Package ‘RnaSeqSampleSize’
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Description RnaSeqSampleSize package provides a sample size calculation method based on negative binomial model and the exact test for assessing differential expression analysis of RNA-seq data
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convertIdOneToOne

Description
A function to convert ID based on the biomaRt package.

Usage
convertIdOneToOne(x, dataset = "hsapiens_gene_ensembl",
filters = "uniprot_swissprot", attributes = c(filters, "entrezgene"),
verbose = FALSE)

Arguments

x
the IDs need to be converted.
dataset
Dataset you want to use. To see the different datasets available within a biomaRt
you can e.g. do: mart = useMart("ensembl"), followed by listDatasets(mart).
filters
Filters (one or more) that should be used in the query. A possible list of filters
can be retrieved using the function listFilters.
attributes
Attributes you want to retrieve. A possible list of attributes can be retrieved
using the function listAttributes.
verbose
Logical. Indicate report extra information on progress or not.

Details
A function to convert ID based on the biomaRt package.

Value
A converted ID character with the same order of parameter x.

Examples
x <- c("Q04837", "P0C0L4", "P0C0L5", "075379", "Q13068", "A2MYD1", "P60709", "P30462", "P30475", "P30479")
convertIdOneToOne(x, filters="uniprot_swissprot", verbose=TRUE)

est_count_dispersion

Description
A function to estimate the gene read count and dispersion distribution of RNA-seq data.

Usage
est_count_dispersion(counts, group = rep(1, NCOL(counts)),
subSampleNum = 20, minAveCount = 1, convertId = FALSE,
dataset = "hsapiens_gene_ensembl", filters = "hgnc_symbol")
est_power

Arguments

counts   numeric matrix of read counts.
group    vector or factor giving the experimental group/condition for each sample/library.
subSampleNum number of samples used to estimate distribution.
minAveCount Only genes with average read counts above this value are used in the estimation of distribution.
convertId logical, whether to convert the gene Id into entrez gene Id. If set as True, then dataset and filters parameter should also be set.
dataset  Dataset you want to use. To see the different datasets available within a biomart you can e.g. do: mart = useMart('ensembl'), followed by listDatasets(mart).
filters Filters (one or more) that should be used in the query. A possible list of filters can be retrieved using the function listFilters.

Details

A function to estimate the gene read count and dispersion distribution of RNA-seq data.

Value

A DEGlist from edgeR package.

Examples

counts<-matrix(sample(1:1000,6000,replace=TRUE),ncol=6)
est_count_dispersion(counts=counts,group=rep(0,6))

Description

A function to estimate the power for differential expression analysis of RNA-seq data.

Usage

est_power(n, w = 1, rho = 2, lambda0 = 5, phi0 = 1, alpha = 0.05, f,
m = 20000, m1 = 200)

Arguments

n       Numer of samples.
w       Ratio of normalization factors between two groups.
rho     minimum fold changes for prognostic genes between two groups.
lambda0 Average read counts for prognostic genes.
phi0     Dispersion for prognostic genes.
alpha    alpha level.
f        FDR level
m        Total number of genes for testing.
m1       Expected number of prognostic genes.
**Value**

Estimate power

**Examples**

\[
n<-63;\rho<-2;\lambda_0<-5;\phi_0<-0.5;f<-0.01 \\
est_power(n=n, \rho=\rho, \lambda_0=\lambda_0, \phi_0=\phi_0,f=f)
\]

---

**Description**

A function to estimate the power curve for differential expression analysis of RNA-seq data.

**Usage**

\[
est_power_curve(n, w = 1, \rho = 2, \lambda_0 = 5, \phi_0 = 1, \\
alpha = 0.05, f = 0.05, \ldots)
\]

**Arguments**

- **n**: Number of samples.
- **w**: Ratio of normalization factors between two groups.
- **\(\rho\)**: Minimum fold changes for prognostic genes between two groups.
- **\(\lambda_0\)**: Average read counts for prognostic genes.
- **\(\phi_0\)**: Dispersion for prognostic genes.
- **\(\alpha\)**: Alpha level.
- **\(f\)**: FDR level
- **\(\ldots\)**: Other parameters for est_power function.

**Value**

A list including parameters, sample size and power.

**Examples**

```r
# Not run:
result1<-est_power_curve(n=63, f=0.01, rho=2, lambda0=5, phi0=0.5)
result2<-est_power_curve(n=63, f=0.05, rho=2, lambda0=5, phi0=0.5)
plot_power_curve(list(result1,result2))
# End(Not run)
```
Description

A function to estimate the power for differential expression analysis of RNA-seq data.

Usage

```r
est_power_distribution(n, f = 0.1, m = 10000, m1 = 100, w = 1,
  rho = 2, repNumber = 100, dispersionDigits = 1, distributionObject,
  libSize, minAveCount = 5, maxAveCount = 2000, seed = 123, selectedGenes,
  pathway, species = "hsa", storeProcess = FALSE,
  countFilterInRawDistribution = TRUE, selectedGeneFilterByCount = FALSE,
  removedGenePower = TRUE)
```

Arguments

- `n`: Number of samples.
- `f`: FDR level.
- `m`: Total number of genes for testing.
- `m1`: Expected number of prognostic genes.
- `w`: Ratio of normalization factors between two groups.
- `rho`: Minimum fold changes for prognostic genes between two groups.
- `repNumber`: Number of genes used in estimation of read counts and dispersion distribution.
- `dispersionDigits`: Digits of dispersion.
- `distributionObject`: A DGEList object generated by `est_count_dispersion` function. RnaSeqSampleSizeData package contains 13 datasets from TCGA, you can set distributionObject as any one of "TCGA_BLCA","TCGA_BRCA","TCGA_CESC","TCGA_COAD","TCGA_HNSC","TCGA_KIRC","TCGA_LGG","TCGA_LUAD","TCGA_LUSC","TCGA_PRAD","TCGA_READ","TCGA_THCA","TCGA_UCEC" to use them.
- `libSize`: numeric vector giving the total count for each sample. If not specified, the libsize in distributionObject will be used.
- `minAveCount`: Minimal average read count for each gene. Genes with smaller read counts will not be used.
- `maxAveCount`: Maximal average read count for each gene. Genes with larger read counts will be taken as maxAveCount.
- `seed`: Optional. A integer, seed for randomly selecting genes.
- `selectedGenes`: Optional. Name of interested genes. Only the read counts and dispersion distribution for these genes will be used in power estimation.
- `pathway`: Optional. ID of interested KEGG pathway. Only the read counts and dispersion distribution for genes in this pathway will be used in power estimation.
- `species`: Optional. Species of interested KEGG pathway.
- `storeProcess`: Logical. Store the power and n in sample size or power estimation process.
countFilterInRawDistribution
   Logical. If the count filter will be applied on raw count distribution. If not, count
   filter will be applied on libSize scaled count distribution.

selectedGeneFilterByCount
   Logical. If the count filter will be applied to selected genes when selectedGenes
   parameter was used.

removedGene0Power
   Logical. When selectedGenes or pathway are used, some genes may have read
   count less than minAveCount and will be removed by count filter. This param-
   eter indicates if they will be used as 0 power in power estimation. If not, they
   will not be used in power estimation.

Details
   A function to estimateme the power for differential expression analysis of RNA-seq data.

Value
   Average power or a list including count ,distribution and power for each gene.

Examples
   ## Not run:
   #Please note here the parameter repNumber was very small (5) to make the example code faster.
   #We suggest repNumber should be at least set as 100 in real analysis.
   est_power_distribution(n=65,f=0.01,rho=2,distributionObject="TCGA_READ",repNumber=5)
   #Power estimation based on some interested genes. We use storeProcess=TRUE to return the details for all selected
   selectedGenes<-names(TCGA_READ$pseudo.counts.mean)[c(1,3,5,7,9,12:30)]
   powerDistribution<-est_power_distribution(n=65,f=0.01,rho=2,distributionObject="TCGA_READ",selectedGenes=sel
   str(powerDistribution)
   mean(powerDistribution$power)
   #Power estimation based on genes in interested pathway
   powerDistribution<-est_power_distribution(n=65,f=0.01,rho=2,distributionObject="TCGA_READ",pathway="00010",
   mean(powerDistribution$power)

   ## End(Not run)

---

optimize_parameter

Description
   A function to optimize the parameters in power or sample size estimation.

Usage
   optimize_parameter(fun = est_power, opt1, opt2, opt1Value, opt2Value, main,
   ...)
Arguments

- **fun**: function to be optimized, can be `est_power`, `sample_size`.
- **opt1**: parameter1 to be optimized.
- **opt2**: parameter2 to be optimized.
- **opt1Value**: values of parameter1 to be optimized.
- **opt2Value**: values of parameter2 to be optimized.
- **main**: Title of optimization result figure.
- **...**: Other parameters for optimized function.

Details

A function to optimize the parameters in power or sample size estimation.

Value

A power or sample size matrix, generated by different pair of two parameters.

Examples

```r
#Optimization for power estimation
result<-optimize_parameter(fun=est_power,opt1="n",opt2="lambda0",opt1Value=c(3,5,10,15,20),opt2Value=c(1:5,10,20))

#Optimization for sample size estimation
## Not run:
result<-optimize_parameter(fun=sample_size,opt1="lambda0",opt2="phi0",opt1Value=c(1,3,5),opt2Value=c(1.5,2,3),power=0.8)
## End(Not run)
```

Description

A function to plot power curves based on the result of `sample_size` or `est_power_curve` function.

Usage

```r
plot_power_curve(result, cexLegend = 1, type = "b", xlab = "Sample Size", ylab = "Power", pch = 16, lwd = 3, las = 1, cex = 1.5, main = "Power Curve", col = "red")
```

Arguments

- **result**: the result of `sample_size` or `est_power_curve` function. The storeProcess parameter should be set as True when performing `sample_size` function. If you want to plot more than one curves in the same figure, the results from `sample_size` function should first be combined into a new list. At most five curves were allowed in one figure.
- **cexLegend**: the cex for legend.
\textbf{sample\_size}

\begin{verbatim}
type \hspace{1cm} 1-character string giving the type of plot desired. The following values are possible, for details, see plot: "p" for points, "l" for lines, "b" for both points and lines, "c" for empty points joined by lines, "o" for overplotted points and lines, "s" and "S" for stair steps and "h" for histogram-like vertical lines. Finally, "n" does not produce any points or lines.

xlab \hspace{1cm} a label for the x axis, defaults to a description of x.
ylab \hspace{1cm} a label for the y axis, defaults to a description of y.
pch \hspace{1cm} Either an integer specifying a symbol or a single character to be used as the default in plotting points.
lwd \hspace{1cm} The line width.
las \hspace{1cm} Numeric in 0,1,2,3; the style of axis labels.
cex \hspace{1cm} A numerical value giving the amount by which plotting text and symbols should be magnified relative to the default.
main \hspace{1cm} a main title for the plot, see also title.
col \hspace{1cm} The line color.
\end{verbatim}

\textbf{Examples}

\begin{verbatim}
result1<-sample\_size(rho=2,phi0=1,lambda0=1,f=0.01,power=0.8,m=20000,m1=500,showMessage=TRUE,storeProcess=TRUE)
result2<-sample\_size(rho=4,phi0=1,lambda0=1,f=0.01,power=0.8,m=20000,m1=500,showMessage=TRUE,storeProcess=TRUE)
plot\_power\_curve(list(result1,result2))
\end{verbatim}

\textbf{Description}

A function to estimate the sample size for differential expression analysis of RNA-seq data.

\textbf{Usage}

\begin{verbatim}
sample\_size(power = 0.8, m = 20000, m1 = 500, f = 0.1, k = 1, w = 1, rho = 2, lambda0 = 5, phi0 = 1, showMessage = FALSE, storeProcess = FALSE)
\end{verbatim}

\textbf{Arguments}

\begin{verbatim}
power \hspace{1cm} Power to detecte prognostic genes.
m \hspace{1cm} Total number of genes for testing.
m1 \hspace{1cm} Expected number of prognostic genes.
f \hspace{1cm} FDR level
k \hspace{1cm} Ratio of sample size between two groups.
w \hspace{1cm} Ratio of normalization factors between two groups.
rho \hspace{1cm} minimum fold changes for prognostic genes between two groups.
lambda0 \hspace{1cm} Average read counts for prognostic genes.
phi0 \hspace{1cm} Dispersion for prognostic genes.
showMessage \hspace{1cm} Logical. Display the message in the estimation process.
storeProcess \hspace{1cm} Logical. Store the power and n in sample size or power estimation process.
\end{verbatim}
**sample_size_distribution**

### Details

A function to estimate the sample size for differential expression analysis of RNA-seq data.

### Value

Estimate sample size or a list including parameters and sample size in the process.

### Examples

```r
power<-0.8; rho<-2; lambda0<-5; phi0<-0.5; f<-0.01
sample_size(power=power, f=f, rho=rho, lambda0=lambda0, phi0=phi0)
```

---

**Description**

A function to estimate the sample size based on read counts and dispersion distribution in real data.

### Usage

```r
sample_size_distribution(power = 0.8, m = 10000, m1 = 100, f = 0.1, k = 1, w = 1, rho = 2, showMessage = FALSE, storeProcess = FALSE, distributionObject, libSize, minAveCount = 5, maxAveCount = 2000, repNumber = 100, dispersionDigits = 1, seed = 123, selectedGenes, pathway, species = "hsa", countFilterInRawDistribution = TRUE, selectedGeneFilterByCount = FALSE)
```

### Arguments

- `power` (Power to detecte prognostic genes.)
- `m` (Total number of genes for testing.)
- `m1` (Expected number of prognostic genes.)
- `f` (FDR level)
- `k` (Ratio of sample size between two groups.)
- `w` (Ratio of normalization factors between two groups.)
- `rho` (minimum fold changes for prognostic genes between two groups.)
- `showMessage` (Logical. Display the message in the estimation process.)
- `storeProcess` (Logical. Store the power and n in sample size or power estimation process.)
- `distributionObject` (A DGEList object generated by est_count_dispersion function. RnaSeqSampleSizeData package contains 13 datasets from TCGA, you can set distributionObject as any one of "TCGA_BLCA", "TCGA_BRCA", "TCGA_CESC", "TCGA_COAD", "TCGA_HNSC", "TCGA_KIRC", "TCGA_LGG", "TCGA_LUAD", "TCGA_LUSC", "TCGA_PRAD", "TCGA_READ", "TCGA_THCA", "TCGA_UCEC" to use them.)
- `libSize` (numeric vector giving the total count for each sample. If not specified, the libsize in distributionObject will be used.)
**sample_size_distribution**

- **minAveCount**: Minimal average read count for each gene. Genes with smaller read counts will not be used.
- **maxAveCount**: Maximal average read count for each gene. Genes with larger read counts will be taken as maxAveCount.
- **repNumber**: Number of genes used in estimation of read counts and dispersion distribution.
- **dispersionDigits**: Digits of dispersion.
- **seed**: Optional. A integer, seed for randomly selecting genes.
- **selectedGenes**: Optional. Name of interested genes. Only the read counts and dispersion distribution for these genes will be used in power estimation.
- **pathway**: Optional. ID of interested KEGG pathway. Only the read counts and dispersion distribution for genes in this pathway will be used in power estimation.
- **species**: Optional. Species of interested KEGG pathway.
- **countFilterInRawDistribution**: Logical. If the count filter will be applied on raw count distribution. If not, count filter will be applied on libSize scaled count distribution.
- **selectedGeneFilterByCount**: Logical. If the count filter will be applied to selected genes when selectedGenes parameter was used.

**Details**

A function to estimate the sample size based on read counts and dispersion distribution in real data.

**Value**

Estimate sample size or a list including parameters and sample size in the process.

**Examples**

```r
## Not run:
# Please note here the parameter repNumber was very small (5) to make the example code faster.
# We suggest repNumber should be at least set as 100 in real analysis.
sample_size_distribution(power=0.8,f=0.01,distributionObject="TCGA_READ",repNumber=5,showMessage=TRUE)
## End(Not run)
```
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