Package 'tMAE'

September 26, 2019

Title Tests and visualize for Mono-allelic expressed variants

Version 0.0.0.9000

Description What the package does (one paragraph).

License What license it uses

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Imports dplyr,
data.table,
magrittr,
tidyr,
GenomicRanges,
SummarizedExperiment,
ggplot2

Depends dplyr,
data.table,
magrittr,
tidyr,
GenomicRanges,
SummarizedExperiment,
ggplot2

R topics documented:

`add_gnomAD_AF` *Add allele frequencies from gnomAD*

Description

Add allele frequency information from gnomAD.

Usage

```
add_gnomAD_AF(data, gene_assembly = c("hg19", "hg38"),
  max_af_cutoff = 0.001, populations = c("AF", "AF_afr", "AF_amr",
  "AF_eas", "AF_nfe"))
```

Arguments

data	A data.frame containing allelic counts.
gene_assembly	either 'hg19' or 'hg38' indicating the genome assembly of the variants.
max_af_cutoff	cutoff for a variant to be considered rare. Default is .001.
populations	

Value

A data.table with the original contents plus columns containing allele frequencies from different gnomAD populations.

Author(s)

Vicente Yepez

Examples

```
file <- system.file("extdata", "demo_MAE_counts.tsv", package = "tMAE", mustWork = TRUE)
maeCounts <- read.table(file)
maeRes <- run_deseq_all_mae(maeCounts)
maeRes <- add_gnomAD_AF(maeCounts, gene_assembly = 'hg19')
```

DESeq4MAE *Run deseq test for MAE*

Description

Uses a negative binomial test to determine if a variant is mono-allelically expressed.

Usage

```
DESeq4MAE(data, minCoverage = 10, disp = 0.05,
  independentFiltering = FALSE)
```

Arguments

data	A data.frame containing allelic counts.
minCoverage	minimum total allelic count. Default is 10.
disp	Gene dispersion for the NB test. Default is 0.05.
independentFiltering	Parameter that affects the multiple testing. Default is FALSE.

Value

Mono-allelic results table containing original counts plus p-value, p-adjusted and freqALT columns.

Author(s)

Vicente Yepez, Christian Mertes

Examples

```
file <- system.file("extdata", "demo_MAE_counts.tsv", package = "tMAE", mustWork = TRUE)
maeCounts <- read.table(file)
run_deseq_all_mae(maeCounts)
```

`plotMA` *plotMA*

Description

Creates an MA plot, ie, Fold Change (ALT/REF) vs Coverage colored by significance (from p adjusted and allelic ratio) or significance and minor allele frequency (if rare_column is provided).

Usage

```
plotMA(data, title = NULL, padjCutoff = 0.05,
  allelicRatioCutoff = 0.8, rare_column = NULL)
```

Arguments

`data`	A data.frame containing the results table from `DESeq4MAE` function
`title`	The plot's title
`padjCutoff`	The significance level
`allelicRatioCutoff`	The minimum allelic ratio ALT/(ALT+REF) to be considered signficant
`rare_column`	The name of the column that indicates if a variant is rare or not. Default is `null` which means it won't be plotted.

Value

A ggplot object containing the MA plot.

Author(s)

Vicente Yepez

Examples

```
file <- system.file("extdata", "demo_MAE_counts.tsv",
 package = "tMAE", mustWork = TRUE)
maeCounts <- read.table(file)
res <- run_deseq_all_mae(maeCounts)
plotMA(res)
```

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