

# Package ‘BALLI’

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**Type** Package

**Title** Expression RNA-Seq Data Analysis Based on Linear Mixed Model

**Version** 0.2.0

**Author** Kyungtaek Park <qkrrudxor147@snu.ac.kr>

**Maintainer** Kyungtaek Park <qkrrudxor147@snu.ac.kr>

**Description** Analysis of gene expression RNA-seq data using Bartlett-Adjusted Likelihood-based LInear model (BALLI). Based on likelihood ratio test, it provides comparisons for effect of one or more variables. See Kyungtaek Park (2018) <doi:10.1101/344929> for more information.

**Depends** R (>= 2.15.0), edgeR, limma, MASS, parallel, stats, methods

**License** GPL

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** CRAN

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balli	<i>BALLI</i>
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### Description

DEG analysis using BALLI algorithm

### Usage

```
balli(object, intV = 2, logcpm = NULL, tecVar = NULL,
      design = NULL, numCores = NULL, threshold = 1e-06, maxiter = 200)
```

### Arguments

object	a TecVarList object
intV	numeric vector designating interest variable(s) which is(are) column number(s) of design matrix
logcpm	logcpm values for each gene and each sample
tecVar	estimated technical variance values for each gene and each sample
design	design matrix with samples in row and covariable(s) to be estimated in column
numCores	number of cores to be used for multithreading. If NULL, a single core is used
threshold	threshold for convergence
maxiter	maximum number of iteration to converge of estimated biological variance. If not, biological variance is estimated by using Brent method

### Value

an Balli object including Result and topGenes list. Following components are shown by Result (same order of genes with input data) and topGenes (ordered by pBALLI in Result) :

log2FC	log2 fold changes of interest variable(s)
lLLI	log-likelihoods estimated by LLI
lBALLI	log-likelihoods estimated by BALLI
pLLI	p-values estimated by LLI
pBALLI	p-values estimated by BALLI
BCF	Bartlett's correction factor

```
expr <- data.frame(t(sapply(1:1000,function(x)rnbinom(20,mu=500,size=50)))) group <- c(rep("A",10),rep("B",10))
design <- model.matrix(~group, data = expr) dge <- DGEList(counts=expr, group=group) dge <-
calcNormFactors(dge) tV <- tecVarEstim(dge,design) balli(tV,intV=2)
```

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Balli-class	<i>Class Balli Class Balli holds results from BALLI</i>
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**Description**

Class Balli Class Balli holds results from BALLI

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balliFit	<i>balliFit</i>
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**Description**

Estimates likelihood and Bartlett correction factor using BALLI algorithm of each gene

**Usage**

```
balliFit(y_mat, x_mat, tecVar, intVar = 2, full = T, cfault = 0,
        miter = 200, conv = 1e-06)
```

**Arguments**

y_mat	numeric vector containing log-cpm values of each gene and each sample
x_mat	design matrix with samples in row and covariable(s) to be estimated in column
tecVar	numeric vector containing estimated technical variance of a gene of each sample
intVar	numeric vector designating interest variable(s) which is(are) column number(s) of x_mat
full	logical value designating full model (TRUE) or reduced model (FALSE).
cfault	initial value of index showing whether converged (0) or not (1).
miter	maximum number of iteration to converge.
conv	threshold for convergence

**Value**

following components are estimated

ll	log-likelihoods
beta	coefficients of interested variable(s)
alpha	coefficients of nuisance variable(s)
BCF	Bartlett's correction factor
cfault	index whether converged or not

**Examples**

```

expr <- data.frame(t(sapply(1:1000,function(x)rnbinom(20,mu=500,size=50))))
group <- c(rep("A",10),rep("B",10))
design <- model.matrix(~group, data = expr)
dge <- DGEList(counts=expr, group=group)
dge <- calcNormFactors(dge)
tV <- tecVarEstim(dge,design)
gtv <- tV$tecVar[1,]
gdat <- data.frame(logcpm=tV$logcpm[1,],design,tecVar=gtv)
gy <- matrix(unlist(gdat[,1]),ncol=1)
gx <- matrix(unlist(gdat[,2:(ncol(gdat)-1)]),ncol=ncol(gdat)-2)
balliFit(y_mat=gy,x_mat=gx,tecVar=gtv,intVar=2,full=TRUE,cfault=0,miter=200,conv=1e-6)

```

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LargeDataObject-class *Class LargeDataObject Class LargeDataObject holds large data such as technical variance and results from BALLI fit*

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**Description**

Class LargeDataObject Class LargeDataObject holds large data such as technical variance and results from BALLI fit

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tecVarEstim *Technical Variance Estimation*

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**Description**

Estimate technical variance by using voom-trend. The code is derived from voom function in limma package

**Usage**

```
tecVarEstim(counts, design = NULL, lib.size = NULL, span = 0.5, ...)
```

**Arguments**

counts	a DGEList object
design	design matrix with samples in row and coefficient(s) to be estimated in column
lib.size	numeric vector containing total library sizes for each sample
span	width of the lowess smoothing window as a proportion
...	other arguments are passed to lmFit.

**Value**

an TecVarList object with the following components:

targets	matrix containing covariables, library sizes and normalization factors of each sample
design	design matrix with samples in row and covariable(s) to be estimated in column
logcpm	logcpm values of each gene and each sample
tecVar	estimated technical variance of each gene and each sample

**Examples**

```
expr <- data.frame(t(sapply(1:1000,function(x)rnbinom(20,mu=500,size=50))))
group <- c(rep("A",10),rep("B",10))
design <- model.matrix(~group, data = expr)
dge <- DGEList(counts=expr, group=group)
dge <- calcNormFactors(dge)
tecVarEstim(dge,design)
```

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TecVarList-class

*Class TecVarList Class TecVarList holds technical variance*

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**Description**

Class TecVarList Class TecVarList holds technical variance

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