

# Package ‘spliceR’

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**Title** Classification of alternative splicing and prediction of coding potential from RNA-seq data.

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**Description** An R package for classification of alternative splicing and prediction of coding potential from RNA-seq data.

**License** GPL (>=2)

**biocViews** GeneExpression, Transcription, AlternativeSplicing, DifferentialExpression, DifferentialSplicing, Sequencing, Visualization

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annotatePTC	<i>PTC and NMD-sensitivity detection from assembled RNA-seq data</i>
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### Description

PTC and NMD-sensitivity detection from assembled RNA-seq data.

### Usage

```
annotatePTC(transcriptData, cds, genomeObject, PTCDistance=50)
```

### Arguments

transcriptData	A SpliceRList object, containing transcript and exon information.
cds	A CDSset object, containing CDS information.
genomeObject	A BSgenome object, containing sequence for the relevant genome. Contained in BSgenome objects, downloadable from BioConductor.
PTCDistance	A numeric giving the premature termination codon-distance: The minimum distance from a STOP to the final exon-exon junction, for a transcript to be marked as NMD-sensitive.

### Details

annotatePTC retrieves sequence data for all exons given in transcriptData, uses the CDS-information in cds to scan for the most upstream reading frame, and translates the mRNA, storing information about the first codon in relation to distance from TTS, distance to the final exon-exon junction, etc. If the STOP distance to the final exon-exon junction is larger than the threshold given in PTCDistance (and the STOP does not fall in the last exon), the STOP is considered premature and the transcript is marked as NMD (nonsense mediated decay) sensitive. For a review of the PTC and NMD mechanism, see Weischenfeldt et al. 2012.

### Value

A SpliceRList, with the transcript\_features object containing additional columns:

spliceR.cdsPosGenomic, the genomic position of the used START codon.

spliceR.stopPosGenomic, the genomic position of the identified STOP codon,

spliceR.ExonWithStart, the exon which the used START codon falls within,

spliceR.ExonWithStop, the exon which the STOP codon falls within.

`spliceR.cdsPosTranscript`, the position relative to transcript start where the used START codon is (measured in nucleotides).

`spliceR.stopPosTranscript`, the position relative to transcript start where the found STOP codon is (measured in nucleotides).

`spliceR.stopDistance`, the distance from the found STOP codon to the last exon-exon junction, relative to transcript start.

`spliceR.junctionIndex`, the exon number in which the found STOP codon falls when compared to the last exon-exon junction, where 0 is the last exon of the transcript, -1 is the second-last, etc NA, if `annotatePTC` was not able to find a ORF.

`spliceR.PTC`, a boolean, indicating whether the transcript is (theoretically) susceptible to nonsense mediated decay. `annotatePTC` sets this value to TRUE if the stop codon falls if any exon other than the last, and the distance to the final downstream exon-exon junction is larger than `PTCDistance` (default 50 nt).

### Author(s)

Kristoffer Vitting-Seerup, Johannes Waage

### References

Vitting-Seerup K, Porse BT, Sandelin A, Waage J. (2014) `spliceR`: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. *BMC Bioinformatics* 15:81.

### Examples

```
## Not run:

#Rebuild cummeRbund's internal dataset
cuffDB <- readCufflinks(dir=system.file("extdata", package="cummeRbund"), gtf=system.file("extdata/chr1_sni

#Generate SpliceRList from cufflinks data
cuffDB_spliceR <- prepareCuff(cuffDB)

# Require BSgenome object, containing genomic sequence
require("BSgenome.Hsapiens.UCSC.hg19",character.only = TRUE)

#Get CDS from UCSC
ucscCDS <- getCDS(selectedGenome="hg19", repoName="UCSC")

#Annotate with PTCs
cuffDB_spliceR_PTC <- annotatePTC(cuffDB_spliceR, cds=ucscCDS, Hsapiens, PTCDistance=50)

## End(Not run)
```

---

CDSSet

*Container for coding sequence (CDS) annotation information*

---

### Description

A container for coding sequence annotation information.

**Usage**

```
CDSset(cds)
```

**Arguments**

`cds` A data.frame object containing CDS annotation. See details for required columns.

**Details**

This object can be generated automatically from [getCDS](#), or can be generated manually by creating a new CDSset from a data.frame with the following columns:

`chrom`, the chromosome name (NB: chromosome names must match when running [annotatePTC](#)), `strand`, the strand, `cdsStart`, the genomic start of the coding sequence (beware of 0/1-frame issues), and `cdsEnd`, the genomic end of the coding sequence (beware of 0/1-frame issues).

The CDSset object is required by [annotatePTC](#) for translation of transcripts and premature termination codon annotation.

For an example, see [annotatePTC](#).

**Value**

A CDSset object.

**Author(s)**

Kristoffer Vitting-Seerup, Johannes Waage

**References**

Vitting-Seerup K, Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. BMC Bioinformatics 15:81.

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conditions

*Returns sample conditions of an SpliceRList or an CuffSet object*

---

**Description**

Returns samples/conditions of an SpliceRList or an CuffSet object.

**Usage**

```
conditions(object)
```

**Arguments**

`object` a SpliceRList object or a CuffSet object.

**Details**

This helper function returns the "conditions" slot of a SpliceRList, or the "sample" slot of a CuffSet.

**Value**

A character vector, giving the samples/conditions.

**Author(s)**

Kristoffer Vitting-Seerup, Johannes Waage

**References**

Vitting-Seerup K , Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. BMC Bioinformatics 15:81.

**Examples**

```
#Load cufflinks example data
cuffDB <- prepareCuffExample()

conditions(cuffDB)

#Generate SpliceRList from cufflinks data
cuffDB_spliceR <- prepareCuff(cuffDB)

conditions(cuffDB_spliceR)
```

---

dim

*Retrieve the Dimensions of a SpliceRList*

---

**Description**

Retrieve the number of (transcripts) contained in SpliceRList.

**Usage**

```
## S3 method for class 'SpliceRList'
dim(x)
## S3 method for class 'SpliceRList'
length(x)
```

**Arguments**

x                    an object of class SpliceRList.

**Details**

As documented in SpliceRList, a SpliceRList contains two objects; a 'transcript\_features' GRanges object, containing transcript information, and a 'exon\_features' object, containing exon information. Dim and length currently only gives information about the number of transcripts in a SpliceRList object, i.e. the length() of the 'transcript\_features' GRanges object.

**Value**

Numeric vector of length 1, indicating the number of transcript comparisons in the SpliceRList.

**See Also**

[dim](#) in the base package.

---

generateGTF

*Generate GTF files for transcript visualization in genome browsers*

---

**Description**

Generate GTF files for transcript visualization in genome browsers.

**Usage**

```
generateGTF(transcriptData, filters=NULL, expressionCutoff=0, scoreMethod="local", filePrefix="sp
```

**Arguments**

- transcriptData** A SpliceRList object, created manually from transcript and exon information, or produced by [prepareCuff](#) from CuffLinks data, and optionally processed by [spliceR](#) and/or [annotatePTC](#).
- filters** Vector, giving the filters that should be applied - any combinations of 'geneOK', 'expressedGenes', 'sigGenes', 'isoOK', 'expressedIso', 'isoClass' and/or 'sigIso'. Works only for data from cufflinks.
- expressionCutoff** Numeric, giving the expression threshold (often in FPKM) used for the 'expressedGenes' and 'expressedIso' filter. Default value is 0.
- scoreMethod** Character, either of 'local' or 'global', indicating whether to score isoform expression values for GTF color coding based on expression of the isoform in relation to the sample (global) or the gene (local).
- filePrefix** Output file name prefix, including path.
- shortDescription** A short description for the GTF track.
- longDescription** A long description for the GTF track.
- useProgressBar** Boolean, indicating whether to use progressbars. For compatibility. Default = TRUE.

**Details**

generateGTF generates GTF files, one for each sample/condition type, and writes these to disk in the current working directory. If the data was generated using cufflinks and the "source\_id" slot of the transcriptData is set to "cufflinks", a number of filters can be applied (see [spliceR](#) for a full description of filters). Transcripts will be colored on a grayscale according to the scoreMethod parameter; for "local", the isoform most expressed for a given gene symbol will be darkest; for "global", the color coding will be relative to each transcripts expression across the sample.

**Author(s)**

Kristoffer Vitting-Seerup, Johannes Waage

## References

Vitting-Seerup K, Porse BT, Sandelin A, Waage JE. (2013) spliceR: An R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. *PeerJ PrePrints* 1:e80v1

## Examples

```
#Load cufflinks example data
cuffDB <- prepareCuffExample()

#Generate SpliceRList from cufflinks data
cuffDB_spliceR <- prepareCuff(cuffDB)

#Reduce dataset size for fast example runtime
cuffDB_spliceR[[1]] <- cuffDB_spliceR[[1]][1:500]

#Run spliceR
mySpliceRList <- spliceR(cuffDB_spliceR, compareTo='preTranscript', filters=c('expressedGenes','geneOK', 'isoOK'))

#Export to GTF
generateGTF(mySpliceRList, filters=c("geneOK", "isoOK", "expressedGenes", "expressedIso"), scoreMethod="local")
```

---

getCDS

*Retrieve CDS information from UCSC*

---

## Description

Retrieve CDS information from a selected repository from UCSC genome browser repositories.

## Usage

```
getCDS(selectedGenome, repoName)
```

## Arguments

**selectedGenome** A character, giving the genome. Currently supported are "hg19" and "mm9".

**repoName** A character, giving the gene model repository. Currently supported are "ensemble", "UCSC" (knownGene), and "refseq".

## Details

For other genomes and/or gene model repositories, please construct a CDSset directly (see [CDSset](#)).  
For a full example of how to use getCDS in a workflow, please see [annotatePTC](#).

## Value

A CDSset containing the annotated CDSs. For a description of the dataframe, see [CDSset](#).

## Author(s)

Kristoffer Vitting-Seerup, Johannes Waage

## References

Vitting-Seerup K , Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. BMC Bioinformatics 15:81.

## Examples

```
## Not run:
mm9UCSC <- getCDS("mm9", "UCSC")

## End(Not run)
```

---

prepareCuff	<i>Prepare assembled RNA-seq data from Cufflinks for spliceR</i>
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---

## Description

Prepare assembled RNA-seq data from Cufflinks for spliceR.

## Usage

```
prepareCuff(cuffDB, fixCufflinksAnnotationProblem=TRUE, removeNonChanonicalChr=TRUE)
```

## Arguments

cuffDB	a cuffDB object, produced by cummeRbund. This object must have been generated with cummeRbund, using the <code>gtf</code> parameter (see example), for spliceR to extract transcript model and exon information.
fixCufflinksAnnotationProblem	Fixes problems with Cufflinks gene symbol annotation. Please see the vignette for additional information.
removeNonChanonicalChr	Removes non-canonical chromosome names.

## Details

NB: prepareCuff is optimized to work with the cummeRbund vs v2.7.2 or later. Please check your version, and update if appropriate. Use prepareCuff to prepare a cummeRbund/Cufflinks DB object for use by spliceR (see example). Often, it's appropriate to prefilter cufflinks data after running prepareCuff with [preSpliceRFilter](#) to reduce overhead on downstream analyses.

## Value

A SpliceRList containing a transcript\_features GRanges object with the following additional metacolumns extracted from the cufflinks DB:

spliceR.isoform_id	Cufflinks unique isoform id
spliceR.sample_1	Sample 1 identifier
spliceR.sample_2	Sample 2 identifier



spliceR.gene\_id  
Cufflinks unique gene id

spliceR.CDS\_id Cufflinks unique CDS id

spliceR.gene\_short\_name  
Cufflinks unique short gene name

spliceR.TSS\_group\_id  
Cufflinks unique TSS id

spliceR.class\_code  
Cufflinks class code (see cufflinks documentation)

spliceR.nearest\_ref\_id  
Nearest reference id

spliceR.length Length of the transcript

spliceR.gene\_status  
Cufflinks gene quantification status

spliceR.gene\_value\_1  
Gene FPKM value for sample 1

spliceR.gene\_value\_2  
Gene FPKM value for sample 2

spliceR.gene\_log2\_fold\_change  
Log2 fold change of gene expression (sample2 / sample1)

spliceR.gene\_p\_value  
P-value for differential testing of difference of gene expression between samples

spliceR.gene\_q\_value  
Adjusted p-value for differential testing of difference of gene expression between samples

spliceR.gene\_significant  
Yes/no; yes if difference of gene expression is significant

spliceR.iso\_status  
Cufflinks isoform quantification status

spliceR.iso\_value\_1  
Isoform FPKM value for sample 1

spliceR.iso\_value\_2  
Isoform FPKM value for sample 2

spliceR.iso\_log2\_fold\_change  
Log2 fold change of isoform expression (sample2 / sample1)

spliceR.iso\_p\_value  
P-value for differential testing of difference of isoform expression between samples

spliceR.iso\_q\_value  
P-value for differential testing of difference of isoform expression between samples

spliceR.iso\_significant  
Yes/no; yes if difference of isoform expression is significant

and a exon\_features GRanges object containing exon model information.

**Author(s)**

Kristoffer Vitting-Seerup, Johannes Waage

## References

Vitting-Seerup K , Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. BMC Bioinformatics 15:81.

## Examples

```
#Load cufflinks example data
cuffDB <- prepareCuffExample()

#Generate SpliceRList from cufflinks data
cuffDB_spliceR <- prepareCuff(cuffDB)
```

---

prepareCuffExample	<i>Prepare the Cufflinks example data</i>
--------------------	---

---

## Description

Prepare the Cufflinks example data set.

## Usage

```
prepareCuffExample()
```

## Details

This helper function prepares the Cufflinks example dataset, including the example GTF-file.

## Value

A CuffSet object.

## Author(s)

Kristoffer Vitting-Seerup, Johannes Waage

## References

Vitting-Seerup K , Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. BMC Bioinformatics 15:81.

## Examples

```
#Load cufflinks example data
cuffDB <- prepareCuffExample()
```

---

preSpliceRFilter      *Filters on spliceR-lists for reduction of data sets*

---

### Description

Applies a number of filters on a spliceR object to reduce data set size before running downstream analyses.

### Usage

```
preSpliceRFilter(spliceRobject, filters, expressionCutoff=0)
```

### Arguments

**spliceRobject**    a SpliceRList object, either created manually from transcript and exon information (see [SpliceRList](#)), or created by [prepareCuff](#) from Cufflinks data.

**filters**            vector, giving the filters that should be applied - any combinations of 'geneOK', 'expressedGenes', 'sigGenes', 'isoOK', 'expressedIso', 'isoClass' and/or 'sigIso'. Works only for data from cufflinks, as a manually generated SpliceRList does not include these metacolumns.

**expressionCutoff**    Numeric, giving the expression threshold (often in FPKM) used for the 'expressedGenes' and 'expressedIso' filter. Default value is 0.

### Details

Often, many genes and isoforms are flagged as not "OK" or "LOWDATA" by Cufflinks, indicating low confidence in these. This function is handy for reducing the data size of a Cufflinks data set to reduce running times for downstream analyses.

Note, that preSpliceRFilter removes transcripts from the dataset permanently, reducing size, while the filter options of [spliceR](#) and [annotatPTC](#) only selects transcripts for analysis, but does not remove any data.

### Value

A SpliceRList with transcripts after filtering.

### Author(s)

Kristoffer Vitting-Seerup, Johannes Waage

### References

Vitting-Seerup K , Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. BMC Bioinformatics 15:81.

**Examples**

```
#Load cufflinks example data
cuffDB <- prepareCuffExample()

#Generate SpliceRList from cufflinks data
cuffDB_spliceR <- prepareCuff(cuffDB)

#Filter
cuffDB_spliceR_filtered <- preSpliceRFilter(cuffDB_spliceR, filters=c("expressedIso", "isoOK", "expressedGenes"))
```

spliceR

*Splice class detection from assembled RNA-seq data***Description**

Splice class detection from assembled RNA-seq data.

**Usage**

```
spliceR(transcriptData, compareTo, filters, expressionCutoff=0, useProgressBar=T)
```

**Arguments**

transcriptData	a SpliceRList object, either created manually from transcript and exon information (see <a href="#">SpliceRList</a> ), or created by <a href="#">prepareCuff</a> from CuffLinks data.
compareTo	a character, either 'preTranscript', for comparison to the hypothetical pre-splicing transcript for each gene, or a character, indicating the reference sample against which to classify splicing events.
filters	vector, giving the filters that should be applied - any combinations of 'geneOK', 'expressedGenes', 'sigGenes', 'isoOK', 'expressedIso', 'isoClass' and/or 'sigIso'. Works only for data from Cufflinks, as a manually generated SpliceRList does not include these metacolumns.
expressionCutoff	Numeric, giving the expression threshold (often in FPKM) used for the 'expressedGenes' and 'expressedIso' filter. Default value is 0.
useProgressBar	Boolean, indicating whether to use progressbars. For compatibility. Default = TRUE.

**Details**

The following filters are allowed for filters: geneOK requires Cufflinks to have reported the quantification of the gene as OK. Only works on transcript data from Cufflinks. expressedGenes requires the parent gene to be expressed. sigGenes requires the parent gene to be expressed in at least one sample. isoOK requires cufflinks to have reported the quantification of the isoform as OK. Only works on transcript data from Cufflinks. expressedIso requires the isoform to be expressed in at least one sample. isoClass removed transcripts marked by cufflinks to be either 'possible pre-mRNA fragment', 'Possible polymerase run-on fragment', or 'Repeat'. Only works on transcript data from Cufflinks. sigIso requires cufflinks to have reported the isoform as significant deregulated between samples. Only works on transcript data from Cufflinks.

**Value**

A SpliceRList, identical to input SpliceRList transcriptData, with the transcript\_features slot containing the following additional columns:

spliceR.major	yes/no, indicating if this isoform is the major isoform expressed of the relevant gene for the reference sample.
spliceR.IF1	Isoform Fraction of total gene expression for sample 1
spliceR.IF2	Isoform Fraction of total gene expression for sample 2
spliceR.dIF	Delta IF (sample 2-sample 1)
spliceR.ESI	Number of exon skipping/inclusion events for this isoform
spliceR.MEE	Number of mutually exclusive exon events for this isoform
spliceR.MESI	Number of multiple exon skipping/inclusion events for this isoform
spliceR.ISI	Number of intron skipping/retention events for this isoform
spliceR.A5	Number of alternative 5' splice site events for this isoform
spliceR.A3	Number of alternative 3' splice site events for this isoform
spliceR.ATSS	0/1, 1 indicating that this isoform uses an alternative transcription start site
spliceR.ATTS	0/1, 1 indicating that this isoform uses an alternative transcription terminating site
spliceR.analyzed	Yes/no, indicating if this isoform was analyzed(yes), or removed in filtering(no)
spliceR.ESI.start	Genomic start location(s) of ESI elements spliced in/out
spliceR.ESI.end	Genomic end location(s) of ESI elements spliced in/out
spliceR.MEE.start	Genomic start location(s) of MEE elements spliced in/out
spliceR.MEE.end	Genomic end location(s) of MEE elements spliced in/out
spliceR.MESI.end	Genomic end location(s) of MESI elements spliced in/out
spliceR.MESI.start	Genomic start location(s) of MESI elements spliced in/out
spliceR.ISI.start	Genomic start location(s) of ISI elements spliced in/out
spliceR.ISI.end	Genomic end location(s) of ISI elements spliced in/out
spliceR.A5.start	Genomic start location(s) of A5 elements spliced in/out
spliceR.A5.end	Genomic end location(s) of A5 elements spliced in/out
spliceR.A3.start	Genomic start location(s) of A3 elements spliced in/out
spliceR.A3.end	Genomic end location(s) of A3 elements spliced in/out
spliceR.ATSS.start	Genomic start location(s) of ATSS elements spliced in/out
spliceR.ATSS.end	Genomic end location(s) of ATSS elements spliced in/out

```
spliceR.ATTS.start
    Genomic start location(s) of ATTS elements spliced in/out
spliceR.ATTS.end
    Genomic end location(s) of ATTS elements spliced in/out
```

### Author(s)

Kristoffer Vitting-Seerup, Johannes Waage

### References

Vitting-Seerup K , Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. BMC Bioinformatics 15:81.

### Examples

```
#Load cufflinks example data
cuffDB <- prepareCuffExample()

#Generate SpliceRList from cufflinks data
cuffDB_spliceR <- prepareCuff(cuffDB)

#Reduce dataset size for fast example runtime
cuffDB_spliceR[[1]] <- cuffDB_spliceR[[1]][1:500]

#Run spliceR
mySpliceRList <- spliceR(cuffDB_spliceR, compareTo='preTranscript', filters=c('expressedGenes', 'geneOK', 'i
```

---

SpliceRList

*Transcript data and annotation object for spliceR*

---

### Description

Creates a SpliceRList object from two GRanges objects, an assembly id, and a source id. The first GRanges, transcript\_features, containing a list of transcripts, and including the columns gene\_id for gene id, tx\_id for transcript id, sample\_1 and sample\_2 for sample identifiers, expression\_1 and expression\_2 for expression values for sample 1 and sample 2, respectively (typically FPKM values or some other normalized count values), and additional optional columns (see prepareCuff). The second, exon\_features, containing a list of exons, and including the columns gene\_id for gene id and tx\_id for transcript id. Assembly id, denoting genome assembly ('hg19', 'hg18', 'mm9', etc.) Source id, denoting source of transcript assembly (currently 'cufflinks' or 'other') Note, that the chromosome identifiers should match the assembly. For experiments

### Usage

```
SpliceRList(transcript_features, exon_features, assembly_id, source_id, conditions, transcripts_p
```

**Arguments**

transcript_features	GRanges object containing transcript features.
exon_features	GRanges object containing transcript features.
assembly_id	character, giving genome assembly.
source_id	A character, either "cufflinks" or "granges", stating source of transcript assembly.
conditions	A character vector, giving the samples or conditions for the RNA-seq experiment.
transcripts_plot	A dataframe, reserved for plotting functions
filter_params	A character vector, reserved for plotting functions.

**Details**

For cufflinks data, call `prepareCuff` to prepare a `SpliceRList`. For other RNA-seq assemblies, use this constructor to create a `SpliceRList`.

See the `spliceR` vignette for an example of creating a `spliceRList` from another source than Cufflinks.

**Value**

A `SpliceRList` object.

**Author(s)**

Kristoffer Vitting-Seerup, Johannes Waage

**References**

Vitting-Seerup K, Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. *BMC Bioinformatics* 15:81.

---

`spliceRPlot`*Plot venn diagrams of alternative splicing events*

---

**Description**

Plot venn diagrams of alternative splicing events vs. samples.

**Usage**

```
spliceRPlot(spliceRobject, evaluate="nr_transcript", asType="All", colors=NULL, alpha=NULL, reset=
```

**Arguments**

<code>spliceRObject</code>	A <code>SpliceRList</code> object, processed and returned by <code>spliceR</code> .
<code>evaluate</code>	A character, giving the evaluation criteria (see details).
<code>asType</code>	The alternative splicing type to visualize, either 'ESI', 'MEE', 'MESI', 'ISI', 'A5', 'A3', 'ATSS', 'ATTS' or 'All'. See <code>spliceR</code> for a full description of alternative splicing types.
<code>colors</code>	Character, giving plot colors for each condition. Must be same length as number of conditions. If NULL, colors from the ColorBrewer "Dark2" palette is used.
<code>alpha</code>	A numeric between 0 and 1, giving the transparency of the plot. If NULL, the alpha will be set optimally depending on number of samples.
<code>reset</code>	A boolean, indicating whether to reinitialize the <code>SpliceRList</code> object for faster replotting.
<code>filters</code>	vector, giving the filters that should be applied - any combinations of 'geneOK', 'expressedGenes', 'sigGenes', 'isoOK', 'expressedIso', 'isoClass' and/or 'sigIso'. Works only for data from cufflinks, as a manually generated <code>SpliceRList</code> does not include these metacolumns.
<code>expressionCutoff</code>	Numeric, giving the expression threshold (often in FPKM) used for the 'expressedGenes' and 'expressedIso' filter. Default value is 0.

**Details**

Upon initial usage of `spliceRPlot`, the `SpliceRList` is initiated with internal data, allowing for faster replotting. If the `SpliceRList` changes because of filtering or other manipulation, rerun `spliceRPlot` with `reset=T`. For the evaluate parameter, the following are valid: 'nr\_transcript', 'nr\_genes', 'nr\_transcript\_pr\_gene', 'nr\_AS', 'mean\_AS\_gene', 'mean\_AS\_transcript', 'mean\_transcript\_exp', 'mean\_gene\_exp'. 'nr\_transcript' outputs number of transcripts, 'nr\_AS' outputs number of alternative splicing events, 'mean\_as' outputs the average number of AS events per gene, 'mean\_transcript\_exp' outputs the mean transcript expression and 'mean\_gene\_exp' output the mean gene expression. For a detailed description of filters, see `spliceR`.

**Value**

A `SpliceRList`, containing additional temporary data for fast subsequent re-plotting.

**Author(s)**

Kristoffer Vitting-Seerup, Johannes Waage

**References**

Vitting-Seerup K, Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. *BMC Bioinformatics* 15:81.

**Examples**

```
#Load cufflinks example data
cuffDB <- prepareCuffExample()

#Generate SpliceRList from cufflinks data
```



```
cuffDB_spliceR <- prepareCuff(cuffDB)

#Reduce dataset size for fast example runtime
cuffDB_spliceR[[1]] <- cuffDB_spliceR[[1]][1:500]

#Run spliceR
mySpliceRList <- spliceR(cuffDB_spliceR, compareTo='preTranscript', filters=c('expressedGenes','geneOK', 'i

#Plot number of exon skipping/inclusion events
mySpliceRList <- spliceRPlot(mySpliceRList, evaluate="nr_AS", asType="ESI")
```

---

topIsoShift	<i>Returns top transcripts in terms of isoform switching</i>
-------------	--

---

## Description

Returns top transcripts in terms of isoform switching.

## Usage

```
topIsoShift(spliceRObject, n=10)
```

## Arguments

**spliceRObject** a SpliceRList object, that has been successfully analyzed and annotated by [spliceR](#).

**n** An integer, giving the number of transcripts to return.

## Details

This helper function returns the transcripts with the highest delta-isoform fraction (dIF) between samples. If the data is based on cufflinks (source\_id=="cufflinks"), only isoforms flagged significantly changing between samples will be returned.

## Value

A dataframe, containing a cast of the GRanges rows of the highest scoring transcripts by dIF.

## Author(s)

Kristoffer Vitting-Seerup, Johannes Waage

## References

Vitting-Seerup K, Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. *BMC Bioinformatics* 15:81.

## Examples

```
#Load cufflinks example data
cuffDB <- prepareCuffExample()

#Generate SpliceRList from cufflinks data
cuffDB_spliceR <- prepareCuff(cuffDB)

#Reduce dataset size for fast example runtime
cuffDB_spliceR[[1]] <- cuffDB_spliceR[[1]][1:500]

#Run spliceR
mySpliceRList <- spliceR(cuffDB_spliceR, compareTo='preTranscript', filters=c('expressedGenes','geneOK', 'i

#Get top dIF transcripts
topIsoShift(mySpliceRList, n=20)
```

---

totalNumberOfAS	<i>Returns total number of alternative splicing events</i>
-----------------	--

---

## Description

Returns total number of alternative splicing events an SpliceRList.

## Usage

```
totalNumberOfAS(spliceRObject)
```

## Arguments

`spliceRObject` a SpliceRList object returned by [spliceRPlot](#).

## Details

This helper function returns number of total number of alternative splicing events. Object must be analyzed by [spliceRPlot](#) first.

## Value

A vector, giving the total number of splicing events for each splice class.

## Author(s)

Kristoffer Vitting-Seerup, Johannes Waage

## References

Vitting-Seerup K, Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. *BMC Bioinformatics* 15:81.

**Examples**

```
#Load cufflinks example data
cuffDB <- prepareCuffExample()

#Generate SpliceRList from cufflinks data
cuffDB_spliceR <- prepareCuff(cuffDB)

#Reduce dataset size for fast example runtime
cuffDB_spliceR[[1]] <- cuffDB_spliceR[[1]][1:500]

#Run spliceR
mySpliceRList <- spliceR(cuffDB_spliceR, compareTo='preTranscript', filters=c('expressedGenes','geneOK', 'i

#Plot number of exon skipping/inclusion events
mySpliceRList <- spliceRPlot(mySpliceRList, evaluate="nr_AS", asType="ESI")

totalNumberOfAS(mySpliceRList)
```

---

transcripts	<i>Returns the transcript or exon GRanges from a SpliceRList object</i>
-------------	---

---

**Description**

Returns the transcript or exon GRanges object from a SpliceRList object.

**Usage**

```
transcripts(transcriptData)
exons(transcriptData)
```

**Arguments**

transcriptData a SpliceRList object.

**Details**

These helper functions returns either the "transcript\_features" or "exon\_features" object of a SpliceRList object.

**Value**

A GRanges object. See SpliceRList for a full description of the contents of a SpliceRList.

**Author(s)**

Kristoffer Vitting-Seerup, Johannes Waage

**References**

Vitting-Seerup K , Porse BT, Sandelin A, Waage J. (2014) spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. BMC Bioinformatics 15:81.

**Examples**

```
#Load cufflinks example data
cuffDB <- prepareCuffExample()

#Generate SpliceRList from cufflinks data
cuffDB_spliceR <- prepareCuff(cuffDB)

myTranscripts <- transcripts(cuffDB_spliceR)
myExons <- exons(cuffDB_spliceR)
```

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