

Package ‘FPSOmics’

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Type Package

Title Ferroptosis Score and associated multi-Omics

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Description

FPSOmics is an R package to calculate ferroptosis score and multidimensional ferroptosis-associated molecular signatures.

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Suggests knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

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FPS

Calculate of ferroptosis score

Description

We firstly calculate enrichment score (ES) of ferroptosis-promote genes(pro-FRGs) and ferroptosis-inhibit genes(anti-FRGs) using single sample gene set enrichment analysis (ssGSEA), then ferroptosis score was defined by the ES of pro-FRGs minus anti-FRGs.

Usage

```
FPS(input_exp_data)
```

Arguments

```
input_exp_data
```

expression matrix (rownames of the variable must be gene symbol, each column is a sample)

Value

data.frame of ferroptosis score, column of pro is pro-ferroptosis score, column of anti is anti-ferroptosis score, column of FPS is Ferroptosis score, column of barcode is samples, column of myclusters is high and low group divided by median ferroptosis score

Examples

```
data(m1_input_mRNA, package='FPSOmics')
FPS_score=FPS(m1_input_mRNA)
```

FPSmultiOmicsSig *Calculation of ferroptosis-associated molecular signatures*

Description

A propensity score matching (PSM) algorithm, which appropriately control the effects of clinical confounding factors, was used to calculate ferroptosis-associated molecular signatures between high and low ferroptosis score group.

Usage

```
FPSmultiOmicsSig(input_Clinical, input_FPS_group, input_omics)
```

Arguments

```
input_Clinical
```

data.frame of the clinical information, the column of barcode is samples and the rest column is each clinical feature (For continuous variables, the name could be age_continuous; For discrete variables, the name could be gender_discrete)

```
input_FPS_group
```

data.frame of high and low group information divided by median ferroptosis score, the column of barcode is samples and the column of myclusters is high and low group information divided by median ferroptosis score

```
input_omics
```

molecular matrix (rownames of the variable must be molecular symbol, each column is a sample)

Value

data.frame of a propensity score matching (PSM) algorithm result with $fdr < 0.05$, column of feature.sig is each gene, column of pvalue.sig is p value, column of fdr.sig is fdr, column of coef.sig is coefficient, column of mean0.sig is mean of low group, column of mean1.sig is mean of high group, column of mean0.sig.w is weighted mean of low group, column of mean1.sig.w is weighted mean of high group

Examples

```
data(m3_input_Clinical, package='FPSOmics')
data(m3_input_FPS_score, package='FPSOmics')
data(m3_input_mRNA, package='FPSOmics')
PSM_result=FPSmultiOmicsSig(m3_input_Clinical, m3_input_FPS_score, m3_input_mRNA)
```

FPSmultiOmicsSigEnrich

Function enrichment

Description

Study the differences of different ferroptosis status in cancer hallmarks, KEGG pathway by Gene Set Enrichment Analysis (GSEA) and GO, KEGG enrichment.

Usage

```
FPSmultiOmicsSigEnrich(input_PSM, input_gs_kegg, temp_folder)
```

Arguments

input_PSM	data.frame of the PSM result from FPSmultiOmicsSig function
input_gs_kegg	the genelist of two column for GSEA enrichment, the first column is term and the second column is gene
temp_folder	the temporal folder for output result

Value

table and figures of GO, KEGG and GSEA enrichment result

Examples

```
data(m4_input_gs_kegg, package='FPSOmics')
data(m4_input_PSM, package='FPSOmics')
enrichment_result=FPSmultiOmicsSigEnrich(m4_input_PSM, m4_input_gs_kegg, 'temp_folder')
```

FPSsurvival

Calculation of ferroptosis score and survival analysis between high and low ferroptosis score groups.

Description

We firstly calculate enrichment score (ES) of ferroptosis-promote genes(pro-FRGs) and ferroptosis-inhibit genes(anti-FRGs) using single sample gene set enrichment analysis (ssGSEA), then ferroptosis score was defined by the ES of pro-FRGs minus anti-FRGs. Secondly, survival analysis between high and low ferroptosis score groups.

Usage

```
FPSsurvival(input_exp_data, input_survival_data)
```

Arguments

input_exp_data

expression matrix (rownames of the variable must be gene symbol, each column is a sample)

input_survival_data

data.frame of the survival time information, the name of first column is barcode which means samples, the name of second column is OS which means censored status, the name of third column is OS.time which means survival time

Value

data.frame of ferroptosis score, column of pro is pro-ferroptosis score, column of anti is anti-ferroptosis score, column of FPS is Ferroptosis score, column of barcode is samples, column of myclusters is high and low group divided by median ferroptosis score; score_MK_plot is MK curve for high and low ferroptosis score

Examples

```
data(m1_input_mRNA, package='FPSOmics') #load mRNA matrix
data(m2_input_survival_data, package='FPSOmics') #load survival time
FPS_survival_result=FPSsurvival(m1_input_mRNA,m2_input_survival_data)
```

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