

Package ‘lfc’

May 8, 2026

Type Package

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

Version 0.2.3

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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](https://doi.org/10.1093/nar/gkv696)> and Erhard (2018) <[doi:10.1093/bioinformatics/bty471](https://doi.org/10.1093/bioinformatics/bty471)>.

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Encoding UTF-8

RoxygenNote 7.2.1

URL <https://github.com/erhard-lab/lfc>

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

Imports stats

Suggests knitr, rmarkdown, DESeq2, SummarizedExperiment

VignetteBuilder knitr

biocViews Bayesian, Transcriptomics, DifferentialExpression

NeedsCompilation no

Repository CRAN

Date/Publication 2023-04-19 18:10:02 UTC

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CenterMedian	<i>Subtract the median of the given vector (for normalizing log2 fold changes).</i>
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Description

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

Usage

```
CenterMedian(1)
```

Arguments

1	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 $P[X \leq x]$, 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, min.sd = 0)
```

Arguments

A	Vector of counts from condition A
B	Vector of counts from condition B
min.sd	minimal standard deviation of the prior

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

1 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,  
  verbose = 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)
verbose	verbose status updates?

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	<i>Logit transformation to obtain the log fold change representation from the proportion representation.</i>
------	--

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

<code>object</code>	the DESeq2DataSet object
<code>contrast</code>	Vector of length 3, specifying the variable and the two levels to compute effect sizes for (<name>,<A>,)
<code>cre</code>	Compute credible intervals as well? (can also be a vector of quantiles)
<code>...</code>	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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