

Package ‘receptLoss’

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Type Package

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

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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

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Depends R (>= 3.6.0)

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Imports dplyr, ggplot2, magrittr, tidyr, SummarizedExperiment

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

VignetteBuilder knitr

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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	<i>Calculate value N std dev away from mean</i>
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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	<i>Plot histogram of genes with expression loss</i>
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Description

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

Usage

```
plotReceptLoss(exprMatrNm1, exprMatrTum, rldf, geneName, addToTitle = "", clr)
```

Arguments

exprMatrNm1	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 exprMatrNm1.
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 exprMatrNm1 and exprMatrTum matrices.
addToTitle	A string that can be added to the title, which includes the gene name.
clr	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
r1 <- receptLoss(exprMatrNml, exprMatrTum, nSdBelow, minPropPerGroup)
clrs <- c("#E78AC3", "#8DA0CB")
plotReceptLoss(exprMatrNml, exprMatrTum, r1, 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

```
exprMatrNm1 <- matrix(abs(rnorm(100, mean=2)), nrow=10)
exprMatrTum <- matrix(abs(rnorm(100)), nrow=10)
geneNames <- paste0(letters[seq_len(nrow(exprMatrNm1))],
  seq_len(nrow(exprMatrNm1)))
rownames(exprMatrNm1) <- rownames(exprMatrTum) <- geneNames
nSdBelow <- 2
minPropPerGroup <- .2
r1 <- receiptLoss(exprMatrNm1, exprMatrTum, nSdBelow, minPropPerGroup)
head(r1)
```

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 `receiptLoss` functions to convert all matrix-like objects to the matrix class.

Usage

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

Arguments

<code>m</code>	Can be a matrix, a data.frame, a <code>DataFrame</code> , or <code>SummarizedExperiment</code> object.
<code>rwnms</code>	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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