Package ‘lfc’

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Type Package

Title Log Fold Change Distribution Tools for Working with Ratios of Counts

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Description Ratios of count data such as obtained from RNA-seq are modelled using Bayesian statistics to derive posteriors for effects sizes. This approach is described in Erhard & Zimmer (2015) <doi:10.1093/nar/gkv696> and Erhard (2018) <doi:10.1093/bioinformatics/bty471>.

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Encoding UTF-8

RoxygenNote 7.1.2

URL `https://github.com/erhard-lab/lfc`

BugReports `https://github.com/erhard-lab/lfc/issues`

Imports stats

Suggests knitr, rmarkdown, DESeq2, SummarizedExperiment, airway

VignetteBuilder knitr

biocViews Bayesian, Transcriptomics, DifferentialExpression

NeedsCompilation no

Repository CRAN

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R topics documented:

`CenterMedian` *Subtract the median of the given vector (for normalizing log2 fold changes).*

Description

Subtract the median of the given vector (for normalizing log2 fold changes).

Usage

```
CenterMedian(l)
```

Arguments

`l`	Vector of effect sizes

Value

A vector of length 2 containing the two parameters

See Also

PsiLFC

Examples

```
CenterMedian(rnorm(1000,200))
```

`dlfc` *The log2 fold change distribution*

Description

Density, distribution function, quantile function and random generation for the log2 fold change distribution with parameters ‘a’ and ‘b’ (corresponding to (pseudo-)counts incremented by 1).

Usage

```
dlfc(x, a, b, log = FALSE)

plfc(q, a, b, lower.tail = TRUE, log.p = FALSE)

qlfc(p, a, b, lower.tail = TRUE, log.p = FALSE)

rlfc(n, a, b)
```

Arguments

`x, q`	vector of quantiles
`a`	non-negative parameter
`b`	non-negative parameter
`log, log.p`	if TRUE, probabilities p are given as log(p)
`lower.tail`	if TRUE (default), probabilities are P[X <= x], otherwise, P[X > x].
`p`	vector of probabilities
`n`	number of observations

Value

The density

Functions

- `dlfc`: Density function
- `plfc`: Distribution function
- `qlfc`: Quantile function
- `rlfc`: random generation

Examples

```
x <- seq (-5,5,by=0.01)
plot(x,dlfc(x,1,1))
```

`EmpiricalBayesPrior` *Computes the prior parameters (i.e. pseudocounts incremented by 1) for the log2 fold change distribution*

Description

Computes the prior parameters (i.e. pseudocounts incremented by 1) for the log2 fold change distribution

Usage

```
EmpiricalBayesPrior(A, B)
```

Arguments

`A`	Vector of counts from condition A
`B`	Vector of counts from condition B

Value

A vector of length 2 containing the two parameters

See Also

PsiLFC

Examples

```
EmpiricalBayesPrior(rnorm(1000,200),rnorm(1000,100))
```

`ltop` *Inverse logit transformation to obtain proportion representation from the log fold change representation.*

Description

Inverse logit transformation to obtain proportion representation from the log fold change representation.

Usage

```
ltop(l)
```

Arguments

`l`	Effect size in log2 fold change representation

Value

The proportion representation of the effect size

See Also

ptol

Other Effect size representations: `ptol()`

Examples

```
ptol(0)
ptol(1)
```

`NormLFC` *Standard LFC effect size estimator*

Description

Computes the standard, normalized log2 fold change with given pseudocounts

Usage

```
NormLFC(A, B, pseudo = c(1, 1), normalizeFun = CenterMedian)
```

Arguments

`A`	Vector of counts from condition A
`B`	Vector of counts from condition B
`pseudo`	Vector of length 2 of the pseudo counts
`normalizeFun`	Function to normalize the obtained effect sizes

Value

The vector containing the estimates

Examples

```
  NormLFC(rnorm(1000,200),rnorm(1000,100))
```

`PsiLFC` *Psi LFC effect size estimator*

Description

Computes the optimal effect size estimate and credible intervals if needed.

Usage

```
PsiLFC(
  A,
  B,
  prior = EmpiricalBayesPrior(A, B),
  normalizeFun = CenterMedian,
  cre = FALSE
)
```

Arguments

`A`	Vector of counts from condition A
`B`	Vector of counts from condition B
`prior`	Vector of length 2 of the prior parameters
`normalizeFun`	Function to normalize the obtained effect sizes
`cre`	Compute credible intervals as well? (can also be a vector of quantiles)

Value

Either a vector containing the estimates, or a data frame containing the credible interval as well

Examples

```
PsiLFC(rnorm(1000,200),rnorm(1000,100))
```

`PsiLFC.se` *Psi LFC effect size estimator*

Description

Computes the optimal effect size estimate and credible intervals if needed for a Bioconductor SummarizedExperiment object

Usage

```
PsiLFC.se(se, contrast, cre = FALSE)
```

Arguments

`se`	SummarizedExperiment object
`contrast`	Vector of length 3 (<name>,<A>,<B>)
`cre`	Compute credible intervals as well? (can also be a vector of quantiles)

Value

Either a vector containing the estimates, or a data frame containing the credible interval as well

Examples

```
## Not run:
   data(airway, package="airway")
   head(PsiLFC.se(airway,contrast=c("dex","untrt","trt")))

## End(Not run)
```

`ptol` *Logit transformation to obtain the log fold change representation from the proportion representation.*

Description

Logit transformation to obtain the log fold change representation from the proportion representation.

Usage

```
ptol(p)
```

Arguments

`p`	Effect size in proportion representation

Value

The log2 fold change representation of the effect size

See Also

ltop

Other Effect size representations: `ltop()`

Examples

```
ptol(0.5)
ptol(2/3)
```

`results` *Psi LFC effect size estimator for DESeq2*

Description

Drop-in replacement for DESeq2's results function for simple settings involving a single variable. Appends the PsiLFC estimate.

Usage

```
results(object, contrast, cre = FALSE, ...)
```

Arguments

`object`	the DESeq2DataSet object
`contrast`	Vector of length 3, specifying the variable and the two levels to compute effect sizes for (<name>,<A>,<B>)
`cre`	Compute credible intervals as well? (can also be a vector of quantiles)
`...`	Handed over to DESeq2's results function

Value

Either a vector containing the estimates, or a data frame containing the credible interval as well

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