

Package ‘edgeRun’

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Type Package

Title More Powerful Unconditional Testing of Negative Binomial Means
for Digital Gene Expression Data

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Author Emmanuel Dimont

Maintainer Emmanuel Dimont <edimont@mail.harvard.edu>

Description Extends edgeR functionality by improving on exactTest using an unconditional exact test of negative binomial means.

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Depends edgeR, data.table

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Repository CRAN

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edgeRun-package *Unconditional exact testing for two-group digital expression data*

Description

This package provides functions for testing for differential expression for digital data (e.g. RNA-Seq, CAGE-Seq, ChIP-Seq, etc.). Exact unconditional tests based on the negative binomial distribution are provided. Similar functionality exists in the Bioconductor package edgeR where a similar but conditional exact test is implemented. The unconditional test is more powerful, especially for lowly expressed genes or when sample size is extremely small.

Details

Package: edgeRun
Type: Package
Version: 1.0.03
Date: 2014-04-09
License: MIT

Users familiar with edgeR can use edgeRun functionality by simply using the UCexactTest function instead of edgeR's exactTest function. We recommend the edgeR workflow that takes input count data and ends up with a DGEList. Please refer to edgeR documentation on how to use that workflow. NOTE: edgeRun can take several hours to run due to computational complexity, and is only recommended for experiments with very few samples where the power benefit of edgeRun is more evident. Power gains for larger sample sizes might not be worth the extra running time, in those cases edgeR is more appropriate and much faster.

Author(s)

Emmanuel Dimont - Hide Laboratory for Computational Biology. Department of Biostatistics, Harvard School of Public Health. Boston, MA 02115, USA.

Maintainer: Emmanuel Dimont <edimont@mail.harvard.edu>

References

Dimont, E., et al. edgeRun: an R package for sensitive, functionally relevant differential expression discovery using an unconditional exact test. bioRxiv doi: <http://dx.doi.org/10.1101/008409>

Robinson, MD, et al. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics* 2010;26:139-140.

See Also

[exactTest](#), [DGEList](#)

Examples

```
# Example taken from edgeR documentation:
# generate raw counts from NB, create list object
# this creates 50 genes across 4 samples, 2 from each group
y <- matrix(rnbinom(50*4, size=1/0.2, mu=10), nrow=50, ncol=4)
d <- DGEList(counts=y, group=c(1,1,2,2), lib.size=colSums(y))
d <- calcNormFactors(d)
d <- estimateCommonDisp(d)
d <- estimateTagwiseDisp(d)

#using edgeR CONDITIONAL exact test
de.edgeR <- exactTest(d)
topTags(de.edgeR)

#using edgeRun, UNCONDITIONAL exact test
#argument 'upper' specifies the number of iterations
```

```
#higher values give more accurate p-values but take longer to run.  
#The example below uses upper=10,000 for speed, but we highly  
#recommend to use at least 50,000.  
#See Supplementary Methods (Dimont, et al. 2014) for details  
de.edgeRun <- UCexactTest(d,upper=10000)  
topTags(de.edgeRun)
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