Package 'iMES'

June 17, 2023

Title Index of methylation-based epigenetic silencing

Version 0.99.1

Description This function calculates an index of methylation-based epigenetic silencing (iMES) using binary DNA methylation status for patients with clear cell renal cell carcinoma.

License MIT + file LICENSE

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.2

Depends R (>= 4.0.1)

Suggests knitr,
rmarkdown,
testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

Imports circlize,
ClassDiscovery,
ComplexHeatmap,
grid,
klaR,
lsr,
RTN

R topics documented:

adaLASSO.coeff *AdaLASSO coefficient*

Description

A data frame storing feature coefficient for model-selected probes

Usage

```
adaLASSO.coeff
```

Format

A data frame with 58 rows (probes relevant to silenced genes) and their corresponding adaLASSO coefficient

contains coefficient to calculate iMES.

iMES *Index of methylation-based epigenetic silencing*

Description

This function calculates an index of methylation-based epigenetic silencing (iMES) using binary DNA methylation status for patients with clear cell renal cell carcinoma.

Usage

```
iMES(bmat = NULL, methcut = 0.2, samples = NULL, quantile = 3)
```

Arguments

bmat	A numeric DNA methylation beta matrix with row features (probes) and sample columns and continuous values as input.
methcut	A numeric value to indicate the methylation cutoff and assign each probe to be either methylated or unmethylated; 0.2 by default.
samples	A string value to indicate the samples that will be used to calculate iMES; all samples will be used by default.
quantile	A numeric value to indicate quantile base to dichotomize samples into iMES-high and iMES-low; 3 (tertile) by default.

Value

A DataFrame with rownames of samples and three columns: iMES (raw iMES score), iMES.mm (minmax normalized iMES score * 10; range from 0-10), iMES.group (dichotomized iMES group)

Author(s)

Xiaofan Lu

lasso_fea_gene *LASSO gene features*

Description

An vector of genes that constitutes iMES

Usage

```
lasso_fea_gene
```

Format

An vector of genes that constitutes iMES
contains 55 genes.

Mids *mRNA list*

Description

An vector including mRNAs

Usage

```
Mids
```

Format

An vector including mRNAs
contains 19,620 mRNAs.

predRegulon *Regulon phenotypes based on genes with epigenetic silencing*

Description

This function inferrs regulon activity of genes that were epigenetically silenced using transcriptomic expression data for patients with clear cell renal cell carcinoma.

Usage

```
predRegulon(
  emat = NULL,
  samples = NULL,
  seed = 20000112,
  fig.path = getwd(),
  fig.name = "heatmap of regulon activity"
)
```

Arguments

emat	A numeric transcritomic gene expression with row features (genes) and sample columns and continuous values as input with proper normalisation (e.g., TPM, FPKM, normalized count, or microarray signals).
samples	A string value to indicate the samples that will be used to calculate regulon activity; all samples will be used by default.
seed	A numeric string to indicate seed for K-mode clustering for reproducibility
fig.path	A string value to indicate the output path for storing the regulon activity heatmap.
fig.name	A string value to indicate the name of the regulon activity heatmap.

Value

A DataFrame with rownames of regulons and colnames of samples with input of regulon activity status, and a predictive regulon phenotype based on K-modes clustering (k=2) with a heatmap.

Author(s)

Xiaofan Lu

---

rtni_kirc *TNI object*

Description

An R object derived from Transcriptional Network Inference

Usage

```
rtni_kirc
```

Format

An object of class TNI

contains TNI an object of class RTN and can be used for external prediction of regulon activity.

Index