Package ‘receptLoss’

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Type Package

Title Unsupervised Identification of Genes with Expression Loss in Subsets of Tumors

Version 1.19.0

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Description receptLoss identifies genes whose expression is lost in subsets of tumors relative to normal tissue. It is particularly well-suited in cases where the number of normal tissue samples is small, as the distribution of gene expression in normal tissue samples is approximated by a Gaussian. Originally designed for identifying nuclear hormone receptor expression loss but can be applied transcriptome wide as well.

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Encoding UTF-8

LazyData true

Depends R (>= 3.6.0)

RoxygenNote 7.1.0

Imports dplyr, ggplot2, magrittr, tidyr, SummarizedExperiment

Suggests knitr, rmarkdown, testthat (>= 2.1.0), here

VignetteBuilder knitr

biocViews GeneExpression, StatisticalMethod

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Contents

`nhrs` *Table of Nuclear Hormone Receptors (NHRs)*

Description

This object contains a table of all known NHRs and was adapted from the 'guidetopharmacology' website (see references). It was joined with a bioMart table to include ensemble gene ids, which are commonly used gene symbols.

Usage

```
nhrs
```

Format

A tibble with 54 rows and 6 variables:

hgnc_symbol the HUGO gene nomenclature committee (HGNC) symbol (letters and numbers, ex. THRB)

hgnc_id the HUGO gene nomenclature committee (HGNC) symbol (a number, ex. 11799)

hgnc_name the HUGO gene nomenclature committee (HGNC) gene name (ex. "Thyroid hormone receptor beta")

entrez_gene_id the entrez gene id (a number, ex. 7068)

ensembl_gene_id the ensembl gene id (ex. ENSG00000151090, always starts with ENSG)

synonyms words or gene symbols in the literature that refer to the same gene

Source

`http://www.guidetopharmacology.org/DATA/targets_and_families.csv`

`http://www.biomart.org/`

`nSdBelowMean` *Calculate value N std dev away from mean*

Description

This function allows you to identify genes with loss of expression

Usage

```
nSdBelowMean(mn, stdv, n)
```

Arguments

`mn`	Mean of distribution
`stdv`	std dev of distribution
`n`	number of std dev below mean to calculate

Value

the value ‘n‘ standard deviations below the mean ‘mn‘

`plotReceptLoss` *Plot histogram of genes with expression loss*

Description

This function allows you to plot histograms of tumor and adj normal data

Usage

```
plotReceptLoss(exprMatrNml, exprMatrTum, rldf, geneName, addToTitle = "", clrs)
```

Arguments

`exprMatrNml`	A matrix of expression values from normal tissue. Each row is a gene, and each column is a patient or sample. Genes should be in same order as exprMatrTum.
`exprMatrTum`	A matrix of expression values from tumor tissue. Each row is a gene, and each column is a patient or sample. Genes should be in same order as exprMatrNml.
`rldf`	The dataframe output from running the receptLoss function
`geneName`	The name of the gene to plot. The name of the gene should correspond to a row name in both exprMatrNml and exprMatrTum matrices.
`addToTitle`	A string that can be added to the title, which includes the gene name.
`clrs`	Vector of length 2 containing colors to use for plot

Value

returns an object of class ‘ggplot‘

Examples

```
exprMatrNml <- matrix(abs(rnorm(100, mean=2)), nrow=10)
exprMatrTum <- matrix(abs(rnorm(100)), nrow=10)
geneNames <- paste0(letters[seq_len(nrow(exprMatrNml))],
seq_len(nrow(exprMatrNml)))
rownames(exprMatrNml) <- rownames(exprMatrTum) <- geneNames
nSdBelow <- 2
minPropPerGroup <- .2
rl <- receptLoss(exprMatrNml, exprMatrTum, nSdBelow, minPropPerGroup)
clrs <- c("#E78AC3", "#8DA0CB")
plotReceptLoss(exprMatrNml, exprMatrTum, rl, geneName="g7", clrs=clrs)
```

`receptLoss` *Identify genes with expression loss*

Description

This function allows you to identify genes with loss of expression

Usage

```
receptLoss(exprMatrNml, exprMatrTum, nSdBelow, minPropPerGroup)
```

Arguments

`exprMatrNml`	A matrix of expression values from normal tissue. Each row is a gene, and each column is a patient or sample. Genes should be in same order as exprMatrTum.
`exprMatrTum`	A matrix of expression values from tumor tissue. Each row is a gene, and each column is a patient or sample. Genes should be in same order as exprMatrNml.
`nSdBelow`	The number of SD below the mean of the adjacent normal tissue to set the boundary between tumor subgroups.
`minPropPerGroup`	A value between 0-1 that represents the minimum proportion of samples that should be present in each of the two subgroups (defined by the boundary set by nSdBelow) for a particular gene.

Value

a nx7 matrix, with n equaling the number of genes. The columns are as follows:

- geneNm - the gene name
- lowerBound - the lower bound, or the value ‘nSdBelow‘ the mean of the normal tissue expression data.

- propTumLessThBound - the proportion of tumor samples with expression levels less than ‘lowerBound‘
- muAb - "mu above", the mean expression value of tumors greater than (ie above) the ‘lowerBound‘.
- ‘muBl‘ - "mu below", the mean expression value of tumors less than (ie below) the ‘lowerBound‘.
- ‘deltaMu‘ - the difference between ‘muAb‘ and ‘muBl‘.
- meetsMinPropPerGrp - a logical indicating whether the proportion of samples in each group is greater than that set by ‘minPropPerGroup‘.

Examples

```
exprMatrNml <- matrix(abs(rnorm(100, mean=2)), nrow=10)
exprMatrTum <- matrix(abs(rnorm(100)), nrow=10)
geneNames <- paste0(letters[seq_len(nrow(exprMatrNml))],
seq_len(nrow(exprMatrNml)))
rownames(exprMatrNml) <- rownames(exprMatrTum) <- geneNames
nSdBelow <- 2
minPropPerGroup <- .2
rl <- receptLoss(exprMatrNml, exprMatrTum, nSdBelow, minPropPerGroup)
head(rl)
```

`toMatrix` *Convert SummarizedExperiment or Dataframe to Matrix*

Description

This function converts SummarizedExperiment objects and dataframes (both S3 and S4) to matrices of expression values. Used within receptLoss functions to convert all matrix-like objects to the matrix class.

Usage

```
toMatrix(m, rwnms = NA)
```

Arguments

`m`	Can be a matrix, a data.frame, a DataFrame, or SummarizedExperiment object.
`rwnms`	the rownames of the object. If NA (the default), assumes that the matrix-like object already has rownames, which in this case do not need to be supplied separately.

Value

A matrix of expression values

Examples

```
m <- as.data.frame(matrix(data=rgamma(n=100, shape=3, rate=2),
nrow=10, ncol=10))
m <- toMatrix(m)
```

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