Package 'refineMIBC'

April 10, 2021

Title Refine muscle-invasive bladder cancer

Version 0.99.1

Description This package is to 1) classify muscle-
invasive bladder cancer (MIBC) to one of the four subtypes identified from multi-
omics integrative clustering; 2) refine basal-like MIBC into either basal-inflamed or basal-
noninflamed subtype.

Depends R (>= 4.0.1)

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Encoding UTF-8

LazyData true

Suggests testthat,
knitr,
rmarkdown,
kableExtra

Remotes github::Lothelab/CMScaller@master

Imports CMScaller,
varSelRF

VignetteBuilder knitr

RoxygenNote 7.1.1

biocViews Classification, CancerData

URL https://github.com/xlucpu/refineMIBC

BugReports https://github.com/xlucpu/refineMIBC/issues

Collate 'refineMIBC.R'
'refineBasal.R'

R topics documented:

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refineBasal   *Refine basal-like muscle invasive bladder cancer*

Description

Refine pre-identified basal-like muscle invasive bladder cancer into either basal-inflamed or basal-noninflamed subtype based on a random forest classifier.

Usage

```
refineBasal(
  expr = NULL,
  isBasal = NULL,
  res.path = getwd(),
  res.name = "REFINED_MIBC_BASAL"
)
```

Arguments

expr	A numeric expression matrix with row features and sample columns.
isBasal	A logic vector to indicate if the sample is basal-like or not. NULL by default and all samples will be assumed as basal-like.
res.path	A string value to indicate the path for saving the prediction result.
res.name	A string value to indicate the name of the output prediction table.

Value

A data.frame storing the random forest prediction results, including 'samID' for sample name, 'prob' for probability as basal-inflamed, and 'basal' for final classifications using 0.5 as cutoff.

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refineMIBC   *Refine muscle-invasive bladder cancer*

Description

Refine muscle-invasive bladder cancer into four subtypes based on transcriptome profile by nearest template prediction algorithm.

Usage

```
refineMIBC(
  expr = NULL,
  scaleFlag = TRUE,
  centerFlag = TRUE,
  distance = "cosine",
  seed = 123456,
  doPlot = FALSE,
  fig.path = getwd(),
  fig.name = "NTP_PREDICTED_HEATMAP",
```

```
    res.path = getwd(),
    res.name = "PREDICTED_MIBC_SUBTYPE"
)
```

Arguments

`expr`	A numeric expression matrix with row features and sample columns.
`scaleFlag`	A logic value to indicate if the expression data should be further scaled. TRUE by default.
`centerFlag`	A logic value to indicate if the expression data should be further centered. TRUE by default.
`distance`	A string value to indicate the distance measurement. Allowed values contain c('cosine', 'pearson', 'spearman', 'kendall'); 'cosine' by default.
`seed`	An integer value for p-value reproducibility; 123456 by default.
`doPlot`	A logic value to indicate whether to produce prediction heatmap; FALSE by default.
`fig.path`	A string value to indicate the output path for storing the nearest template prediction heatmap.
`fig.name`	A string value to indicate the name of the nearest template prediction heatmap.
`res.path`	A string value to indicate the path for saving the prediction result.
`res.name`	A string value to indicate the name of the output prediction table.

Value

A figure of predictive heatmap by NTP (.pdf) and a data.frame storing the results of nearest template prediction (see ntp).

References

Hoshida, Y. (2010). Nearest Template Prediction: A Single-Sample-Based Flexible Class Prediction with Confidence Assessment. PLoS ONE 5, e15543.

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rfClassifier	*Random forest classifier for refining basal-like MIBC*

Description

An R object derived from varSelRF.

Usage

```
rfClassifier
```

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templates   *Template for classifying MIBC using NTP*

Description

A data frame storing the subtype-specific markers for MIBC.

Usage

```
templates
```

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