# xtail

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`xtail` *A tool to analyze differential translation using ribosome profiling data.*

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## Description

By pairwise comparisons of ribosome profiling data, xtail identifies differentially translated genes.

## Usage

```
xtail(mrna,rpf,condition,baseLevel=NA,minMeanCount=1,ci=0.95,...)
```

## Arguments

| | |
|---|---|
| `mrna` | a matrix or data frame of raw mRNA count data whose rows correspond to genes and columns correspond to samples. |
| `rpf` | a matrix or data frame of raw (not normalized) RPF count data whose rows correspond to genes and columns correspond to samples. |
| `condition` | condition lavels corresponding to the samples in mrna and rpf. There must be exactly two unique values. |
| `baseLevel` | The baseLevel is a label that assign the condition be compared. If `xtail` is run without specifying baseLevel, it will return the comparison of the second condition over the first condition. |
| `minMeanCount` | `xtail` uses the average expression level of each gene, across all samples as filter criterion and it omits all genes with mean counts below minMeanCount. |
| `ci` | The level credible intervals of log2 fold change of translational efficiency (TE). Default is 95%. |
| `normalize` | If normalization should be done (TRUE \ FALSE). Default is to apply the median-of-ratios normlazation method. |
| `method.adjust` | The method to use for adjusting multiple comparisons, see `?p.adjust` |
| `threads` | The number of CPU cores used. By default, all available cores are used. |
| `bins` | The number of bins used for calculate the probability density of log2FC or log2R. (default is 10000) This paramater will determine accuracy of pvalue.Set it small for a very quick test run. |

## Details

No missing values are allowed.

Duplicate row names (gene names or gene ids) are not allowed.

`xtail` takes in raw read counts of RPF and mRNA, and performs median-of-ratios normalization. Alternatively, users can provide normalized read counts and skip the built-in normal by setting "normalize" to FALSE.

The step of estimation of the probability distributions, for log2FC or log2R, will execute slowly in the current implementation, but can be speeded up by running on multiple cores using the parallel library. By default, the "detectCores" function in parallel library is used to determine the number of CPU cores in the machine on which R is running. To adjust the number of cores used, use "threads" argument to assign.

## Author(s)

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## References

Zhengtao Xiao, Qin Zou, Yu Liu, and Xuerui Yang: Genome-wide assessment of differential translations with ribosome profiling data.

## Examples

```
data(xtaildata)
#Get the mrna count data and rpf count data
test.mrna <- xtaildata$mrna
test.rpf <- xtaildata$rpf
#Assign condition labels to samples.
condition <- c("control","control","treat","treat")
#run xtail
test.results <- xtail(test.mrna,test.rpf,condition)
#save the results
write.table(test.results,"test_results.txt",quote=F,sep="\t")
```

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