

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'
'dataset.R'
'global.R'

R topics documented:

refineBasal	2
refineMIBC	3
rfClassifier	4
templates	4

Index	5
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refineBasal	<i>Refine basal-like muscle invasive bladder cancer</i>
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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.

Examples

```
library(refineMIBC)
load(system.file("extdata", "demo.RData", package = "refineMIBC", mustWork = TRUE)) # load example data
expr <- demo$MIBC.expr
subt <- demo$MIBC.subt
isbasal <- subt$TCGA == "Basal_squamous"
iBasal <- refineBasal(expr = expr,
                      isBasal = isbasal)
head(iBasal)
```

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.

References

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

Eide, P.W., Bruun, J., Lothe, R.A. et al. CMScaller: an R package for consensus molecular subtyping of colorectal cancer pre-clinical models. Sci Rep 7, 16618 (2017).

Examples

```
library(refineMIBC)
load(system.file("extdata", "demo.RData", package = "refineMIBC", mustWork = TRUE)) # load example data
expr <- demo$MIBC.expr
subt <- demo$MIBC.subt
iCS <- refineMIBC(expr      = expr,
                  scaleFlag = TRUE,
                  centerFlag = TRUE,
                  doPlot    = FALSE)

head(iCS)
```

rfClassifier	<i>Random forest classifier for refining basal-like MIBC</i>
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Description

An R object derived from varSelRF.

Usage

```
rfClassifier
```

Format

An object of class varSelRF
contains rfClassifier an object of class varSelRF and can be used for external prediction.

templates	<i>Template for classifying MIBC using NTP</i>
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Description

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

Usage

```
templates
```

Format

A data frame with 120 rows (30 markers for each subtype) and 3 variables.
contains templates the subtype-specific up-regulated markers for MIBC.

Index

- * **datasets**
 - rfClassifier, [4](#)
 - templates, [4](#)
- refineBasal, [2](#)
- refineMIBC, [3](#)
- rfClassifier, [4](#)
- templates, [4](#)