Package ‘diffUTR’

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Type Package

Title diffUTR: Streamlining differential exon and 3' UTR usage

Version 1.12.0

Depends R (>= 4.0)

Description The diffUTR package provides a uniform interface and plotting functions for limma/edgeR/DEXSeq-powered differential bin/exon usage. It includes in addition an improved version of the limma::diffSplice method. Most importantly, diffUTR further extends the application of these frameworks to differential UTR usage analysis using poly-A site databases.

Imports S4Vectors, SummarizedExperiment, limma, edgeR, DEXSeq, GenomicRanges, Rsubread, ggplot2, rtracklayer, ComplexHeatmap, ggrepel, stringi, methods, stats, GenomeInfoDb, dplyr, matrixStats, IRanges, ensembldb, viridisLite

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biocViews GeneExpression

BugReports https://github.com/ETHZ-INS/diffUTR

VignetteBuilder knitr

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addNormalizedAssays

Description
addNormalizedAssays

Usage
addNormalizedAssays(se, readLength = 50L)

Arguments
se A bin-wise ‘SummarizedExperiment’ as produced by countFeatures
readLength Used as a minimum width to estimate read density (default 50).

Value
The ‘se’ object with populated ‘logcpm’ and ‘logNormDensity’ assays.

Examples
data(example_bin_se)
example_bin_se <- addNormalizedAssays(example_bin_se)
countFeatures

Description

countFeatures

Usage

```r
countFeatures(
  bamfiles,
  bins,
  strandSpecific = 0,
  readLength = 50L,
  allowMultiOverlap = TRUE,
  inclNormalized = TRUE,
  tmpDir = tempdir(),
  ...
)
```

Arguments

- **bamfiles**: A vector of paths to bam files
- **bins**: A GRanges of bins in which to count reads (or path to a rds file containing such an object)
- **strandSpecific**: Passed to `Rsubread::featureCounts`
- **readLength**: Used as a minimum width to estimate read density.
- **allowMultiOverlap**: Passed to `Rsubread::featureCounts`
- **inclNormalized**: Logical; whether to include normalized assays (needed for plotting)
- **tmpDir**: Passed to `Rsubread::featureCounts`
- **...**: Passed to `Rsubread::featureCounts`

Value

A `RangedSummarizedExperiment-class`

Examples

```r
data("example_gene_annotation", package="diffUTR")
bins <- prepareBins(example_gene_annotation)
bam_files <- list.files(system.file("extdata", package="diffUTR"),
  pattern="bam$", full=TRUE)
# not run
# se <- countFeatures(bam_files, bins, verbose=FALSE)
```
**Description**

deuBinPlot

**Usage**

deuBinPlot(
  se,
  gene,
  type = c("summary", "condition", "sample"),
  intronSize = 2,
  exonSize = c("sqrt", "linear", "log"),
  y = NULL,
  condition = NULL,
  size = "type",
  lineSize = 1,
  colour = NULL,
  alpha = NULL,
  removeAmbiguous = TRUE,
  minDensityRatio = 0.1
)

**Arguments**

- `se`: A bin-wise SummarizedExperiment as produced by `countFeatures` and including bin-level tests (i.e. having been passed through one of the DEU wrappers such as `diffSpliceWrapper` or `DEXSeqWrapper`)
- `gene`: The gene of interest
- `type`: Either 'summary' (plot DEU summary), 'sample' (plot sample-wise data), or 'condition' (plot data aggregate by condition)
- `intronSize`: Intron plot size. If <=3, intron size will be this fraction of the mean exon size. If >3, each intron will have the given size.
- `exonSize`: Scaling for exon sizes, either 'sqrt', 'log', or 'linear'.
- `y`: Value to plot on the y-axis. If 'type="summary"', this should be a column of `rowData(se)`, otherwise should be an assay name of 'se'.
- `condition`: The colData column containing the samples’ condition.
- `size`: rowData variable to use to determine the thickness of the bins.
- `lineSize`: Size of the line connecting the bins. Use ‘lineSize=0’ to omit the line.
- `colour`: rowData variable to use to determine the colour of the bins. If 'type="condition"', can also be "condition"; if 'type="sample"' can be any colData column.
- `alpha`: Alpha level, passed to ggplot.
**Description**

This is a small improvement to the `diffSplice` function written by Gordon Smyth and Charity Law.

**Usage**

```
diffSplice2(fit, geneid, exonid = NULL, robust = FALSE, verbose = TRUE)
```

**Arguments**

- **fit** an `MArrayLM-class` fitted model object produced by `lmFit` or `contrasts.fit`, with rows corresponding to exons.
- **geneid** gene identifiers (as in `diffSplice`)
- **exonid** exon identifiers (as in `diffSplice`)
- **robust** logical, should the estimation of the empirical Bayes prior parameters be robustified against outlier sample variances?
- **verbose** logical, if TRUE will output some diagnostic information

**Value**

An `MArrayLM-class` object containing both exon level and gene level tests. Results are sorted by geneid and by exonid within gene.
diffSpliceDGEWrapper

Examples
library(SummarizedExperiment)
library(edgeR)
data(example_bin_se)
se <- example_bin_se
design <- model.matrix(~condition, data=as.data.frame(colData(se)))
dds <- calcNormFactors(DGEList(assays(se)$counts))
dds <- voom(dds, design)
dds <- lmFit(dds, design)
res <- diffSplice2(dds, geneid=rowData(se)$gene, exonid=row.names(se))
topSplice(res)

### diffSpliceDGEWrapper

#### Description
Wrappers around commonly-used DEU methods (`diffSpliceDGE`, `DEXSeq` and an improved version of `diffSplice`)

#### Usage

```r
diffSpliceDGEWrapper(
  se,
  design,
  coef = NULL,
  QLF = TRUE,
  robust = TRUE,
  countFilter = TRUE,
  excludeTypes = NULL
)
```

```r
diffSpliceWrapper(
  se,
  design,
  coef = NULL,
  robust = TRUE,
  improved = TRUE,
  countFilter = TRUE,
  excludeTypes = NULL
)
```

```r
DEXSeqWrapper(
  se,
  design = ~sample + exon + condition:exon,
  reducedModel = ~sample + exon,
  excludeTypes = NULL,
)```
Arguments

- `se`: A bin-wise SummarizedExperiment as produced by `countFeatures`.
- `design`: A formula (using columns of `colData(se)`) or (for `diffSpliceWrapper` or `diffSpliceDGEWrapper` only) a model.matrix.
- `coef`: The coefficient to be tested (ignored for `DEXSeqWrapper`).
- `QLF`: Logical; whether to use edgeR’s quasi-likelihood negative binomial (applicable only to `diffSpliceDGEWrapper`).
- `robust`: Logical; whether to use robust fitting for the dispersion trend (ignored for `DEXSeqWrapper`).
- `countFilter`: Logical; whether to filter out low-count bins (ignored for `DEXSeqWrapper`).
- `excludeTypes`: A vector of bin types to ignore for testing. To test for any kind of differential usage, leave empty. To test for differential UTR usage, use `excludeTypes=c("CDS","non-coding")` (or see `geneLevelStats` for more options).
- `improved`: Logical; whether to use `diffSplice2` instead of the original `diffSplice` (default TRUE).
- `reducedModel`: A reduced formula (applicable only to `DEXSeqWrapper`).
- `...`: Further arguments (passed to `testForDEU` and `estimateExonFoldChanges`) of `DEXSeq`. Can for instance be used to enable multithreading, by passing `BPPARAM=BiocParallel::MulticoreParam(ncores)`.

Value

The `se` object with additional rowData columns contain bin (i.e. exon) -level statistics, and a metadata slot containing gene level p-values.

Examples

```r
library(SummarizedExperiment)
data(example_bin_se)
se <- diffSpliceWrapper(example_bin_se, ~condition)
head(rowData(se))
```

Description

An object produced by `countFeatures` containing small subset of genes from mouse hippocampal slices undergoing Forskolin-induced long-term potentiation (GSE84643).
Value

a ‘RangedSummarizedExperiment’

References

https://www.nature.com/articles/s41598-017-17407-w

declaration of a geneBinHeatmap

text

description

An example gene annotation containing only a small subset of mouse genes.

Value

a ‘GRanges’ object

description of geneBinHeatmap

Usage

geneBinHeatmap(
  se,
  gene,
  what = NULL,
  anno_rows = c("type", "logWidth", "meanLogDensity", "log10PValue", "geneAmbiguous"),
  anno_columns = c(),
  anno_colors = list(),
  removeAmbiguous = FALSE,
  merge_legends = TRUE,
  cluster_columns = FALSE,
  minDensityRatio = 0.1,
  left_annotation = NULL,
  top_annotation = NULL,
  ...
)

(remaining code...)
Arguments

se  A bin-wise SummarizedExperiment as produced by `countFeatures`
gene  The gene of interest
what  Type of values (i.e. assay) to plot
anno_rows  Row annotation columns (i.e. columns of ‘rowData(se)’) to plot
anno_columns  Column annotation columns (i.e. columns of ‘colData(se)’) to plot
anno_colors  Annotation colors, as a list named with the row/column annotations, see ‘SingleAnnotation’ for details. Ignored if ‘left_annotation’ and/or ‘top_annotation’ are given directly.
removeAmbiguous  Logical; whether to remove bins that are gene-ambiguous (i.e. overlap multiple genes).
merge_legends  Logical; whether to merge legends. This effectively calls ‘draw(..., merge_legends=TRUE)’ around the heatmap.
cluster_columns  Logical; whether to cluster columns (passed to `Heatmap`)
minDensityRatio  Minimum ratio of read density (with respect to the gene’s average) for a bin to be plotted.
left_annotation  Passed to `Heatmap`, overrides ‘anno_rows’.
top_annotation  Passed to `Heatmap`, overrides ‘anno_columns’.
...  Passed to ‘ComplexHeatmap’ (see `Heatmap`)

Value

A `Heatmap`

Examples

data(example_bin_se)
se <- diffSpliceWrapper(example_bin_se, ~condition)
geneBinHeatmap(se, "Jund")

diffSpliceWrapper
geneLevelStats

Usage

geneLevelStats(
  se,
  coef = NULL,
  excludeTypes = NULL,
  includeTypes = NULL,
  returnSE = TRUE,
  minDensityRatio = 0.1,
  minWidth = 20,
  excludeGeneAmbiguous = TRUE
)

Arguments

se A ‘RangedSummarizedExperiment’ containing the results of one of the DEU wrappers.
coef The coefficients tested (if the model included more than one term).
excludeTypes Vector of bin types to exclude.
includeTypes Vector of bin types to include (overrides ‘excludeTypes’)
returnSE Logical; whether to return the updated ‘se’ object (default), or the gene-level table.
minDensityRatio Minimum ratio of read density (with respect to the gene’s average) for a bin to be included.
minWidth Minimum bin width to include
excludeGeneAmbiguous Logical; whether to exclude bins which are ambiguous (i.e. can be from different genes)

Value

If ‘returnSE=TRUE’ (default), returns the ‘se’ object with an updated ‘metadata(se)$geneLevel’ slot, otherwise returns the gene-level data.frame.

Examples

library(SummarizedExperiment)
data(example_bin_se)
se <- diffSpliceWrapper(example_bin_se, ~condition)
se <- geneLevelStats(se, includeTypes="3UTR")
head(metadata(se)$geneLevel)
Description

plotTopGenes

Usage

plotTopGenes(se, n = 10, FDR = 0.05, diffUTR = FALSE, alpha = 1, ...)

Arguments

se            A bin-wise SummarizedExperiment as produced by countFeatures and including bin-level tests (i.e. having been passed through one of the DEU wrappers such as diffSpliceWrapper or DEXSeqWrapper)
n            The maximum number of genes for which to plot labels
FDR            The FDR threshold above which to plot labels
diffUTR        Logical; if FALSE, uses absolute coefficients (appropriate for normal differential exon usage); if TRUE, uses non-absolute (ie changes should be in the same direction across significant bins) and width-weighted scores (i.e. larger bins have more weight) – this is relevant only when testing UTR usage.
alpha         Points transparency
...            Passed to geom_label_repel; this can for instance be used to increase ‘max.overlaps’ when not all desired gene labels are displayed)

Value

A ggplot

Examples

data(example_bin_se)
se <- diffSpliceWrapper(example_bin_se, ~condition)
plotTopGenes(se)
**Description**

prepareBins

**Usage**

```r
def prepareBins(
g,APA = NULL,
onlyMainChr = TRUE,
removeAntisense = TRUE,
chrStyle = NULL,
maxUTRbinSize = 15000,
codingOnly = FALSE,
genewise = FALSE,
stranded = FALSE,
verbose = TRUE
)
```

**Arguments**

- `g`: A GRanges (or path to RDS file containing a GRanges) or path to a gtf file or EnsDb object containing the gene annotation.
- `APA`: A GRanges (or path to a GRanges in RDS format) or bed file containing the alternative poly-A site database
- `onlyMainChr`: Logical; whether to keep only main chromosomes
- `removeAntisense`: Logical; whether to remove antisense APA sites
- `chrStyle`: Chromosome notation to convert to (default no conversion)
- `maxUTRbinSize`: Max width of new alternative UTR bins
- `codingOnly`: Logical, whether to keep only coding transcripts
- `genewise`: Logical, whether annotation should be flattened genewise
- `stranded`: Logical, whether to perform disjoin in a stranded fashion.
- `verbose`: Logical, whether to print run information

**Details**

See the vignette for more details.

**Value**

A ‘GRanges’ object.
**rn6_PAS**

**Author(s)**
Stefan Greber

**Examples**
```r
data(example_gene_annotation)
bins <- prepareBins(example_gene_annotation)
```

---

**rn6_PAS**

*Poly-A sites compendium for Rattus Norvegicus (Rno6)*

**Description**
These are the sites from polyA_DB release 3.2, downloaded from [https://exon.apps.wistar.org/PolyA_DB/v3/download/3.2/rat_pas.zip](https://exon.apps.wistar.org/PolyA_DB/v3/download/3.2/rat_pas.zip), and lifted over to Rno6.

**Value**
a `GRanges` object

---

**simesAggregation**

**simesAggregation**

**Description**
Simes p-value correction and aggregation, adapted from [limma](https://www.bioconductor.org/packages/release/bioc/html/diffSplice.html)

**Usage**
```r
simesAggregation(p.value, geneid)
```

**Arguments**
- `p.value` A vector of p-values
- `geneid` A vector of group labels such as gene identifiers

**Value**
A named vector of aggregated p-values

**Examples**
```r
p <- runif(50)
genes <- sample(LETTERS,50,replace=TRUE)
simesAggregation(p, genes)
```
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