Package 'babel'

October 12, 2022

Version 0.3-0

Title Ribosome Profiling Data Analysis

Author Adam B. Olshen, Richard A. Olshen, Barry S. Taylor

Maintainer Adam B. Olshen <adam.olshen@ucsf.edu>

Depends R (>= 2.14.0), edgeR

Imports parallel

Suggests R.rsp, R.devices, R.utils

VignetteBuilder R.rsp

Description Included here are babel routines for identifying unusual ribosome protected fragment counts given mRNA counts.

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NeedsCompilation no

Repository CRAN

Date/Publication 2016-06-23 09:05:13

R topics documented:

`babel` *Ribosome Profiling Analysis Program*

Description

From paired mRNA and ribosome protected fragment count data run Babel analysis to detect changes in translation.

Usage

```
babel(rna,rp,group,nreps,method.adjust="BH",min.rna=10,nSD=3,...)
```

Arguments

rna	a matrix or data frame of raw (not normalized) mRNA count data whose rows correspond to genes and whose columns correspond to samples.
rp	a matrix or data frame of raw ribosome protected fragment count data whose rows correspond to genes and whose columns correspond to samples. The row names and column names (if specified) must be the same as for rna.
group	class labels corresponding to the samples in rna and rp. There must be exactly two unique values.
nreps	number of permutations for within comparison. Must be divisible by 10,000.
method.adjust	method of adjustment for multiple comparisons used by p.adjust.
min.rna	minimum number of rna counts across all samples for a gene to be included. Default is 10.
nSD	Number of SDs from mean such that gene is included in standard error calculation. Should be between 2 and 3, lower leads to more power. Default is 3.
...	Additional arguments.

Details

No missing values are allowed.

Making nreps larger gives more precise estimates. At least 100,000 is required. A million would be better, and ten million would be ideal, but will execute slowly in the current implementation.

Computations can be speeded up by running on multiple cores of the same node using the mclappy command of the parallel library. By default, two cores are used. Windows cannot use the fork command so it can run on only one core. To adjust the number of cores used, use 'options(mc.cores=x)', where x is the number of cores to use.

Value

A list with the following named components:

within	A list with one component per sample that is named after the sample that contains a data frame consisting of a gene id, direction (1 for translation greater than expected, -1 for less than expected), a one-sided p-value for the same, a two-sided p-value, and the corresponding FDR.
combined	A list with two components (one per group label) that is named after the group label that contains a data frame consisting of a gene id, direction (1 for translation greater than expected, -1 for less than expected), a (two-sided) p-value, and the corresponding FDR.
between	A list of data frames corresponding to every pairwise comparison between groups named after the comparison consisting of a gene id, p-value, corresponding FDR, and direction (1 for translation higher in first group label, -1 for lower

in first group label). If there is at least two samples per group there are three addition variables: rna log fold-change, rna FDR, and change type (translation only or both rna and translation).

References

Olshen, A. B., Hsieh, A. C., Stumpf, C. R., Olshen R. A., Ruggero, D., Taylor, B. S. (2013). Assessing gene-level translation control from ribosome profiling. *Bioinformatics*.

Examples

```
data(ribo.prof)
#Get rna count data
test.rna <- ribo.prof$test.rna
#Read in rp count data, if rownames or colnames differ from rna count
# data, adjust them so that they are the same
test.rp <- ribo.prof$test.rp
#Assign group labels to samples.  All groups will be tested pairwise.
test.group=c("A","B","A","B")
#Set the seed so the result is reproducibile
set.seed(12345)
#Run babel with 100000 repetitions.
## Not run:
test.babel <- babel(test.rna,test.rp,group=test.group,nreps=100000,min.rna=10)
#Extract within sample p-values (is translation expected given mRNA level per sample)
within.babel <- test.babel$within
#Extract within group combined p-values (is translation expected given
# mRNA level per group label)
Combined.babel <- test.babel$combined
#Extract between group p-values (is translation given mRNA level the same between group)
between.babel <- test.babel$between

## End(Not run)
```

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ribo.prof *Sample ribosome profiling data*

Description

Sample ribosome profiling data for 1000 genes and 4 samples.

Usage

```
ribo.prof
```

Format

A list containing two data frames, test.rna that has sample mRNA data and test.rp that has sample RPF data.

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