

# 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** ImmunoOncology, Sequencing, RNASeq, DifferentialExpression, Software, SAGE

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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
```

**Arguments**

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

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**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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