

# Package ‘GeneStructureTools’

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**Type** Package

**Title** Tools for spliced gene structure manipulation and analysis

**Version** 1.25.0

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**Description** GeneStructureTools can be used to create in silico alternative splicing events, and analyse potential effects this has on functional gene products.

**License** BSD\_3\_clause + file LICENSE

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---

addBroadTypes	<i>Change transcript biotypes to a broader set</i>
---------------	--

---

**Description**

Change transcript biotypes to a broader set in a GRanges GTF object

**Usage**

addBroadTypes(gtf)

**Arguments**

gtf GRanges object of the GTF

**Value**

GRanges object of the GTF with new transcript types

**Author(s)**

Beth Signal

**See Also**

Other gtf manipulation: [UTR2UTR53](#), [exonsToTranscripts](#), [filterGtfOverlap](#), [removeDuplicateTranscripts](#), [removeSameExon](#), [reorderExonNumbers](#)

**Examples**

```
gtfFile <- system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools")
gtf <- rtracklayer::import(gtfFile)
gtf <- addBroadTypes(gtf)
```

---

addIntronInTranscript *Add a retained intron to the transcripts it is skipped by*

---

**Description**

Add a retained intron to the transcripts it is skipped by

**Usage**

```
addIntronInTranscript(flankingExons, exons, whippetDataSet = NULL,
  match = "exact", glueExons = TRUE)
```

**Arguments**

flankingExons data.frame generated by findIntronContainingTranscripts()  
 exons GRanges object made from a GTF with ONLY exon annotations (no gene, transcript, CDS etc.)  
 whippetDataSet whippetDataSet generated from readWhippetDataSet()  
 match what type of match replacement should be done? exact: exact matches to the intron only retain: keep non-exact intron match coordinates in spliced sets, and retain them in retained sets replace: replace non-exact intron match coordinates with event coordinates in spliced sets, and retain in retained sets  
 glueExons Join together exons that are not separated by introns?

**Value**

GRanges with transcripts containing retained introns

**Author(s)**

Beth Signal

**See Also**

Other whippet splicing isoform creation: [findExonContainingTranscripts](#), [findIntronContainingTranscripts](#), [findJunctionPairs](#), [replaceJunction](#), [skipExonInTranscript](#)

**Examples**

```
whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)
wds <- filterWhippetEvents(wds)

gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10

wds.intronRetention <- filterWhippetEvents(wds, eventTypes="RI")
exons.intronRetention <- findIntronContainingTranscripts(wds.intronRetention, exons)
IntronRetentionTranscripts <- addIntronInTranscript(exons.intronRetention, exons,
  whippetDataSet=wds.intronRetention)

exonsFromGRanges <- exons[exons$transcript_id=="ENSMUST00000139129.8" &
  exons$exon_number %in% c(3,4)]
intronFromGRanges <- exonsFromGRanges[1]
GenomicRanges::start(intronFromGRanges) <-
  GenomicRanges::end(exonsFromGRanges[exonsFromGRanges$exon_number==3])
GenomicRanges::end(intronFromGRanges) <-
  GenomicRanges::start(exonsFromGRanges[exonsFromGRanges$exon_number==4])
exons.intronRetention <- findIntronContainingTranscripts(intronFromGRanges, exons)

IntronRetentionTranscripts <-
  addIntronInTranscript(exons.intronRetention, exons, match="retain")
```

---

 addSets

*Add set numbers to introns*


---

**Description**

Converts a group of introns into non-overlapping sets

**Usage**

```
addSets(clusterGRanges)
```

**Arguments**

`clusterGRanges` Granges object with a cluster of intron locations

**Value**

GRanges object with a cluster of intron locations and corresponding set numbers

**Author(s)**

Beth Signal

---

alternativeIntronUsage

*Create transcripts with alternative intron usage*

---

**Description**

Creates transcript isoforms from alternative intron usage tested by leafcutter

**Usage**

```
alternativeIntronUsage(altIntronLocs, exons)
```

**Arguments**

altIntronLocs	data.frame containing information from the per_intron_results.tab file output from leafcutter. Note that only one cluster of alternative introns can be processed at a time.
exons	GRanges object made from a GTF with ONLY exon annotations (no gene, transcript, CDS etc.)

**Value**

GRanges object with all potential alternative isoforms skipping the introns specified in either the upregulated or downregulated locations

**Author(s)**

Beth Signal

**Examples**

```
leafcutterFiles <- list.files(system.file("extdata", "leafcutter/"),
  package = "GeneStructureTools"), full.names = TRUE)
leafcutterIntrons <- read.delim(leafcutterFiles[grep("intron_results",
  leafcutterFiles)], stringsAsFactors=FALSE)
gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf"),
  package = "GeneStructureTools")
exons <- gtf[gtf$type=="exon"]
# single cluster processing
cluster <- leafcutterIntrons[leafcutterIntrons$cluster=="chr16:clu_1396",]
altIsoforms1396 <- alternativeIntronUsage(cluster, exons)
unique(altIsoforms1396$transcript_id)
cluster <- leafcutterIntrons[leafcutterIntrons$cluster=="chr16:clu_1395",]
altIsoforms1395 <- alternativeIntronUsage(cluster, exons)
unique(altIsoforms1395$transcript_id)
```

```
# multiple cluster processing
altIsoforms1396plus1395 <- alternativeIntronUsage(cluster, c(exons, altIsoforms1396))
unique(altIsoforms1396plus1395$transcript_id)
```

---

annotateGeneModel	<i>Annotate a GRanges gene model with ORF boundaries for visualisation with Gviz</i>
-------------------	--

---

### Description

Annotate a GRanges gene model with ORF boundaries for visualisation with Gviz

### Usage

```
annotateGeneModel(transcripts, orfs)
```

### Arguments

transcripts	GRanges of gene model to be visualised
orfs	ORF predictions. Created by getORFs()

### Value

data.frame of a gene model for visualisation

### Author(s)

Beth Signal

### See Also

Other Gviz gene structure visualisation: [makeGeneModel](#)

### Examples

```
gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
package="GeneStructureTools"))
transcript <- gtf[gtf$type=="exon" & gtf$gene_name=="Neur11a"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10
# longest ORF for each transcripts
orfs <- getOrfs(transcript, BSgenome = g, returnLongestOnly = TRUE)
geneModelAnnotated <- annotateGeneModel(transcript, orfs)
```

---

attrChangeAltSpliced *Evaluate the change in an attribute between a set of 'normal' transcripts and 'alternative' transcripts*

---

## Description

Evaluate the change in an attribute between a set of 'normal' transcripts and 'alternative' transcripts

## Usage

```
attrChangeAltSpliced(orphsX, orfsY, attribute = "orf_length",
  compareBy = "gene", useMax = TRUE, compareUTR = FALSE)
```

## Arguments

orphsX	orf information for 'normal' transcripts. Generated by getOrfs()
orphsY	orf information for 'alternative' transcripts. Generated by getOrfs()
attribute	attribute to compare
compareBy	compare by 'transcript' isoforms or by 'gene' groups
useMax	use max as the summary function when multiple isoforms are aggregated? If FALSE, will use min instead.
compareUTR	compare the UTR lengths between transcripts? Only runs if attribute = "orf_length"

## Value

data.frame with attribute changes

## Author(s)

Beth Signal

## See Also

Other transcript isoform comparisons: [orfDiff](#), [transcriptChangeSummary](#)

## Examples

```
whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)
wds <- filterWhippetEvents(wds)

gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
transcripts <- gtf[gtf$type=="transcript"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10

wds.exonSkip <- filterWhippetEvents(wds, eventTypes="CE", psiDelta = 0.2)
exons.exonSkip <- findExonContainingTranscripts(wds.exonSkip, exons,
  variableWidth=0, findIntrons=FALSE, transcripts)
```

```

ExonSkippingTranscripts <- skipExonInTranscript(exons.exonSkip, exons, whippetDataSet=wds.exonSkip)

orfsSkipped <- getOrfs(ExonSkippingTranscripts[ExonSkippingTranscripts$set=="skipped_exon"],
  BSgenome = g)
orfsIncluded <- getOrfs(ExonSkippingTranscripts[ExonSkippingTranscripts$set=="included_exon"],
  BSgenome = g)
attrChangeAltSpliced(orfsSkipped, orfsIncluded, attribute = "orf_length")

```

---

coordinates

*Method coordinates*


---

## Description

Method coordinates

## Usage

```

coordinates(whippetDataSet)

## S4 method for signature 'whippetDataSet'
coordinates(whippetDataSet)

```

## Arguments

whippetDataSet whippetDataSet generated from readWhippetDataSet()

## Value

whippet splicing event coordinates as a GRanges object

## See Also

Other whippet data processing: [diffSplicingResults](#), [filterWhippetEvents](#), [formatWhippetEvents](#), [junctions](#), [readCounts](#), [readWhippetDIFffiles](#), [readWhippetDataSet](#), [readWhippetJNCfiles](#), [readWhippetPSIfiles](#), [whippetTranscriptChangeSummary](#)

## Examples

```

whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)

coordinates <- coordinates(wds)

```

---

cumsumANDpad	<i>Cumulative sum of a sequence of numbers, padded with NA</i>
--------------	--

---

**Description**

Cumulative sum of a sequence of numbers, padded with NA

**Usage**

```
cumsumANDpad(x, padLength)
```

**Arguments**

x	input numeric vector
padLength	length to pad output to

**Value**

vector with cumulative sum, padded with NA

**Author(s)**

Beth Signal

---

DEXSeqIdsToGeneIds	<i>Convert DEXSeq ids to gene ids</i>
--------------------	---------------------------------------

---

**Description**

Convert DEXSeq ids to gene ids

**Usage**

```
DEXSeqIdsToGeneIds(DEXSeqIds, removeVersion = FALSE, containsE = TRUE)
```

**Arguments**

DEXSeqIds	vector of DEXSeq group or exon ids
removeVersion	remove the version (.xx) of the gene?
containsE	do the DEXSeq exons ids contain :E00X?

**Value**

vector of unique gene ids

**Author(s)**

Beth Signal

**See Also**

Other DEXSeq processing methods: [findDEXexonType](#), [summariseExonTypes](#)

**Examples**

```
# multiple genes in name
DEXSeqId <- "ENSMUSG00000027618.17+ENSMUSG00000098950.7+ENSMUSG00000089824.10+ENSMUSG00000074643.12"
DEXSeqIdsToGeneIds(DEXSeqId)

# exonic part number in id
DEXSeqIdsToGeneIds("ENSMUSG0000001017.15:E013", removeVersion=TRUE)
```

---

diffSplicingResults    *Method diffSplicingResults*

---

**Description**

Method diffSplicingResults

**Usage**

```
diffSplicingResults(whippetDataSet)

## S4 method for signature 'whippetDataSet'
diffSplicingResults(whippetDataSet)
```

**Arguments**

whippetDataSet    whippetDataSet generated from readWhippetDataSet()

**Value**

differential splicing results data.frame (originally from a whippet .diff file)

**See Also**

Other whippet data processing: [coordinates](#), [filterWhippetEvents](#), [formatWhippetEvents](#), [junctions](#), [readCounts](#), [readWhippetDIFFfiles](#), [readWhippetDataSet](#), [readWhippetJNCfiles](#), [readWhippetPSIfiles](#), [whippetTranscriptChangeSummary](#)

**Examples**

```
whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)

diffSplicingResults <- diffSplicingResults(wds)
```

---

exonsToTranscripts	<i>Convert an exon-level gtf annotation to a transcript-level gtf annotation</i>
--------------------	--

---

**Description**

Convert an exon-level gtf annotation to a transcript-level gtf annotation

**Usage**

```
exonsToTranscripts(exons)
```

**Arguments**

exons                   GRanges object with exons

**Value**

GRanges object with transcripts

**Author(s)**

Beth Signal

**See Also**

Other gtf manipulation: [UTR2UTR53](#), [addBroadTypes](#), [filterGtfOverlap](#), [removeDuplicateTranscripts](#), [removeSameExon](#), [reorderExonNumbers](#)

**Examples**

```
gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon" & gtf$transcript_id=="ENSMUST00000126412.1"]
exons
transcripts <- exonsToTranscripts(exons)
transcripts
```

---

filterGtfOverlap	<i>Filter a GTF overlap to remove exons when exon is annotated as a CDS/UTR</i>
------------------	---

---

**Description**

Filter a GTF overlap to remove exons when exon is annotated as a CDS/UTR

**Usage**

```
filterGtfOverlap(gtf.from)
```

**Arguments**

gtf.from GRanges object of the GTF produced from an overlap

**Value**

GRanges object of the GTF with redundant exons removed

**Author(s)**

Beth Signal

**See Also**

Other gtf manipulation: [UTR2UTR53](#), [addBroadTypes](#), [exonsToTranscripts](#), [removeDuplicateTranscripts](#), [removeSameExon](#), [reorderExonNumbers](#)

**Examples**

```
gtfFile <- system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools")
gtf <- rtracklayer::import(gtfFile)
overlap <- as.data.frame(GenomicRanges::findOverlaps(gtf[which(gtf$type=="CDS")][1], gtf))
table(gtf$type[overlap$subjectHits])
overlapFiltered <- filterGtfOverlap(gtf[overlap$subjectHits])
table(overlapFiltered$type[overlap$subjectHits])
overlap <- as.data.frame(GenomicRanges::findOverlaps(gtf[which(
  gtf$transcript_type=="retained_intron")][1], gtf))
table(gtf$type[overlap$subjectHits])
overlapFiltered <- filterGtfOverlap(gtf[overlap$subjectHits])
table(overlapFiltered$type[overlap$subjectHits])
```

---

filterWhippetEvents *Filter out significant events from a whippet diff comparison*

---

**Description**

Filter out significant events from a whippet diff comparison

**Usage**

```
filterWhippetEvents(whippetDataSet, probability = 0.95, psiDelta = 0.1,
  eventTypes = "all", idList = NA, minCounts = NA, medianCounts = NA,
  sampleTable)
```

**Arguments**

whippetDataSet whippetDataSet generated from readWhippetDataSet()  
 probability minimum probability required to call event as significant  
 psiDelta minimum change in psi required to call an event as significant  
 eventTypes which event type to filter for? default = "all"  
 idList (optional) list of gene ids to filter for

minCounts	minimum number of counts for all replicates in at least one condition to call an event as significant
medianCounts	median count for all replicates in at least one condition to call an event as significant
sampleTable	data.frame with sample names and conditions. Only needed if filtering with counts.

**Value**

filtered whippet differential comparison data.frame

**Author(s)**

Beth Signal

**See Also**

Other whippet data processing: [coordinates](#), [diffSplicingResults](#), [formatWhippetEvents](#), [junctions](#), [readCounts](#), [readWhippetDIFFfiles](#), [readWhippetDataSet](#), [readWhippetJNCfiles](#), [readWhippetPSIfiles](#), [whippetTranscriptChangeSummary](#)

**Examples**

```
whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)
wds <- filterWhippetEvents(wds)
```

---

findDEXexonType      *Find a DEXSeq exons' biotype*

---

**Description**

Find a DEXSeq exons' biotype

**Usage**

```
findDEXexonType(DEXSeqExonId, DEXSeqGtf, gtf, set = "overlap")
```

**Arguments**

DEXSeqExonId	vector of DEXSeq exon ids
DEXSeqGtf	GRanges object of the DEXSeq formatted gtf
gtf	GRanges object of the GTF annotated with exon biotypes - i.e. exon, CDS, UTR
set	which overlapping set of exon biotypes to return - to, from, and/or overlap

**Value**

overlapping types

**Author(s)**

Beth Signal

**See Also**Other DEXSeq processing methods: [DEXSeqIdsToGeneIds](#), [summariseExonTypes](#)**Examples**

```
gtfFile <- system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools")
DEXSeqGtfFile <- system.file("extdata", "gencode.vM14.dexseq.gtf",
  package = "GeneStructureTools")

gtf <- rtracklayer::import(gtfFile)
gtf <- UTR2UTR53(gtf)
DEXSeqGtf <- rtracklayer::import(DEXSeqGtfFile)

findDEXexonType("ENSMUSG0000032366.15:E028", DEXSeqGtf, gtf)

DEXSeqResultsFile <- system.file("extdata", "dexseq_results_significant.txt",
  package = "GeneStructureTools")
DEXSeqResults <- read.table(DEXSeqResultsFile, sep="\t")

findDEXexonType(rownames(DEXSeqResults), DEXSeqGtf, gtf)
```

---

**findExonContainingTranscripts***Given the location of a whole spliced in exon, find transcripts which can splice out this exon*

---

**Description**

Given the location of a whole spliced in exon, find transcripts which can splice out this exon

**Usage**

```
findExonContainingTranscripts(input, exons, variableWidth = 0,
  findIntrons = FALSE, transcripts)
```

**Arguments**

input	whippetDataSet generated from readWhippetDataSet() or a Granges of exon coordinates
exons	GRanges object made from a GTF containing exon coordinates
variableWidth	How many nts overhang is allowed for finding matching exons (default = 0, i.e. complete match)
findIntrons	Find transcripts where the event occurs within the intron?
transcripts	GRanges object made from a GTF containing transcript coordinates (only required if findIntrons=TRUE)

**Value**

data.frame with all overlapping exons

**Author(s)**

Beth Signal

**See Also**

Other whippet splicing isoform creation: [addIntronInTranscript](#), [findIntronContainingTranscripts](#), [findJunctionPairs](#), [replaceJunction](#), [skipExonInTranscript](#)

**Examples**

```
whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)
wds <- filterWhippetEvents(wds)

gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
transcripts <- gtf[gtf$type=="transcript"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10

wds.exonSkip <- filterWhippetEvents(wds, eventTypes="CE", psiDelta = 0.2)
exons.exonSkip <- findExonContainingTranscripts(wds.exonSkip, exons,
  variableWidth=0, findIntrons=FALSE, transcripts)

exonFromGRanges <- exons[exons$exon_id == "ENSMUSE00001271768.1"]
exons.exonSkip <- findExonContainingTranscripts(exonFromGRanges, exons,
  variableWidth=0, findIntrons=FALSE, transcripts)
```

---

**findIntronContainingTranscripts**

*Given the location of a whole retained intron, find transcripts which splice out this intron*

---

**Description**

Given the location of a whole retained intron, find transcripts which splice out this intron

**Usage**

```
findIntronContainingTranscripts(input, exons, match = "exact")
```

**Arguments**

input	whippetDataSet generated from readWhippetDataSet() or a GRanges of intron coordinates
exons	GRanges object made from a GTF with ONLY exon annotations (no gene, transcript, CDS etc.)

**match** what type of matching to perform? exact = only exons which bound the intron exactly, introns = any exon pairs which overlap the intron, all = any exon pairs AND single exons which overlap the intron

### Value

data.frame with all flanking exon pairs

### Author(s)

Beth Signal

### See Also

Other whippet splicing isoform creation: [addIntronInTranscript](#), [findExonContainingTranscripts](#), [findJunctionPairs](#), [replaceJunction](#), [skipExonInTranscript](#)

### Examples

```
whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)
wds <- filterWhippetEvents(wds)

gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10

wds.intronRetention <- filterWhippetEvents(wds, eventTypes="RI")
exons.intronRetention <- findIntronContainingTranscripts(input=wds.intronRetention, exons)

exonsFromGRanges <- exons[exons$transcript_id=="ENSMUST00000139129.8" &
  exons$exon_number %in% c(3,4)]
intronFromGRanges <- exonsFromGRanges[1]
GenomicRanges::start(intronFromGRanges) <-
  GenomicRanges::end(exonsFromGRanges[exonsFromGRanges$exon_number==3])
GenomicRanges::end(intronFromGRanges) <-
  GenomicRanges::start(exonsFromGRanges[exonsFromGRanges$exon_number==4])
exons.intronRetention <- findIntronContainingTranscripts(intronFromGRanges, exons)
```

---

findJunctionPairs      *Find alternative junctions for Whippet alternative splicing events*

---

### Description

Find junctions that pair with each end of an AA (alt. acceptor) or AD (alt. donor) whippet range  
 Find junctions that pair with the upstream/downstream exon of an AF (alt. first exon) or an AL (alt. last exon)

### Usage

```
findJunctionPairs(whippetDataSet, jncCoords, type = NA)
```

**Arguments**

whippetDataSet whippetDataSet generated from readWhippetDataSet()  
 jncCoords GRanges object with Whippet junctions. Generated by readWhippetJNCfiles()  
 type type of Whippet event (AA/AD/AF/AL). Note only one event type should be processed at a time.

**Value**

GRanges object with alternative junctions. Each event should have a set of X (for which the psi measurement is reported) junctions, and alternative Y junctions.

**Author(s)**

Beth Signal

**See Also**

Other whippet splicing isoform creation: [addIntronInTranscript](#), [findExonContainingTranscripts](#), [findIntronContainingTranscripts](#), [replaceJunction](#), [skipExonInTranscript](#)

**Examples**

```
whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)
wds <- filterWhippetEvents(wds)

gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
transcripts <- gtf[gtf$type=="transcript"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10

wds.altAce <- filterWhippetEvents(wds, eventTypes="AA")
jncPairs.altAce <- findJunctionPairs(wds.altAce, type="AA")

wds.altDon <- filterWhippetEvents(wds, eventTypes="AD")
jncPairs.altDon <- findJunctionPairs(wds.altDon, type="AD")

wds.altFirst <- filterWhippetEvents(wds, eventTypes="AF", psiDelta=0.2)
jncPairs.altFirst <- findJunctionPairs(wds.altFirst, type="AF")

wds.altLast <- filterWhippetEvents(wds, eventTypes="AL", psiDelta=0.2)
jncPairs.altLast <- findJunctionPairs(wds.altLast, type="AL")
```

---

formatWhippetEvents     *Format Whippet co-ordinates as a GRanges object*

---

**Description**

Format Whippet co-ordinates as a GRanges object

**Usage**

```
formatWhippetEvents(whippet)
```

**Arguments**

whippet            data.frame containing event location information. May be generated by readWhippetDIFFfiles()

**Value**

GRanges object with events

**Author(s)**

Beth Signal

**See Also**

Other whippet data processing: [coordinates](#), [diffSplicingResults](#), [filterWhippetEvents](#), [junctions](#), [readCounts](#), [readWhippetDIFFfiles](#), [readWhippetDataSet](#), [readWhippetJNCfiles](#), [readWhippetPSIfiles](#), [whippetTranscriptChangeSummary](#)

**Examples**

```
whippetFiles <- list.files(system.file("extdata","whippet/"),
  package = "GeneStructureTools"), full.names = TRUE)
diffFiles <- whippetFiles[grepl(".diff", whippetFiles)]
whippetDiffSplice <- readWhippetDIFFfiles(diffFiles)
whippetCoords <- formatWhippetEvents(whippetDiffSplice)
```

---

getOrfs

*Get open reading frames for transcripts*

---

**Description**

Get open reading frames for transcripts

**Usage**

```
getOrfs(transcripts, BSgenome = NULL, returnLongestOnly = TRUE,
  allFrames = FALSE, longest = 1, exportFasta = FALSE, fastaFile = NULL,
  uORFs = FALSE)
```

**Arguments**

transcripts        GRanges object with ONLY exon annotations (no gene, transcript, CDS etc.) with all transcripts for orf retrieval

BSgenome           BSgenome object

returnLongestOnly    only return longest ORF?

allFrames            return longest ORF for all 3 frames?

longest	return x longest ORFs (regardless of frames)
exportFasta	export a .fa.gz file with nucleotide sequences for each transcript?
fastaFile	file name for .fa.gz export
uORFs	get uORF summaries?

**Value**

data.frame with longest orf details

**Author(s)**

Beth Signal

**See Also**

Other ORF annotation: [getUOrfs](#), [maxLocation](#), [orfSimilarity](#)

**Examples**

```
gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
package="GeneStructureTools"))
transcript <- gtf[gtf$type=="exon" & gtf$gene_name=="Neur11a"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10
# longest ORF for each transcripts
orfs <- getOrfs(transcript, BSgenome = g, returnLongestOnly = TRUE)
# longest ORF in all 3 frames for each transcript
orfs <- getOrfs(transcript, BSgenome = g, allFrames = TRUE)
# longest 3 ORFs in each transcript
orfs <- getOrfs(transcript, BSgenome = g, returnLongestOnly = FALSE, longest=3)
```

---

getUOrfs	<i>Get upstream open reading frames for transcripts with annotated main ORFs</i>
----------	--

---

**Description**

Get upstream open reading frames for transcripts with annotated main ORFs

**Usage**

```
getUOrfs(transcripts, BSgenome = NULL, orfs, findExonB = FALSE)
```

**Arguments**

transcripts	GRanges object with ONLY exon annotations (no gene, transcript, CDS etc.) with all transcripts for orf retrieval
BSgenome	BSgenome object
orfs	orf annotation for the transcripts object. Generated by <code>getOrfs(transcripts, ...)</code>
findExonB	find the distance to and exon number of the downstream (B) junction?

**Value**

data.frame with all upstream ORF details.

**Author(s)**

Beth Signal

**See Also**

Other ORF annotation: [getOrfs](#), [maxLocation](#), [orfSimilarity](#)

**Examples**

```
gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
  package="GeneStructureTools"))
transcript <- gtf[gtf$type=="exon" & gtf$gene_name=="Neur11a"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10
# longest ORF for each transcripts
orfs <- getOrfs(transcript, BSgenome = g, returnLongestOnly = FALSE)
uORFS <- getUOrfs(transcript, BSgenome = g, orfs = orfs, findExonB = TRUE)
```

---

junctions

*Method junctions*

---

**Description**

Method junctions

**Usage**

```
junctions(whippetDataSet)

## S4 method for signature 'whippetDataSet'
junctions(whippetDataSet)
```

**Arguments**

whippetDataSet whippetDataSet generated from readWhippetDataSet()

**Value**

junctions GRanges object (originally from a whippet .jnc file)

**See Also**

Other whippet data processing: [coordinates](#), [diffSplicingResults](#), [filterWhippetEvents](#), [formatWhippetEvents](#), [readCounts](#), [readWhippetDIFFfiles](#), [readWhippetDataSet](#), [readWhippetJNCfiles](#), [readWhippetPSIfiles](#), [whippetTranscriptChangeSummary](#)

**Examples**

```
whippetFiles <- system.file("extdata", "whippet/",  
  package = "GeneStructureTools")  
wds <- readWhippetDataSet(whippetFiles)  
  
junctions <- junctions(wds)
```

---

leafcutterTranscriptChangeSummary

*Compare open reading frames for whippet differentially spliced events*

---

**Description**

Compare open reading frames for whippet differentially spliced events

**Usage**

```
leafcutterTranscriptChangeSummary(significantEvents,  
  combineGeneEvents = FALSE, exons, BSGenome, NMD = FALSE,  
  showProgressBar = TRUE, exportGTF = NULL)
```

**Arguments**

significantEvents	data.frame containing information from the per_intron_results.tab file output from leafcutter.
combineGeneEvents	combine clusters occurring in the same gene? Currently not recommended.
exons	GRanges gtf annotation of exons
BSGenome	BSGenome object containing the genome for the species analysed
NMD	Use NMD predictions? (Note: notNMD must be installed to use this feature)
showProgressBar	show a progress bar of alternative isoform generation?
exportGTF	file name to export alternative isoform GTFs (default=NULL)

**Value**

data.frame containing significant whippet diff data and ORF change summaries

**Author(s)**

Beth Signal

**Examples**

```
leafcutterFiles <- list.files(system.file("extdata", "leafcutter/",
package = "GeneStructureTools"), full.names = TRUE)
leafcutterIntrons <- read.delim(leafcutterFiles[
grep("intron_results", leafcutterFiles)], stringsAsFactors=FALSE)
gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10
leafcutterTranscriptChangeSummary(significantEvents = leafcutterIntrons,
exons=exons, BSgenome = g, NMD=FALSE)
```

---

makeGeneModel

---

*Convert GRanges gene model to data.frame for visualisation with Gviz*


---

**Description**

Convert GRanges gene model to data.frame for visualisation with Gviz

**Usage**

```
makeGeneModel(transcript)
```

**Arguments**

transcript      GRanges of gene model to be visualised

**Value**

data.frame of a gene model for visualisation

**Author(s)**

Beth Signal

**See Also**

Other Gviz gene structure visualisation: [annotateGeneModel](#)

**Examples**

```
gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
package="GeneStructureTools"))
transcript <- gtf[gtf$type=="exon" & gtf$gene_name=="Neurl1a"]
geneModel <- makeGeneModel(transcript)
```

---

maxLocation	<i>Find the largest distance between two vectors of numbers Helper function for get_orfs</i>
-------------	--

---

### Description

Find the largest distance between two vectors of numbers Helper function for get\_orfs

### Usage

```
maxLocation(startSite, stopSite, longest = 1)
```

### Arguments

startSite	vector of start sites - i.e Met amino acid positions
stopSite	vector of stop sites - i.e Stop (*) amino acid positions
longest	which pair to return (1 = longest pair, 2= 2nd longest pair etc.)

### Value

sequential start site and end site with the greatest difference

### Author(s)

Beth Signal

### See Also

Other ORF annotation: [getOrfs](#), [getUOrfs](#), [orfSimilarity](#)

### Examples

```
starts <- c(1,10,15,25)
stops <- c(4,16,50,55)
# longest start site = 25, longest stop site = 50
maxLocation(starts, stops, longest = 1)
starts <- c(1,10,15,25)
stops <- c(4,14,50,55)
# longest start site = 15, longest stop site = 50
maxLocation(starts, stops, longest = 1)
# 2nd longest start site = 10, 2nd longest stop site = 14
maxLocation(starts, stops, longest = 2)
```

---

 orfDiff

*Evaluate changes to ORFs caused by alternative splicing*


---

**Description**

Evaluate changes to ORFs caused by alternative splicing

**Usage**

```
orfDiff(orfX, orfY, filterNMD = TRUE, geneSimilarity = TRUE,
        compareUTR = TRUE, compareBy = "gene", allORFs = NULL)
```

**Arguments**

orfX	orf information for 'normal' transcripts. Generated by getOrfs()
orfY	orf information for 'alternative' transcripts. Generated by getOrfs()
filterNMD	filter orf information for transcripts not targeted by nmd first?
geneSimilarity	compare orf to all orfs in gene?
compareUTR	compare UTRs?
compareBy	compare by 'transcript' isoforms or by 'gene' groups
allORFs	orf information for all transcripts for novel sequence comparisons. Generated by getOrfs()

**Value**

data.frame with orf changes

**Author(s)**

Beth Signal

**See Also**

Other transcript isoform comparisons: [attrChangeAltSpliced](#), [transcriptChangeSummary](#)

**Examples**

```
whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)
wds <- filterWhippetEvents(wds)

gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
transcripts <- gtf[gtf$type=="transcript"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10

orfProteinCoding <- getOrfs(exons[exons$gene_name=="Prex2" &
  exons$transcript_type=="protein_coding"], BSgenome = g)
orfNMD <- getOrfs(exons[exons$gene_name=="Prex2" &
```

```

exons$transcript_type=="nonsense_mediated_decay"], BSgenome = g)
orfDiff(orphsProteinCoding, orfsNMD, filterNMD=FALSE)

wds.exonSkip <- filterWhippetEvents(wds, eventTypes="CE",psiDelta = 0.2)
exons.exonSkip <- findExonContainingTranscripts(wds.exonSkip, exons,
variableWidth=0, findIntrons=FALSE, transcripts)
ExonSkippingTranscripts <- skipExonInTranscript(exons.exonSkip, exons, whippetDataSet=wds.exonSkip)

orphsSkipped <- getOrfs(ExonSkippingTranscripts[ExonSkippingTranscripts$set=="skipped_exon"],
BSgenome = g)
orphsIncluded <- getOrfs(ExonSkippingTranscripts[ExonSkippingTranscripts$set=="included_exon"],
BSgenome = g)
orfDiff(orphsSkipped, orfsIncluded, filterNMD=FALSE)

```

---

orfSimilarity                    *calculate percentage of orfB contained in orfA*

---

### Description

calculate percentage of orfB contained in orfA

### Usage

```
orfSimilarity(orfA, orfB, substitutionCost = 100)
```

### Arguments

orfA	character string of ORF amino acid sequence
orfB	character string of ORF amino acid sequence
substitutionCost	cost for substitutions in ORF sequences. Set to 1 if substitutions should be weighted equally to insertions and deletions.

### Value

percentage of orfB contained in orfA

### Author(s)

Beth Signal

### See Also

Other ORF annotation: [getOrfs](#), [getUOrfs](#), [maxLocation](#)

### Examples

```

orfSimilarity("MFGLDIYAGTRSSFRQFSLT", "MFGLDIYAGTRSSFRQFSLT")
orfSimilarity("MFGLDIYAGTRSSFRQFSLT", "MFGLDIYAFRQFSLT")
orfSimilarity("MFGLDIYAFRQFSLT", "MFGLDIYAGTRSSFRQFSLT")
orfSimilarity("MFGLDIYAGTRXXFRQFSLT", "MFGLDIYAGTRSSFRQFSLT")
orfSimilarity("MFGLDIYAGTRXXFSLT", "MFGLDIYAGTRSSFRQFSLT", 1)

```

---

overlapTypes	<i>Annotate introns and exonic parts by overlapping exon biotype</i>
--------------	--

---

**Description**

Annotate introns and exonic parts by overlapping exon biotype

**Usage**

```
overlapTypes(queryCoords, gtf, set = c("from", "to", "overlap"))
```

**Arguments**

queryCoords	GRanges object of the query regions
gtf	GRanges object of the GTF annotated with exon biotypes - i.e. exon, CDS, UTR
set	which overlapping set of exon biotypes to return - to, from, and/or overlap

**Value**

overlapping types in a data.frame

**Author(s)**

Beth Signal

**Examples**

```
gtfFile <- system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools")
DEXSeqGtfFile <- system.file("extdata", "gencode.vM14.dexseq.gtf",
  package = "GeneStructureTools")

gtf <- rtracklayer::import(gtfFile)
gtf <- UTR2UTR53(gtf)
DEXSeqGtf <- rtracklayer::import(DEXSeqGtfFile)

overlapTypes(DEXSeqGtf[1:10], gtf)
```

---

readCounts	<i>Method readCounts</i>
------------	--------------------------

---

**Description**

Method readCounts

**Usage**

```
readCounts(whippetDataSet)

## S4 method for signature 'whippetDataSet'
readCounts(whippetDataSet)
```

**Arguments**

whippetDataSet whippetDataSet generated from readWhippetDataSet()

**Value**

whippet read count data.frame (originally from a whippet .psi file)

**See Also**

Other whippet data processing: [coordinates](#), [diffSplicingResults](#), [filterWhippetEvents](#), [formatWhippetEvents](#), [junctions](#), [readWhippetDIFFfiles](#), [readWhippetDataSet](#), [readWhippetJNCfiles](#), [readWhippetPSIfiles](#), [whippetTranscriptChangeSummary](#)

**Examples**

```
whippetFiles <- system.file("extdata", "whippet/",  
  package = "GeneStructureTools")  
wds <- readWhippetDataSet(whippetFiles)  
  
readCounts <- readCounts(wds)
```

---

readWhippetDataSet     *Import whippet results files as a whippetDataSet*

---

**Description**

Import whippet results files as a whippetDataSet

**Usage**

```
readWhippetDataSet(filePath = ".")
```

**Arguments**

filePath            path to whippet output files

**Value**

whippetDataSet

**Author(s)**

Beth Signal

**See Also**

Other whippet data processing: [coordinates](#), [diffSplicingResults](#), [filterWhippetEvents](#), [formatWhippetEvents](#), [junctions](#), [readCounts](#), [readWhippetDIFFfiles](#), [readWhippetJNCfiles](#), [readWhippetPSIfiles](#), [whippetTranscriptChangeSummary](#)

## Examples

```
whippetFiles <- system.file("extdata", "whippet/",  
package = "GeneStructureTools")  
wds <- readWhippetDataSet(whippetFiles)
```

---

readWhippetDIFFfiles *Read in a list of whippet .diff.gz files and format as a data.frame*

---

## Description

Read in a list of whippet .diff.gz files and format as a data.frame

## Usage

```
readWhippetDIFFfiles(files)
```

## Arguments

files            vector of \*.diff.gz file names

## Value

data.frame with junction counts for all files

## Author(s)

Beth Signal

## See Also

Other whippet data processing: [coordinates](#), [diffSplicingResults](#), [filterWhippetEvents](#), [formatWhippetEvents](#), [junctions](#), [readCounts](#), [readWhippetDataSet](#), [readWhippetJNCfiles](#), [readWhippetPSIfiles](#), [whippetTranscriptChangeSummary](#)

## Examples

```
whippetFiles <- list.files(system.file("extdata", "whippet/",  
package = "GeneStructureTools"), full.names = TRUE)  
diffFiles <- whippetFiles[grep(".diff", whippetFiles)]  
whippetDiffSplice <- readWhippetDIFFfiles(diffFiles)
```

---

readWhippetJNCfiles     *Read in a list of whippet .jnc.gz files and format as a GRanges object*

---

**Description**

Read in a list of whippet .jnc.gz files and format as a GRanges object

**Usage**

```
readWhippetJNCfiles(files)
```

**Arguments**

files                    vector of \*.jnc.gz file names

**Value**

GRanges object with junctions

**Author(s)**

Beth Signal

**See Also**

Other whippet data processing: [coordinates](#), [diffSplicingResults](#), [filterWhippetEvents](#), [formatWhippetEvents](#), [junctions](#), [readCounts](#), [readWhippetDIFFfiles](#), [readWhippetDataSet](#), [readWhippetPSIfiles](#), [whippetTranscriptChangeSummary](#)

**Examples**

```
whippetFiles <- list.files(system.file("extdata","whippet/"),
  package = "GeneStructureTools"), full.names = TRUE)
jncFiles <- whippetFiles[grep(".jnc", whippetFiles)]
whippetJNC <- readWhippetJNCfiles(jncFiles)
```

---

readWhippetPSIfiles     *Read in a list of whippet .psi.gz files and format as a data.frame*

---

**Description**

Read in a list of whippet .psi.gz files and format as a data.frame

**Usage**

```
readWhippetPSIfiles(files, attribute = "Total_Reads", maxNA = NA)
```

**Arguments**

files                    vector of \*.psi.gz file names  
 attribute                which attribute from the PSI files to use (Total\_Reads, Psi, CI\_width)  
 maxNA                    maximum number of NA values allowed before a site is removed

**Value**

data.frame with junction counts for all files

**Author(s)**

Beth Signal

**See Also**

Other whippet data processing: [coordinates](#), [diffSplicingResults](#), [filterWhippetEvents](#), [formatWhippetEvents](#), [junctions](#), [readCounts](#), [readWhippetDIFFfiles](#), [readWhippetDataSet](#), [readWhippetJNCfiles](#), [whippetTranscriptChangeSummary](#)

**Examples**

```
whippetFiles <- list.files(system.file("extdata","whippet/",
package = "GeneStructureTools"), full.names = TRUE)
psiFiles <- whippetFiles[grep(".psi", whippetFiles)]
whippetPSI <- readWhippetPSIfiles(psiFiles)
```

---

```
removeDuplicateTranscripts
      Remove transcript duplicates
```

---

**Description**

Removes Structural duplicates of transcripts in a GRanges object Note that duplicates must have different transcript ids.

**Usage**

```
removeDuplicateTranscripts(transcripts)
```

**Arguments**

transcripts      GRanges object with transcript structures in exon form

**Value**

GRanges object with unique transcript structures in exon form

**Author(s)**

Beth Signal

**See Also**

Other gtf manipulation: [UTR2UTR53](#), [addBroadTypes](#), [exonsToTranscripts](#), [filterGtfOverlap](#), [removeSameExon](#), [reorderExonNumbers](#)

## Examples

```
gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
exons.altName <- exons
exons.altName$transcript_id <- paste(exons.altName$transcript_id, "duplicated", sep="_")
exons.duplicated <- c(exons, exons.altName)
length(exons.duplicated)
exons.deduplicated <- removeDuplicateTranscripts(exons.duplicated)
length(exons.deduplicated)
```

---

removeSameExon	<i>Remove exon duplicates</i>
----------------	-------------------------------

---

## Description

Removes structural duplicates of exons in a GRanges object

## Usage

```
removeSameExon(exons)
```

## Arguments

exons                    GRanges object with exons

## Value

GRanges object with unique exons

## Author(s)

Beth Signal

## See Also

Other gtf manipulation: [UTR2UTR53](#), [addBroadTypes](#), [exonsToTranscripts](#), [filterGtfOverlap](#), [removeDuplicateTranscripts](#), [reorderExonNumbers](#)

## Examples

```
gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
exons.duplicated <- c(exons[1:4], exons[1:4])
length(exons.duplicated)
exons.deduplicated <- removeSameExon(exons.duplicated)
length(exons.deduplicated)
```

---

removeVersion	<i>Remove version number from ensembl gene/transcript ids</i>
---------------	---

---

**Description**

Remove version number from ensembl gene/transcript ids

**Usage**

```
removeVersion(ids)
```

**Arguments**

ids	vector of ensembl ids
-----	-----------------------

**Value**

vector of ensembl ids without the version number

**Author(s)**

Beth Signal

**Examples**

```
removeVersion("ENSMUSG00000001017.15")
```

---

reorderExonNumbers	<i>Reorder the exon numbers in a gtf annotation</i>
--------------------	---

---

**Description**

Reorder the exon numbers in a gtf annotation

**Usage**

```
reorderExonNumbers(exons, by = "transcript_id")
```

**Arguments**

exons	GRanges object made from a GTF with ONLY exon annotations (no gene, transcript, CDS etc.)
by	what column are the transcripts grouped by?

**Value**

The same input GRanges, but with exon numbers reordered.

**Author(s)**

Beth Signal

**See Also**

Other gtf manipulation: [UTR2UTR53](#), [addBroadTypes](#), [exonsToTranscripts](#), [filterGtfOverlap](#), [removeDuplicateTranscripts](#), [removeSameExon](#)

**Examples**

```
gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
exons <- reorderExonNumbers(exons)
```

---

replaceJunction	<i>Find transcripts containing/overlapping junctions and replace them with alternative junctions</i>
-----------------	--

---

**Description**

Find transcripts containing/overlapping junctions and replace them with alternative junctions

**Usage**

```
replaceJunction(whippetDataSet, junctionPairs, exons, type = NA)
```

**Arguments**

whippetDataSet	whippetDataSet generated from <code>readWhippetDataSet()</code>
junctionPairs	GRanges object with alternative Whippet junctions. Generated by <code>findJunctionPairs()</code>
exons	GRanges object made from a GTF containing exon coordinates
type	type of Whippet event (AA/AD/AF/AL). Note only one event type should be processed at a time.

**Value**

GRanges object with transcripts containing alternative junctions.

**Author(s)**

Beth Signal

**See Also**

Other whippet splicing isoform creation: [addIntronInTranscript](#), [findExonContainingTranscripts](#), [findIntronContainingTranscripts](#), [findJunctionPairs](#), [skipExonInTranscript](#)

**Examples**

```

whippetFiles <- system.file("extdata", "whippet/",
package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)
wds <- filterWhippetEvents(wds)

gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
transcripts <- gtf[gtf$type=="transcript"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10

wds.altAce <- filterWhippetEvents(wds, eventTypes="AA")
jncPairs.altAce <- findJunctionPairs(wds.altAce, type="AA")
transcripts.altAce <- replaceJunction(wds.altAce, jncPairs.altAce, exons, type="AA")

wds.altDon <- filterWhippetEvents(wds, eventTypes="AD")
jncPairs.altDon <- findJunctionPairs(wds.altDon, type="AD")
transcripts.altDon <- replaceJunction(wds.altDon, jncPairs.altDon, exons, type="AD")

wds.altFirst <- filterWhippetEvents(wds, eventTypes="AF", psiDelta=0.2)
jncPairs.altFirst <- findJunctionPairs(wds.altFirst, type="AF")
transcripts.altFirst <- replaceJunction(wds.altFirst, jncPairs.altFirst, exons, type="AF")

wds.altLast <- filterWhippetEvents(wds, eventTypes="AL", psiDelta=0.2)
jncPairs.altLast <- findJunctionPairs(wds.altLast, type="AL")
transcripts.altLast <- replaceJunction(wds.altLast, jncPairs.altLast, exons, type="AL")

```

---

skipExonInTranscript *Remove and include a skipped exon from the transcripts it overlaps*

---

**Description**

Remove and include a skipped exon from the transcripts it overlaps

**Usage**

```

skipExonInTranscript(skippedExons, exons, glueExons = TRUE,
whippetDataSet = NULL, match = "exact")

```

**Arguments**

skippedExons	data.frame generated by findExonContainingTranscripts()
exons	GRanges object made from a GTF with ONLY exon annotations (no gene, transcript, CDS etc.)
glueExons	Join together exons that are not separated by exons?
whippetDataSet	whippetDataSet generated from readWhippetDataSet()
match	what type of match replacement should be done? exact: exact matches to the skipped event only, also removes any intron overlaps skip: keep non-exact exon match coordinates in included sets, and skip them in skipped sets replace: replace non-exact exon match coordinates with event coordinates in included sets, and skip them in skipped sets

**Value**

GRanges with transcripts skipping exons

**Author(s)**

Beth Signal

**See Also**

Other whippet splicing isoform creation: [addIntronInTranscript](#), [findExonContainingTranscripts](#), [findIntronContainingTranscripts](#), [findJunctionPairs](#), [replaceJunction](#)

**Examples**

```
whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)
wds <- filterWhippetEvents(wds)

gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
transcripts <- gtf[gtf$type=="transcript"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10

wds.exonSkip <- filterWhippetEvents(wds, eventTypes="CE", psiDelta = 0.2)
exons.exonSkip <- findExonContainingTranscripts(wds.exonSkip, exons,
  variableWidth=0, findIntrons=FALSE, transcripts)
ExonSkippingTranscripts <- skipExonInTranscript(exons.exonSkip, exons, whippetDataSet=wds.exonSkip)

exonFromGRanges <- exons[exons$exon_id == "ENSMUSE00001271768.1"]
exons.exonSkip <- findExonContainingTranscripts(exonFromGRanges, exons,
  variableWidth=0, findIntrons=FALSE, transcripts)
ExonSkippingTranscripts <- skipExonInTranscript(exons.exonSkip, exons, match="skip")
```

---

summariseExonTypes      *Summarise exon biotypes to broader categories*

---

**Description**

Summarise exon biotypes to broader categories

**Usage**

```
summariseExonTypes(types)
```

**Arguments**

types                      vector of exon biotypes

**Value**

vector of broader exon biotypes

**Author(s)**

Beth Signal

**See Also**Other DEXSeq processing methods: [DEXSeqIdsToGeneIds](#), [findDEXexonType](#)**Examples**

```
gtfFile <- system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools")
DEXSeqGtfFile <- system.file("extdata", "gencode.vM14.dexseq.gtf",
  package = "GeneStructureTools")

gtf <- rtracklayer::import(gtfFile)
gtf <- UTR2UTR53(gtf)
DEXSeqGtf <- rtracklayer::import(DEXSeqGtfFile)

findDEXexonType("ENSMUSG0000032366.15:E028", DEXSeqGtf, gtf)

DEXSeqResultsFile <- system.file("extdata", "dexseq_results_significant.txt",
  package = "GeneStructureTools")
DEXSeqResults <- read.table(DEXSeqResultsFile, sep="\t")

types <- findDEXexonType(rownames(DEXSeqResults), DEXSeqGtf, gtf)
summarisedTypes <- summariseExonTypes(types)
table(types, summarisedTypes)
```

---

transcriptChangeSummary

*Compare open reading frames for two sets of paired transcripts*


---

**Description**

Compare open reading frames for two sets of paired transcripts

**Usage**

```
transcriptChangeSummary(transcriptsX, transcriptsY, BSgenome, exons,
  NMD = FALSE, NMDModel = NULL, compareBy = "gene",
  orfPrediction = "allFrames", compareToGene = FALSE,
  whippetDataSet = NULL, exportGTF = NULL)
```

**Arguments**

transcriptsX	GRanges object with exon annotations for all transcripts to be compared for the 'normal' condition
transcriptsY	GRanges object with exon annotations for all transcripts to be compared for the 'alternative' condition
BSgenome	BSGenome object containing the genome for the species analysed
exons	GRanges object made from a GTF containing exon coordinates

NMD	Use NMD predictions? (Note: notNMD must be installed to use this feature)
NMDModel	Use the "base" or "lncRNA" NMD model?
compareBy	compare isoforms by 'transcript' id, or aggregate all changes occurring by 'gene'
orfPrediction	What type of orf predictions to return. default= "allFrames"
compareToGene	compare alternative isoforms to all normal gene isoforms (in exons)
whippetDataSet	whippetDataSet generated from readWhippetDataSet() Use if PSI directionality should be taken into account when comparing isoforms.
exportGTF	file name to export alternative isoform GTFs (default=NULL)

**Value**

Summarised ORF changes data.frame

**Author(s)**

Beth Signal

**See Also**

Other transcript isoform comparisons: [attrChangeAltSpliced](#), [orfDiff](#)

**Examples**

```
whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)
wds <- filterWhippetEvents(wds)

gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools"))
exons <- gtf[gtf$type=="exon"]
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10

wds.exonSkip <- filterWhippetEvents(wds, eventTypes="CE", psiDelta = 0.2)

exons.exonSkip <- findExonContainingTranscripts(wds.exonSkip, exons,
  variableWidth=0, findIntrons=FALSE, transcripts)
ExonSkippingTranscripts <- skipExonInTranscript(exons.exonSkip, exons, whippetDataSet=wds.exonSkip)
transcriptChangeSummary(ExonSkippingTranscripts[ExonSkippingTranscripts$set=="included_exon"],
  ExonSkippingTranscripts[ExonSkippingTranscripts$set=="skipped_exon"],
  BSgenome=g, exons)
```

---

 UTR2UTR53

---

*Annotate UTRs from Gencode GTF as 5' or 3'*


---

**Description**

Annotate UTRs from Gencode GTF as 5' or 3'

**Usage**

```
UTR2UTR53(gtf)
```

**Arguments**

gtf GRanges object of the GTF

**Value**

gtf annotation GRanges object

**Author(s)**

Beth Signal

**See Also**

Other gtf manipulation: [addBroadTypes](#), [exonsToTranscripts](#), [filterGtfOverlap](#), [removeDuplicateTranscripts](#), [removeSameExon](#), [reorderExonNumbers](#)

**Examples**

```
gtfFile <- system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools")
gtf <- rtracklayer::import(gtfFile)
gtf <- UTR2UTR53(gtf)
table(gtf$type)
```

---

whippetDataSet-class *Class whippetDataSet*

---

**Description**

Class whippetDataSet contains information read from whippet output files

---

whippetTranscriptChangeSummary  
*Compare open reading frames for whippet differentially spliced events*

---

**Description**

Compare open reading frames for whippet differentially spliced events

**Usage**

```
whippetTranscriptChangeSummary(whippetDataSet, gtf.all = NULL, BSgenome,
  eventTypes = "all", exons = NULL, transcripts = NULL, NMD = FALSE,
  exportGTF = NULL)
```

**Arguments**

whippetDataSet	whippetDataSet generated from readWhippetDataSet()
gtf.all	GRanges gtf annotation (can be used instead of specifying exons and transcripts)
BSgenome	BSGenome object containing the genome for the species analysed
eventTypes	which event type to filter for? default = "all"
exons	GRanges gtf annotation of exons
transcripts	GRanges gtf annotation of transcripts
NMD	Use NMD predictions? (Note: notNMD must be installed to use this feature)
exportGTF	file name to export alternative isoform GTFs (default=NULL)

**Value**

data.frame containing significant whippet diff data and ORF change summaries

**Author(s)**

Beth Signal

**See Also**

Other whippet data processing: [coordinates](#), [diffSplicingResults](#), [filterWhippetEvents](#), [formatWhippetEvents](#), [junctions](#), [readCounts](#), [readWhippetDIFFfiles](#), [readWhippetDataSet](#), [readWhippetJNCfiles](#), [readWhippetPSIfiles](#)

**Examples**

```
whippetFiles <- system.file("extdata", "whippet/",
  package = "GeneStructureTools")
wds <- readWhippetDataSet(whippetFiles)
wds <- filterWhippetEvents(wds)

gtf <- rtracklayer::import(system.file("extdata", "example_gtf.gtf",
  package = "GeneStructureTools"))
g <- BSgenome.Mmusculus.UCSC.mm10::BSgenome.Mmusculus.UCSC.mm10
whippetTranscriptChangeSummary(wds, gtf.all=gtf, BSgenome = g)
```

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