

# Package ‘diffUTR’

September 3, 2025

**Type** Package

**Title** diffUTR: Streamlining differential exon and 3' UTR usage

**Version** 1.17.0

**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

**Suggests** BiocStyle, knitr, rmarkdown

**biocViews** GeneExpression

**BugReports** <https://github.com/ETHZ-INS/diffUTR>

**VignetteBuilder** knitr

**License** GPL-3

**Encoding** UTF-8

**RoxygenNote** 7.1.2

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**Author** Pierre-Luc Germain [cre, aut] (ORCID:  
<<https://orcid.org/0000-0003-3418-4218>>),  
Stefan Gerber [aut]

**Maintainer** Pierre-Luc Germain <pierre-luc.germain@hest.ethz.ch>

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|                     |                            |
|---------------------|----------------------------|
| addNormalizedAssays | <i>addNormalizedAssays</i> |
|---------------------|----------------------------|

---

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

*countFeatures***Description**

countFeatures

**Usage**

```
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**

```
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)
```

deuBinPlot

*deuBinPlot***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 <a href="#">countFeatures</a> and including bin-level tests (i.e. having been passed through one of the DEU wrappers such as <a href="#">diffSpliceWrapper</a> or <a href="#">DEXSeqWrapper</a> ) |
| 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 $\leq 3$ , 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.                                                                                                                                                                                                                   |
| removeAmbiguous | Logical; whether to remove bins that are gene-ambiguous (i.e. overlap multiple genes).                                                                                                                                                           |
| minDensityRatio | Minimum ratio of read density (with respect to the gene's average) for a bin to be plotted.                                                                                                                                                      |

**Value**

A ggplot object

**Examples**

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

---

|             |                    |
|-------------|--------------------|
| diffSplice2 | <i>diffSplice2</i> |
|-------------|--------------------|

---

**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 <a href="#">MArrayLM-class</a> fitted model object produced by <a href="#">lmFit</a> or 'contrasts.fit', with rows corresponding to exons. |
| geneid  | gene identifiers (as in <a href="#">diffSplice</a> )                                                                                          |
| exonid  | exon identifiers (as in <a href="#">diffSplice</a> )                                                                                          |
| 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.

**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    *DEUwrappers*


---

## Description

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

## Usage

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

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

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

## Arguments

|             |                                                                                                                        |
|-------------|------------------------------------------------------------------------------------------------------------------------|
| se          | A bin-wise SummarizedExperiment as produced by <a href="#">countFeatures</a>                                           |
| 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 <a href="#">geneLevelStats</a> for more options). |
| improved     | Logical; whether to use <a href="#">diffSplice2</a> instead of the original <a href="#">diffSplice</a> (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**

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

---

|                |                                                       |
|----------------|-------------------------------------------------------|
| example_bin_se | <i>Example bin-level 'RangedSummarizedExperiment'</i> |
|----------------|-------------------------------------------------------|

---

**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>

---

|                         |                                |
|-------------------------|--------------------------------|
| example_gene_annotation | <i>Example gene annotation</i> |
|-------------------------|--------------------------------|

---

**Description**

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

**Value**

a 'GRanges' object

---

|                |                       |
|----------------|-----------------------|
| geneBinHeatmap | <i>geneBinHeatmap</i> |
|----------------|-----------------------|

---

## Description

A wrapper around ‘ComplexHeatmap’.

## 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,
  ...
)
```

## Arguments

|                 |                                                                                                                                                                                                    |
|-----------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| se              | A bin-wise SummarizedExperiment as produced by <a href="#">countFeatures</a>                                                                                                                       |
| 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 ‘ <a href="#">SingleAnnotation</a> ’ 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 <a href="#">Heatmap</a> )                                                                                                                           |
| minDensityRatio | Minimum ratio of read density (with respect to the gene’s average) for a bin to be plotted.                                                                                                        |
| left_annotation | Passed to <a href="#">Heatmap</a> , overrides ‘anno_rows’.                                                                                                                                         |
| top_annotation  | Passed to <a href="#">Heatmap</a> , overrides ‘anno_columns’.                                                                                                                                      |
| ...             | Passed to ‘ComplexHeatmap’ (see <a href="#">Heatmap</a> )                                                                                                                                          |

**Value**

A [Heatmap](#)

**Examples**

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

---

|                |                       |
|----------------|-----------------------|
| geneLevelStats | <i>geneLevelStats</i> |
|----------------|-----------------------|

---

**Description**

Aggregates bin-level statistics to the gene-level

**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)
```

---

|              |                     |
|--------------|---------------------|
| plotTopGenes | <i>plotTopGenes</i> |
|--------------|---------------------|

---

Description

plotTopGenes

Usage

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

Arguments

|         |                                                                                                                                                                                                                                                                                                               |
|---------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| se      | A bin-wise SummarizedExperiment as produced by <a href="#">countFeatures</a> and including bin-level tests (i.e. having been passed through one of the DEU wrappers such as <a href="#">diffSpliceWrapper</a> or <a href="#">DEXSeqWrapper</a> )                                                              |
| 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 <a href="#">geom_label_repel</a> ; 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)
```

prepareBins

*prepareBins***Description**

prepareBins

**Usage**

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

**Arguments**

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

**Details**

See the vignette for more details.

**Value**

A ‘GRanges’ object.

**Author(s)**

Stefan Greber

Examples

```
data(example_gene_annotation)
bins <- prepareBins(example_gene_annotation)
```

---

|         |                                                             |
|---------|-------------------------------------------------------------|
| rn6_PAS | <i>Poly-A sites compendium for Rattus Norvegicus (Rno6)</i> |
|---------|-------------------------------------------------------------|

---

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 | <i>simesAggregation</i> |
|------------------|-------------------------|

---

Description

Simes p-value correction and aggregation, adapted from `link[limma]{diffSplice}`

Usage

```
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

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

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