

# Package ‘lncDIFF’

August 7, 2018

**Title** lncRNA Normalized Counts Differential Expression Analysis

**Version** 0.0.0.1

**Description**

Differential expression analysis on long non coding RNA (lncRNA), using GLM with Zero-Inflated (exponential) Quasi Maximum Likelihood (ZIQLM) estimator and likelihood ratio test. This package only applies to DE analysis on normalized counts.

**Depends** R (>= 3.5.0)

**License** GPL(>=2)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.0

**NeedsCompilation** no

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design	<i>Design matrix for matched tumor-normal samples in tcga.hnsc.match.edata.</i>
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**Description**

Design matrix for matched tumor-normal samples in tcga.hnsc.match.edata.

**Usage**

```
design
```

**Format**

A model matrix with 80 rows (i.e. samples) and 2 columns (tumor vs normal).

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tcga.hnsc.match.edata	<i>TCGA head and neck squamous cell carcinomas (HNSC) lncRNA Reads Per Killobase per Million (RPKM).</i>
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**Description**

TCGA head and neck squamous cell carcinomas (HNSC) lncRNA Reads Per Killobase per Million (RPKM).

**Usage**

```
tcga.hnsc.match.edata
```

**Format**

A data frame of lncRNA RPKM with 1322 rows (i.e. genes) and 80 columns (i.e. samples ).

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ZIQML.fit	<i>Group effect estimate on lncRNA normalized counts</i>
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**Description**

ZIQML.fit estimates the group effect on genes using zero-inflated exponential quasi likelihood.

**Usage**

```
ZIQML.fit(edata, design.matrix, link = "log")
```

**Arguments**

edata	Normalized counts matrix with genes in rows and samples in columns.
design.matrix	Design matrix for groups, generated by model.matrix().
link	Link function for the generalized linear model and likelihood function, either 'log' or 'identity'. The default is 'log'.

**Value**

Estimates	Estimated group effect on input genes by zero-inflated exponential quasi maximum likelihood (ZIQML) estimator.
logLikelihood	The value of zero-inflated quasi likelihood at estimated group effect.
edata	The input gene expression matrix.
design.matrix	The input design matrix.
link	The specified link function.

## Examples

```
data('tcga.hnsc.match.edata','design')
# 'tcga.hnsc.match.edata' contains RPKM of 1132 lncRNA genes and 80 samples
# 'design' is the design matrix for tumor vs normal tissue.

fit.log=ZIQML.fit(edata=tcga.hnsc.match.edata,design.matrix=design,link='log')
# Fit GLM by ZIQML with logarithmic link function

fit.identity=ZIQML.fit(edata=tcga.hnsc.match.edata,design.matrix=design,link='identity')
# Fit GLM by ZIQML with identity link function
```

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ZIQML.LRT	<i>Likelihood ratio test based on ZIQML.fit()</i>
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## Description

ZIQML.LRT returns the likelihood ratio test results based on the object returned by ZIQML.fit().

## Usage

```
ZIQML.LRT(ZIQML.fit, coef = NULL, simulated.pvalue = FALSE,
           permutation = 100)
```

## Arguments

ZIQML.fit	Object returned by ZIQML.fit()
coef	An integer or vector indicating the coefficient(s) in design matrix to be tested. coef=1 is the intercept (i.e. baseline group effect), and should not be tested.
simulated.pvalue	If empirical p-values are computed, simulated.pvalue=TRUE. The default is FALSE.
permutation	The number of permutations used in simulating pvalues. The default value is 100.

## Value

test.results	Likelihood ratio test results with test statistics, p-value, FDR (or adjusted p-values). If simulated.pvalue=TRUE, test.results also includes simulated p-value and FDR.
Estimates	Estimated group effect in object ZIQML.fit.

## Examples

```
data('tcga.hnsc.match.edata','design')
# 'tcga.hnsc.match.edata' contains RPKM of 1132 lncRNA genes and 80 samples.
# 'design' is the design matrix for tumor vs normal tissue.

fit.log=ZIQML.fit(edata=tcga.hnsc.match.edata,design.matrix=design,link='log')
# Fit GLM by ZIQML with logarithmic link function
```

```
LRT.results=ZIQML.LRT(fit.log,coef=2)
# Likelihood ratio test on tumor vs normal, using observed p-values.

# Include simulated p-values
fit.log.sim=ZIQML.fit(edata=tcga.hnsc.match.edata[1:10,],design.matrix=design,link='log')
LRT.results.sim=ZIQML.LRT(fit.log.sim,coef=2,simulated.pvalue=TRUE,permutation=200)
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