Package ‘derfinderHelper’

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Type Package

Title derfinder helper package

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Suggests devtools (>= 1.6), knitcitations (>= 1.0.1), knitr (>= 1.6), BiocStyle, rmarkdown (>= 0.3.3), testthat

VignetteBuilder knitr

Description Helper package for speeding up the derfinder package when using multiple cores.

License Artistic-2.0

LazyData false

URL https://github.com/leekgroup/derfinderHelper

BugReports https://support.bioconductor.org/t/derfinderHelper

biocViews DifferentialExpression, Sequencing, RNASeq, Software

RoxygenNote 5.0.1

NeedsCompilation no

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derfinderHelper-package

*derfinder helper package*

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**Description**

Helper package for speeding up the derfinder package when using multiple cores.

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**fstats.apply**

*Calculate F-statistics per base by extracting chunks from a DataFrame*

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**Description**

Extract chunks from a DataFrame and get the F-statistics on the rows of data, comparing the models mod (alternative) and mod0 (null).

**Usage**

```r
fstats.apply(index = Rle(TRUE, nrow(data)), data, mod, mod0, adjustF = 0,
lowMemDir = NULL, method = "Matrix", scalefac = 32)
```

**Arguments**

- `index`: An index (logical Rle is the best for saving memory) indicating which rows of the DataFrame to use.
- `data`: The DataFrame containing the coverage information. Normally stored in coveragePrep$coverageProcessed from derfinder::preprocessCoverage. Could also be the full data from derfinder::loadCoverage.
- `mod`: The design matrix for the alternative model. Should be m by p where p is the number of covariates (normally also including the intercept).
- `mod0`: The design matrix for the null model. Should be m by p_0.
- `adjustF`: A single value to adjust that is added in the denominator of the F-stat calculation. Useful when the Residual Sum of Squares of the alternative model is very small.
- `lowMemDir`: The directory where the processed chunks are saved when using derfinder::preprocessCoverage with a specified lowMemDir.
- `method`: Has to be either 'Matrix' (default), 'Rle' or 'regular'. See details.
- `scalefac`: The scaling factor used in derfinder::preprocessCoverage. It is only used when method='Matrix'.
Details

If `lowMemDir` is specified then `index` is expected to specify the chunk number.

`fstats.apply` has three different implementations which are controlled by the `method` parameter. `method='regular'` coerces the data to a standard `matrix` object. `method='Matrix'` coerces the data to a `sparseMatrix` which reduces the required memory. This method is only usable when the projection matrices have row sums equal to 0. Note that these row sums are not exactly 0 due to how the computer works, thus leading to very small numerical differences in the F-statistics calculated versus `method='regular'`. Finally, `method='Rle'` calculates the F-statistics using the Rle compressed data without coercing it to other types of objects, thus using less memory that the other methods. However, it’s speed is affected by the number of samples (n) as the current implementation requires n (n + 1) operations, so it’s only recommended for small data sets. `method='Rle'` does result in small numerical differences versus `method='regular'`.

Overall `method='Matrix'` is faster than the other options and requires less memory than `method='regular'`. With tiny example data sets, `method='Matrix'` can be slower than `method='regular'` because the coercion step is slower.

In derfinder versions <= 0.0.62, `method='regular'` was the only option available.

Value

A numeric Rle with the F-statistics per base for the chunk in question.

Author(s)

Leonardo Collado-Torres, Jeff Leek

Examples

```r
## Create some toy data
library('IRanges')
toyData <- DataFrame(
  'sample1' = Rle(sample(0:10, 1000, TRUE)),
  'sample2' = Rle(sample(0:10, 1000, TRUE)),
  'sample3' = Rle(sample(0:10, 1000, TRUE)),
  'sample4' = Rle(sample(0:10, 1000, TRUE)))

## Create the model matrices
mod.toy <- model.matrix(~ group)
mod0.toy <- model.matrix(~ 0 + rep(1, 4))

## Get the F-statistics
fstats <- fstats.apply(data = toyData, mod = mod.toy, mod0 = mod0.toy,
                       scalefac = 1)

## Example with data from derfinder package
## Not run:
## Load the data
library('derfinder')

## Create the model matrices
mod <- model.matrix(~ genomeInfo$pop)
mod0 <- model.matrix(~ 0 + rep(1, nrow(genomeInfo)))
```
## Run the function

```r
system.time(fstats.Matrix <- fstats.apply(data=genomeData$coverage, mod=mod,
    mod0=mod0, method='Matrix', scalefac = 1))
fstats.Matrix
```

## Compare methods

```r
system.time(fstats.regular <- fstats.apply(data=genomeData$coverage,
    mod=mod, mod0=mod0, method='regular'))
system.time(fstats.Rle <- fstats.apply(data=genomeData$coverage, mod=mod,
    mod0=mod0, method='Rle'))
```

## Small numerical differences can occur

```r
summary(fstats.regular - fstats.Matrix)
summary(fstats.regular - fstats.Rle)
```

## You can make the effect negligible by appropriately rounding `findRegions(cutoff)` so the DERs will be the same regardless of the method used.

## Extra comparison, although the method to compare against is 'regular'

```r
summary(fstats.Rle - fstats.Matrix)
```

## End(Not run)
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