Package: BADER (via r-universe)

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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.

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Suggests pasilla (>= 0.2.10)

biocViews ImmunoOncology, Sequencing, RNASeq, DifferentialExpression, Software, SAGE

Repository https://bioc.r-universe.dev

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BADER *Bayesian Analysis of RNA Sequencing Data*

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 repetions
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.

- mode = 0: Only posterior means are returned for every parameter
- mode = 1: Full posterior distribution for log fold change parameter is returned
- mode = 2: Posterior distibutions for the following parameters are returned: log fold change log mean and log dispersion

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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