

# Package ‘BADER’

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**Type** Package

**Title** Bayesian Analysis of Differential Expression in RNA Sequencing Data

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**Description** For RNA sequencing count data, BADER fits a Bayesian hierarchical model. The algorithm returns the posterior probability of differential expression for each gene between two groups A and B. The joint posterior distribution of the variables in the model can be returned in the form of posterior samples, which can be used for further down-stream analyses such as gene set enrichment.

**License** GPL-2

**Suggests** pasilla (>= 0.2.10)

**biocViews** Sequencing, RNASeq, DifferentialExpression, Software, SAGE

**NeedsCompilation** yes

## R topics documented:

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BADER	<i>Bayesian Analysis of RNA Sequencing Data</i>
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### Description

This function estimates the posterior distribution of various parameters regarding RNA Sequencing data. The most interesting parameter is the probability of differential expression (DE) between two groups A and B. But also estimates for the log mean and the log dispersion parameter of the underlying poisson - log-normal model can be returned.

**Usage**

```
BADER(x, design, sizeFactors = TRUE, start = NULL, burn = 1000, reps = 10000, printEvery = 100, saveEvery = 100)
```

**Arguments**

<code>x</code>	<code>m x n</code> matrix: Every column should contain count data for a subject with <code>m</code> genes or tags.
<code>design</code>	Factor specifying the samples' treatment groups. The first level of 'design' corresponds to the treatment group A, the second level to treatment group B
<code>sizeFactors</code>	boolean: Whether size factors should be estimated (TRUE) or all set to 1 (FALSE)
<code>start</code>	list containing start values for MCMC sampler
<code>burn</code>	Number of burning in steps
<code>reps</code>	Number of repetitions
<code>printEvery</code>	After every <code>printEvery</code> iteration the current step is being printed
<code>saveEvery</code>	Every <code>saveEvery</code> -th step is saved for inference
<code>t0</code>	Warming up time for Metropolis-Hastings
<code>mode</code>	How much data should be returned? Returning all posterior distributions requires large memory. <ul style="list-style-type: none"> <li>• <code>mode = 0</code>: Only posterior means are returned for every parameter</li> <li>• <code>mode = 1</code>: Full posterior distribution for log fold change parameter is returned</li> <li>• <code>mode = 2</code>: Posterior distributions for the following parameters are returned: log fold change log mean and log dispersion</li> </ul>

**Value**

A list with posterior distributions / posterior means

**Author(s)**

Andreas Neudecker

**Examples**

```
set.seed(21)

## log mean expression
muA <- rnorm(100,4,1)
gam <- c(rnorm(10,0,2),rep(0,90))
muB <- muA + gam

## log dispersion
alphaA <- alphaB <- rnorm(100,-2,1)

## count tables for treatment group a and b
kA <- t(matrix(rnbinom(300,mu=exp(muA),size=exp(-alphaA)),nrow=3,byrow=TRUE))
kB <- t(matrix(rnbinom(300,mu=exp(muB),size=exp(-alphaB)),nrow=3,byrow=TRUE))

x <- cbind(kA,kB)
design <- factor(c("A","A","A","B","B","B"))
```

```
results <- BADER(x,design,burn=1000, reps=2000)

## Not run:
plot(results$diffProb,xlab="Index",ylab="posterior DE prob.")

## End(Not run)
```

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