHuman". Default is NULL (do not use any negative controls).
KEEPTMP	Keep temporary files.
PATHWAY	Treat genes in –GENE option as a pathway. In other words, the averaged expression of these genes will be used for testing.
SAVEPATH	The save path of result. Default save path is the current working directory. If you don't need save the result, set SAVEPATH as NULL.

Value

The result for object RDS

Examples

```
### BARCODE file contains cell identity information, generated from the cell identity collection step
 BARCODE <- system.file("extdata","barcode_rec.txt",package = "scMAGeCK")

### RDS can be a Seurat object or local RDS file path that contains the scRNA-seq dataset
 RDS <- system.file("extdata","singles_dox_mki67_v3.RDS",package = "scMAGeCK")

 target_gene <- "MKI67"

 rra_result <- scmageck_rra(BARCODE=BARCODE, RDS=RDS, GENE=target_gene,
        LABEL='dox_mki67', NEGCTRL=NULL, KEEPTMP=FALSE, PATHWAY=FALSE, SAVEPATH=NULL)
 head(rra_result)
```

Index