

Package ‘consensusOV’

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Type Package

Title Gene expression-based subtype classification for high-grade serous ovarian cancer

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Description This package implements four major subtype classifiers for high-grade serous (HGS) ovarian cancer as described by Helland et al. (PLoS One, 2011), Bentink et al. (PLoS One, 2012), Verhaak et al. (J Clin Invest, 2013), and Konecny et al. (J Natl Cancer Inst, 2014). In addition, the package implements a consensus classifier, which consolidates and improves on the robustness of the proposed subtype classifiers, thereby providing reliable stratification of patients with HGS ovarian tumors of clearly defined subtype.

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Imports Biobase, GSVA, gdata, genefu, limma, matrixStats, randomForest, stats, utils

Depends R (>= 3.4)

URL <http://www.pmggenomics.ca/bhklab/software/consensusOV>

Suggests knitr, ggplot2

VignetteBuilder knitr

RoxygenNote 6.0.1

LazyData true

biocViews Classification, Clustering, DifferentialExpression, GeneExpression, Microarray, Transcriptomics

BugReports <https://github.com/bhklab/consensusOV/issues>

git_url <https://git.bioconductor.org/packages/consensusOV>

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dataset.merging	<i>Merging all individual esets and merging them into a big eset</i>
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Description

Merging all individual esets and merging them into a big eset

Usage

```
dataset.merging(esets, method = c("union", "intersect"),
  standardization = c("quantile", "robust.scaling", "scaling", "none"),
  nthread = 1)
```

Arguments

esets	The list containing all GSE file that need to be merged.
method	either "unique" or "intersect" is use to for selecting geneid
standardization	choose between "quantile", "robust.scaling", "scaling" or "none"
nthread	number of threads (1 by default)

Value

The merging eset

get.bentink.subtypes	<i>Get ovarian cancer subtypes as defined by Bentink et al., 2012</i>
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Description

Get ovarian cancer subtypes as defined by Bentink et al., 2012

Usage

```
get.bentink.subtypes(expression.matrix, entrez.ids)
```

Arguments

`expression.matrix`
A matrix of gene expression values with rows as genes, columns as samples.

`entrez.ids` A vector of Entrez Gene IDs, corresponding to the rows of `expression.matrix`

Value

A list with first value `Bentink.subtypes` containing a factor of subtype names; and second value `angio` containing the output of `genefu::ovcAngiogenic`

References

Bentink et al. *Angiogenic mRNA and microRNA gene expression signature predicts a novel subtype of serous ovarian cancer*. PloS one (2012).

Examples

```
library(Biobase)
library(genefu)
data(GSE14764.eset)
expression.matrix <- exprs(GSE14764.eset)
entrez.ids <- as.character(fData(GSE14764.eset)$EntrezGene.ID)
get.bentink.subtypes(expression.matrix, entrez.ids)
```

```
get.consensus.subtypes
```

Get consensusOV ovarian cancer subtypes

Description

Get consensusOV ovarian cancer subtypes

Usage

```
get.consensus.subtypes(expression.matrix, entrez.ids,
  concordant.tumors.only = TRUE, remove.using.cutoff = FALSE,
  percentage.dataset.removed = 0.75,
  .training.dataset = consensus.training.dataset.full,
  .dataset.names.to.keep = names(esets.rescaled.classified.filteredgenes))
```

Arguments

`expression.matrix`
A matrix of gene expression values with rows as genes, columns as samples.

`entrez.ids` A vector of Entrez Gene IDs, corresponding to the rows of `expression.matrix`

`concordant.tumors.only`
Logical. Should the classifier trained only on tumors that are concordantly classified by Helland, Konecny, and Verhaak? Defaults to TRUE.

`remove.using.cutoff`
Specify whether to classify NA for samples that do not meet a margin cutoff

percentage.dataset.removed
 If remove.using.cutoff is TRUE, then classify this percentage of samples to NA based on margin values

.training.dataset
 ExpressionSet containing the training data. Defaults to the pooled dataset across selected MetaGxOvarian datasets.

.dataset.names.to.keep
 Names of MetaGxOvarian datasets to use for training

Value

A list with first value consensusOV.subtypes containing a factor of subtype names; and second value rf.probs containing a matrix of subtype probabilities

Examples

```
library(Biobase)
data(GSE14764.eset)
expression.matrix <- exprs(GSE14764.eset)
entrez.ids <- as.character(fData(GSE14764.eset)$EntrezGene.ID)
get.consensus.subtypes(expression.matrix, entrez.ids)
```

get.helland.subtypes *Get ovarian cancer subtypes as defined by Helland et al., 2011*

Description

Get ovarian cancer subtypes as defined by Helland et al., 2011

Usage

```
get.helland.subtypes(expression.matrix, entrez.ids)
```

Arguments

expression.matrix
 A matrix of gene expression values with rows as genes, columns as samples.

entrez.ids
 A vector of Entrez Gene IDs, corresponding to the rows of expression.matrix

Value

A list with first value Helland.subtypes containing a factor of subtype names; and second value subtype.scores containing a matrix of subtype scores

References

Helland et al. *Deregulation of MYCN, LIN28B and LET7 in a molecular subtype of aggressive high-grade serous ovarian cancers*. PloS one (2011).

Examples

```
library(Biobase)
data(GSE14764.eset)
expression.matrix <- exprs(GSE14764.eset)
entrez.ids <- as.character(fData(GSE14764.eset)$EntrezGene.ID)
get.helland.subtypes(expression.matrix, entrez.ids)
```

get.konecny.subtypes *Get ovarian cancer subtypes as defined by Konecny et al., 2014*

Description

Get ovarian cancer subtypes as defined by Konecny et al., 2014

Usage

```
get.konecny.subtypes(expression.matrix, entrez.ids)
```

Arguments

`expression.matrix` A matrix of gene expression values with rows as genes, columns as samples.
`entrez.ids` A vector of Entrez Gene IDs, corresponding to the rows of `expression.matrix`

Value

A list with first value `Konecny.subtypes` containing a factor of subtype names; and second value `spearman.cc.vals` containing the Spearman correlation values per subtype

References

Konecny et al. *Prognostic and therapeutic relevance of molecular subtypes in high-grade serous ovarian cancer*. Journal of the National Cancer Institute (2014).

Examples

```
library(Biobase)
data(GSE14764.eset)
expression.matrix <- exprs(GSE14764.eset)
entrez.ids <- as.character(fData(GSE14764.eset)$EntrezGene.ID)
get.konecny.subtypes(expression.matrix, entrez.ids)
```

get.subtypes *Get ovarian cancer subtypes*

Description

Get ovarian cancer subtypes

Usage

```
get.subtypes(expression.dataset, entrez.ids = NULL,
             method = c("consensusOV", "Helland", "Verhaak", "Konecny", "Bentink"), ...)
```

Arguments

expression.dataset	Either a matrix of gene expression values with rows as genes, columns as samples; or a BioBase::ExpressionSet object from MetaGxOvarian. If expression.dataset is a matrix, then entrez.ids must have length equal to the number of rows of expression.dataset.
entrez.ids	A vector of Entrez Gene IDs, corresponding to the rows of expression.dataset
method	The subtyping method to use
...	Optional parameters to be passed to the low level function

Value

A list with first value Konecny.subtypes containing a factor of subtype names; and second value spearman.cc.vals containing the Spearman correlation values per subtype

Examples

```
library(Biobase)
data(GSE14764.eset)
expression.matrix <- exprs(GSE14764.eset)
entrez.ids <- as.character(fData(GSE14764.eset)$EntrezGene.ID)
get.subtypes(expression.matrix, entrez.ids, method="Konecny")
```

get.verhaak.subtypes *Get ovarian cancer subtypes as defined by Verhaak et al., 2013*

Description

Get ovarian cancer subtypes as defined by Verhaak et al., 2013

Usage

```
get.verhaak.subtypes(expression.matrix, entrez.ids)
```

Arguments

`expression.matrix` A matrix of gene expression values with rows as genes, columns as samples.

`entrez.ids` A vector of Entrez Gene IDs, corresponding to the rows of `expression.matrix`

Value

A list with first value `Verhaak.subtypes` containing a factor of subtype names; and second value `gsva` containing the GSVA subtype scores

References

Verhaak et al. *Prognostically relevant gene signatures of high-grade serous ovarian carcinoma*. The Journal of Clinical Investigation (2013)

Examples

```
library(Biobase)
data(GSE14764.eset)
expression.matrix <- exprs(GSE14764.eset)
entrez.ids <- as.character(fData(GSE14764.eset)$EntrezGene.ID)
get.konecny.subtypes(expression.matrix, entrez.ids)
```

GSE14764.eset *Sample ExpressionSet from MetaGxOvarian*

Description

A `Biobase::ExpressionSet` from package `MetaGxOvarian` for the dataset GSE14764

Usage

```
GSE14764.eset
```

Format

A `Biobase::ExpressionSet` object

Source

<http://biorxiv.org/content/biorxiv/early/2016/05/12/052910.full.pdf>

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