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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Depends R (>= 3.6)

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

URL http://www.pmgenomics.ca/bhklab/software/consensusOV

Suggests BiocStyle, ggplot2, knitr, rmarkdown

VignetteBuilder knitr

Encoding UTF-8

RoxygenNote 6.1.1

LazyData true

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

BugReports https://github.com/bhklab/consensusOV/issues
dataset.merging

Merging all individual esets and merging them into a big eset

**Description**

Merging all individual esets and merging them into a big eset

**Usage**

```r
dataset.merging(esets, method = c("union", "intersect"),
standardization = c("quantile", "robust.scaling", "scaling", "none"),
ntthread = 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"
- `ntthread` number of threads (1 by default)

**Value**

The merging eset
get.bentink.subtypes

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

**Description**

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

**Usage**

```r
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**


**Examples**

```r
library(Biobase)  
library(genefu)  
data(GSE14764.eset)  
extpression.matrix <- exprs(GSE14764.eset)  
extrez.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
get.consensus.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))

margin(rf.probs)

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
rf.probs  
  random forest probabilities for each subtype as returned by `get.consensus.subtypes`

Value

get.consensus.subtypes returns a list with first value consensusOV.subtypes containing a factor of subtype labels; and second value rf.probs containing a matrix of subtype probabilities.

margin returns a numeric vector containing the classification margin scores, i.e. the difference between the top two subtype scores for each tumor.

Examples

library(Biobase)
data(GSE14764.eset)
extension.matrix <- exprs(GSE14764.eset)
extrez.ids <- as.character(fData(GSE14764.eset)$EntrezGene.ID)
sts <- get.consensus.subtypes(expression.matrix, entrez.ids)
margins <- margin(rf.probs)
get.hao.subtypes  

Get ovarian cancer subtypes as defined by Hao et al., 2017

Description
Get ovarian cancer subtypes as defined by Hao et al., 2017

Usage
get.hao.subtypes(expression.matrix, entrez.ids)

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

Details
Hao et al., 2017 derived a gene signature to predict the tissue of origin of ovarian tumors as either fallopian tube (FT) or ovarian surface epithelium (OSE).

The authors found that expression patterns of tissue-specific genes, prognostic genes, and molecular markers support a dualistic tissue origin of ovarian cancer, from either FT or OSE.

The subtype classifier considers 112 signature genes including 37 genes upregulated in FT and 75 genes upregulated in OSE. A score is computed that is designed to range from 0 to 1 for FT tumors, while OSE tumors have a score ranging from -1 to 0.

Value
A list with first value tissue containing a factor of subtype names (tissue of origin); and second value score containing the tissue-of-origin score.

Author(s)
Ludwig Geistlinger

References

Examples
library(Biobase)
data(GSE14764.eset)
expression.matrix <- exprs(GSE14764.eset)
entrez.ids <- as.character(fData(GSE14764.eset)$EntrezGene.ID)
get.hao.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**


**Examples**

```r
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)
```
get.subtypes

## 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


## Examples

```r
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

```r
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
get.verhaak.subtypes

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

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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