

# Package ‘refineMIBC’

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**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)

**License** GPL-3 + file LICENSE

**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:

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refineBasal

*Refine basal-like muscle invasive bladder cancer*


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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.

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refineMIBC

*Refine muscle-invasive bladder cancer*


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### 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).

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rfClassifier

*Random forest classifier for refining basal-like MIBC*


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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.

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`templates`*Template for classifying MIBC using NTP*

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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.

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