

# Package ‘GenomicFeatures’

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**Title** Tools for making and manipulating transcript centric annotations

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**License** Artistic-2.0

**Description** A set of tools and methods for making and manipulating transcript centric annotations. With these tools the user can easily download the genomic locations of the transcripts, exons and cds of a given organism, from either the UCSC Genome Browser or a BioMart database (more sources will be supported in the future). This information is then stored in a local database that keeps track of the relationship between transcripts, exons, cds and genes. Flexible methods are provided for extracting the desired features in a convenient format.

**Maintainer** Bioconductor Package Maintainer <maintainer@bioconductor.org>

**Depends** BiocGenerics (>= 0.1.0), S4Vectors (>= 0.7.17), IRanges (>= 2.3.21), GenomeInfoDb (>= 1.5.16), GenomicRanges (>= 1.21.32), AnnotationDbi (>= 1.27.9)

**Imports** methods, utils, tools, DBI (>= 0.2-5), RSQLite (>= 0.8-1), RCurl, XVector, Biostrings (>= 2.23.3), rtracklayer (>= 1.29.24), biomaRt (>= 2.17.1), Biobase (>= 2.15.1)

**Suggests** org.Mm.eg.db, org.Hs.eg.db, BSgenome, BSgenome.Hsapiens.UCSC.hg19 (>= 1.3.17), BSgenome.Celegans.UCSC.ce2, BSgenome.Dmelanogaster.UCSC.dm3 (>= 1.3.17), mirbase.db, FDb.UCSC.tRNAs, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Dmelanogaster.UCSC.dm3.ensGene (>= 2.7.1), TxDb.Mmusculus.UCSC.mm10.knownGene, TxDb.Hsapiens.UCSC.hg19.lincRNAsTranscripts, TxDb.Hsapiens.UCSC.hg38.knownGene, SNPlocs.Hsapiens.dbSNP141.GRCh38, Rsamtools, pasillaBamSubset (>= 0.0.5), GenomicAlignments, RUnit, BiocStyle, knitr

**Collate** utils.R TxDb-SELECT-helpers.R Ensembl.utils.R  
findCompatibleMarts.R TxDb-class.R FeatureDb-class.R makeTxDb.R  
makeTxDbFromUCSC.R makeTxDbFromBiomart.R makeTxDbFromGRanges.R  
makeTxDbFromGFF.R makeFeatureDbFromUCSC.R id2name.R

transcripts.R transcriptsBy.R transcriptsByOverlaps.R  
 transcriptLengths.R disjointExons.R features.R microRNAs.R  
 extractTranscriptSeqs.R extractUpstreamSeqs.R  
 getPromoterSeq-methods.R makeTxDbPackage.R select-methods.R  
 nearest-methods.R transcriptLocs2refLocs.R  
 coordinate-mapping-methods.R coverageByTranscript.R  
 test\_GenomicFeatures\_package.R

**VignetteBuilder** knitr

**biocViews** Genetics, Infrastructure, Annotation, Sequencing,  
 GenomeAnnotation

**NeedsCompilation** no

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as-format-methods      *Coerce to file format structures*

---

## Description

These functions coerce a `TxDb` object to a `GRanges` object with metadata columns encoding transcript structures according to the model of a standard file format. Currently, BED and GFF models are supported. If a `TxDb` is passed to `export`, when targeting a BED or GFF file, this coercion occurs automatically.

## Usage

```
## S4 method for signature 'TxDb'  
asBED(x)  
## S4 method for signature 'TxDb'  
asGFF(x)
```

## Arguments

x                      A `TxDb` object to coerce to a `GRanges`, structured as BED or GFF.

## Value

For `asBED`, a `GRanges`, with the columns `name`, `thickStart`, `thickEnd`, `blockStarts`, `blockSizes` added. The thick regions correspond to the CDS regions, and the blocks represent the exons. The transcript IDs are stored in the `name` column. The ranges are the transcript bounds.

For `asGFF`, a `GRanges`, with columns `type`, `Name`, `ID`, and `Parent`. The gene structures are expressed according to the conventions defined by the GFF3 spec. There are elements of each type of feature: “gene”, “mRNA”, “exon” and “cds”. The `Name` column contains the `gene_id` for genes, `tx_name` for transcripts, and exons and cds regions are NA. The `ID` column uses `gene_id` and `tx_id`, with the prefixes “GeneID” and “TxID” to ensure uniqueness across types. The exons and cds regions have NA for ID. The `Parent` column contains the IDs of the parent features. A feature may have multiple parents (the column is a `CharacterList`). Each exon belongs to one or more mRNAs, and mRNAs belong to a gene.

## Author(s)

Michael Lawrence

## Examples

```
txdb_file <- system.file("extdata", "hg19_knownGene_sample.sqlite",  
                          package="GenomicFeatures")  
txdb <- loadDb(txdb_file)  
  
asBED(txdb)  
asGFF(txdb)
```

---

coverageByTranscript    *Compute coverage by transcript (or CDS) of a set of ranges*

---

### Description

coverageByTranscript computes the transcript (or CDS) coverage of a set of ranges.  
 pcoverageByTranscript is a version of coverageByTranscript that operates element-wise.

### Usage

```
coverageByTranscript(x, transcripts, ignore.strand=FALSE)
```

```
pcoverageByTranscript(x, transcripts, ignore.strand=FALSE, ...)
```

### Arguments

- |               |  |
|---------------|--|
| x             | <p>An object representing a set of ranges (typically aligned reads). <a href="#">GRanges</a>, <a href="#">GRangesList</a>, <a href="#">GAlignments</a>, <a href="#">GAlignmentPairs</a>, and <a href="#">GAlignmentsList</a> objects are supported.</p> <p>More generally, for coverageByTranscript x can be any object for which <a href="#">seqinfo()</a> and <a href="#">coverage()</a> are supported (e.g. a <a href="#">BamFile</a> object). Note that, for such objects, coverage() is expected to return an <a href="#">RleList</a> object whose names are seqlevels(x).</p> <p>More generally, for pcoverageByTranscript x can be any object for which <a href="#">grglist()</a> is supported. It should have the length of transcripts or length 1. If the latter, it is recycled to the length of transcripts.</p>   |
| transcripts   | <p>A <a href="#">GRangesList</a> object representing the exons of each transcript for which to compute coverage. For each transcript, the exons must be ordered by <i>ascending rank</i>, that is, by their position in the transcript. This means that, for a transcript located on the minus strand, the exons should typically be ordered by descending position on the reference genome. If transcripts was obtained with <a href="#">exonsBy</a>, then the exons are guaranteed to be ordered by ascending rank. See <a href="#">?exonsBy</a> for more information.</p> <p>Alternatively transcripts can be any object for which <a href="#">exonsBy</a> is implemented (e.g. a <a href="#">TxDb</a> object), in which case it is replaced by the <a href="#">GRangesList</a> object returned by <a href="#">exonsBy(transcripts, by="tx", use.names=TRUE)</a>.</p> <p>For pcoverageByTranscript, transcripts should have the length of x or length 1. If the latter, it is recycled to the length of x).</p> |
| ignore.strand | <p>TRUE or FALSE. If FALSE (the default) then the strand of a range in x and exon in transcripts must be the same in order for the range to contribute coverage to the exon. If TRUE then the strand is ignored.</p>   |
| ...           | <p>Additional arguments passed to the internal call to <a href="#">grglist()</a>. More precisely, when x is not a <a href="#">GRanges</a> or <a href="#">GRangesList</a> object, pcoverageByTranscript replace it by the <a href="#">GRangesList</a> object returned by <a href="#">grglist(x, ...)</a>.</p>   |

### Value

An [RleList](#) object *parallel* to transcripts, that is, the i-th element in it is an integer-[Rle](#) representing the coverage of the i-th transcript in transcripts. Its [elementLengths\(\)](#) is guaranteed to be identical to [sum\(width\(transcripts\)\)](#). The names and metadata columns on transcripts are propagated to it.

**Author(s)**

H. Pages

**See Also**

- [extractTranscriptSeqs](#) for extracting transcript (or CDS) sequences from chromosome sequences.
- [transcriptLengths](#) for extracting the transcript lengths from a [TxDb](#) object.
- The [RleList](#) class defined and documented in the **IRanges** package.
- The [GRangesList](#) class defined and documented in the **GenomicRanges** package.
- The [coverage](#) methods defined in the **GenomicRanges** package.
- The [exonsBy](#) function for extracting exon ranges grouped by transcript.
- [findCompatibleOverlaps](#) in the **GenomicAlignments** package for finding which reads are *compatible* with the splicing of which transcript.

**Examples**

```
## -----
## 1. COMPUTE TRANSCRIPTOME COVERAGE OF A SET OF ALIGNED READS
## -----

## Load the aligned reads:
library(pasillaBamSubset)
library(GenomicAlignments)
reads <- readGAlignments(untreated1_chr4())

## Load the transcripts:
library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
txdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
transcripts <- exonsBy(txdb, by="tx", use.names=TRUE)

## Compute the transcript coverage with coverageByTranscript():
tx_cvg <- coverageByTranscript(reads, transcripts, ignore.strand=TRUE)
tx_cvg

## A sanity check:
stopifnot(identical(elementLengths(tx_cvg), sum(width(transcripts))))

## We can also use pcoverageByTranscript() to compute 'tx_cvg'.
## For this we first create a GAlignmentsList object "parallel" to
## 'transcripts' where the i-th list element contains the aligned reads
## that overlap with the i-th transcript:
hits <- findOverlaps(reads, transcripts, ignore.strand=TRUE)
tx2reads <- setNames(as(t(hits), "List"), names(transcripts))
reads_by_tx <- extractList(reads, tx2reads) # GAlignmentsList object
reads_by_tx

## Call pcoverageByTranscript():
tx_cvg2 <- pcoverageByTranscript(reads_by_tx, transcripts,
                                ignore.strand=TRUE)
stopifnot(identical(tx_cvg, tx_cvg2))

## A more meaningful coverage is obtained by counting for each
## transcript only the reads that are *compatible* with its splicing:
```

```

compat_hits <- findCompatibleOverlaps(reads, transcripts)
tx2reads <- setNames(as(t(compat_hits), "List"), names(transcripts))
compat_reads_by_tx <- extractList(reads, tx2reads)

tx_compat_cvg <- pcoverageByTranscript(compat_reads_by_tx,
                                     transcripts,
                                     ignore.strand=TRUE)

## A sanity check:
stopifnot(all(all(tx_compat_cvg <= tx_cvg)))

## -----
## 2. COMPUTE CDS COVERAGE OF A SET OF ALIGNED READS
## -----

## coverageByTranscript() can also be used to compute CDS coverage:
cds <- cdsBy(txdb, by="tx", use.names=TRUE)
cds_cvg <- coverageByTranscript(reads, cds, ignore.strand=TRUE)
cds_cvg

## A sanity check:
stopifnot(identical(elementLengths(cds_cvg), sum(width(cds))))

## -----
## 3. ALTERNATIVELY, THE CDS COVERAGE CAN BE OBTAINED FROM THE
##     TRANSCRIPT COVERAGE BY TRIMMING THE 5' AND 3' UTRS
## -----

tx_lens <- transcriptLengths(txdb, with.utr5_len=TRUE, with.utr3_len=TRUE)
stopifnot(identical(tx_lens$tx_name, names(tx_cvg))) # sanity

## Keep the rows in 'tx_lens' that correspond to a list element in
## 'cds_cvg' and put them in the same order as in 'cds_cvg':
m <- match(names(cds_cvg), names(tx_cvg))
tx_lens <- tx_lens[m, ]
utr5_width <- tx_lens$utr5_len
utr3_width <- tx_lens$utr3_len

trimListElements <- function(x, ltrim=0, rtrim=0)
{
  x_ellens <- elementLengths(x)
  n1 <- pmax(x_ellens - rtrim, 0)
  n2 <- pmax(n1 - ltrim, 0)
  ptail(phead(x, n=n1), n=n2)
}

cds_cvg2 <- trimListElements(tx_cvg[m], utr5_width, utr3_width)

## A sanity check:
stopifnot(identical(cds_cvg2, cds_cvg))

```

**Description**

The DEFAULT\_CIRC\_SEQS character vector contains strings that are normally used by major repositories as the names of chromosomes that are typically circular, it is available as a convenience so that users can use it as a default value for circ\_seqs arguments, and append to it as needed.

**Usage**

```
DEFAULT_CIRC_SEQS
```

**See Also**

[makeTxDbFromUCSC](#), [makeTxDbFromBiomart](#)

**Examples**

```
DEFAULT_CIRC_SEQS
```

---

disjointExons	<i>Extract non-overlapping exon parts from an object</i>
---------------	--

---

**Description**

disjointExons extracts the non-overlapping exon parts from a [TxDb](#) object or any other supported object.

**Usage**

```
disjointExons(x, ...)

## S4 method for signature 'TxDb'
disjointExons(x, aggregateGenes=FALSE,
              includeTranscripts=TRUE, ...)
```

**Arguments**

x	A <a href="#">TxDb</a> object or any other supported object.
...	Arguments to be passed to methods.
aggregateGenes	For disjointExons : A logical. When FALSE (default) exon fragments that overlap multiple genes are dropped. When TRUE, all fragments are kept and the gene_id metadata column includes all gene ids that overlap the exon fragment.
includeTranscripts	For disjointExons : A logical. When TRUE (default) a tx_name metadata column is included that lists all transcript names that overlap the exon fragment.

**Details**

disjointExons creates a [GRanges](#) of non-overlapping exon parts with metadata columns of gene\_id and exonic\_part. Exon parts that overlap more than 1 gene can be dropped with aggregateGenes=FALSE. When includeTranscripts=TRUE a tx\_name metadata column is included that lists all transcript names that overlap the exon fragment. This function replaces prepareAnnotationForDEXSeq in the **DEXSeq** package.

**Value**

A [GRanges](#) object.

**Author(s)**

disjointExons was originally implemented by Mike Love and Alejandro Reyes and then moved (and adapted) to **GenomicFeatures** by Valerie Obenchain.

**See Also**

- [transcripts](#), [transcriptsBy](#), and [transcriptsByOverlaps](#) for the core genomic features extractors.
- The [TxDb](#) class.

**Examples**

```
## TODO
```

---

```
extractTranscriptSeqs Extract transcript (or CDS) sequences from chromosome sequences
```

---

**Description**

extractTranscriptSeqs extracts transcript (or CDS) sequences from an object representing a single chromosome or a collection of chromosomes.

**Usage**

```
extractTranscriptSeqs(x, transcripts, ...)

## S4 method for signature 'DNAString'
extractTranscriptSeqs(x, transcripts, strand="+")

## S4 method for signature 'ANY'
extractTranscriptSeqs(x, transcripts)
```

**Arguments**

- |             |   |
|-------------|---|
| x           | An object representing a single chromosome or a collection of chromosomes. More precisely, x can be a <a href="#">DNAString</a> object (single chromosome), or a <a href="#">BSgenome</a> object (collection of chromosomes).<br>Other objects representing a collection of chromosomes are supported (e.g. <a href="#">FaFile</a> objects in the <b>Rsamtools</b> package) as long as <a href="#">seqinfo</a> and <a href="#">getSeq</a> work on them. |
| transcripts | An object representing the exon ranges of each transcript to extract.<br>More precisely: <ul style="list-style-type: none"> <li>• If x is a <a href="#">DNAString</a> object, then transcripts must be an <a href="#">RangesList</a> object.</li> </ul>   |



- If `x` is a [BSgenome](#) object or any object representing a collection of chromosomes, then transcripts must be a [GRangesList](#) object or any object for which [exonsBy](#) is implemented (e.g. a [TxDb](#) object). If the latter, then it's first turned into a [GRangesList](#) object with `exonsBy(transcripts, by="tx", use.names=TRUE)`.

Note that, for each transcript, the exons must be ordered by ascending rank, that is, by their position in the transcript. This means that, for a transcript located on the minus strand, the exons should typically be ordered by descending position on the reference genome. If transcripts was obtained with [exonsBy](#) (see above), then the exons are guaranteed to be ordered by ascending rank. See [?exonsBy](#) for more information.

...

Additional arguments, for use in specific methods.

strand

Only supported when `x` is a [DNASTring](#) object.

Can be an atomic vector, a factor, or an [Rle](#) object, in which case it indicates the strand of each transcript (i.e. all the exons in a transcript are considered to be on the same strand). More precisely: it's turned into a factor (or factor-[Rle](#)) that has the "standard strand levels" (this is done by calling the [strand](#) function on it). Then it's recycled to the length of [RangesList](#) object transcripts if needed. In the resulting object, the *i*-th element is interpreted as the strand of all the exons in the *i*-th transcript.

strand can also be a list-like object, in which case it indicates the strand of each exon, individually. Thus it must have the same *shape* as [RangesList](#) object transcripts (i.e. same length plus `strand[[i]]` must have the same length as `transcripts[[i]]` for all *i*).

strand can only contain "+" and/or "-" values. "\*" is not allowed.

### Value

A [DNASTringSet](#) object *parallel* to transcripts, that is, the *i*-th element in it is the sequence of the *i*-th transcript in transcripts.

### Author(s)

H. Pages

### See Also

- [coverageByTranscript](#) for computing coverage by transcript (or CDS) of a set of ranges.
- [transcriptLengths](#) for extracting the transcript lengths from a [TxDb](#) object.
- The [transcriptLocs2refLocs](#) function for converting transcript-based locations into reference-based locations.
- The [available.genomes](#) function in the [BSgenome](#) package for checking availability of BSgenome data packages (and installing the desired one).
- The [DNASTring](#) and [DNASTringSet](#) classes defined and documented in the [Biostrings](#) package.
- The [translate](#) function in the [Biostrings](#) package for translating DNA or RNA sequences into amino acid sequences.
- The [GRangesList](#) class defined and documented in the [GenomicRanges](#) package.
- The [RangesList](#) class defined and documented in the [IRanges](#) package.
- The [exonsBy](#) function for extracting exon ranges grouped by transcript.
- The [TxDb](#) class.

**Examples**

```

## -----
## 1. A TOY EXAMPLE
## -----

library(Biostrings)

## A chromosome of length 30:
x <- DNASTring("ATTTAGGACTCCCTGAGGACAAGACCCC")

## 2 transcripts on 'x':
tx1 <- IRanges(1, 8)           # 1 exon
tx2 <- c(tx1, IRanges(12, 30)) # 2 exons
transcripts <- IRangesList(tx1=tx1, tx2=tx2)
extractTranscriptSeqs(x, transcripts)

## By default, all the exons are considered to be on the plus strand.
## We can use the 'strand' argument to tell extractTranscriptSeqs()
## to extract them from the minus strand.

## Extract all the exons from the minus strand:
extractTranscriptSeqs(x, transcripts, strand="-")

## Note that, for a transcript located on the minus strand, the exons
## should typically be ordered by descending position on the reference
## genome in order to reflect their rank in the transcript:
extractTranscriptSeqs(x, IRangesList(tx1=tx1, tx2=rev(tx2)), strand="-")

## Extract the exon of the 1st transcript from the minus strand:
extractTranscriptSeqs(x, transcripts, strand=c("-", "+"))

## Extract the 2nd exon of the 2nd transcript from the minus strand:
extractTranscriptSeqs(x, transcripts, strand=list("-", c("+", "-")))

## -----
## 2. A REAL EXAMPLE
## -----

## Load a genome:
library(BSgenome.Hsapiens.UCSC.hg19)
genome <- BSgenome.Hsapiens.UCSC.hg19

## Load a TxDb object:
txdb_file <- system.file("extdata", "hg19_knownGene_sample.sqlite",
                        package="GenomicFeatures")
txdb <- loadDb(txdb_file)

## Check that 'txdb' is based on the hg19 assembly:
txdb

## Extract the exon ranges grouped by transcript from 'txdb':
transcripts <- exonsBy(txdb, by="tx", use.names=TRUE)

## Extract the transcript sequences from the genome:
tx_seqs <- extractTranscriptSeqs(genome, transcripts)
tx_seqs

```

```

## A sanity check:
stopifnot(identical(width(tx_seqs), unname(sum(width(transcripts))))))

## -----
## 3. USING extractTranscriptSeqs() TO EXTRACT CDS SEQUENCES
## -----

cds <- cdsBy(txdb, by="tx", use.names=TRUE)
cds_seqs <- extractTranscriptSeqs(genome, cds)
cds_seqs

## A sanity check:
stopifnot(identical(width(cds_seqs), unname(sum(width(cds))))))

## Note that, alternatively, the CDS sequences can be obtained from the
## transcript sequences by removing the 5' and 3' UTRs:
tx_lens <- transcriptLengths(txdb, with.utr5_len=TRUE, with.utr3_len=TRUE)
stopifnot(identical(tx_lens$tx_name, names(tx_seqs))) # sanity
## Keep the rows in 'tx_lens' that correspond to a sequence in 'cds_seqs'
## and put them in the same order as in 'cds_seqs':
m <- match(names(cds_seqs), names(tx_seqs))
tx_lens <- tx_lens[m, ]
utr5_width <- tx_lens$utr5_len
utr3_width <- tx_lens$utr3_len
cds_seqs2 <- narrow(tx_seqs[m],
                    start=utr5_width+1L, end=-(utr3_width+1L))
stopifnot(identical(as.character(cds_seqs2), as.character(cds_seqs)))

## -----
## 4. TRANSLATE THE CDS SEQUENCES
## -----

prot_seqs <- translate(cds_seqs, if.fuzzy.codon="solve")

## Note that, by default, translate() uses The Standard Genetic Code to
## translate codons into amino acids. However, depending on the organism,
## a different genetic code might be needed to translate CDS sequences
## located on the mitochondrial chromosome. For example, for vertebrates,
## the following code could be used to correct 'prot_seqs':
SGC1 <- getGeneticCode("SGC1")
chrM_idx <- which(all(seqnames(cds) == "chrM"))
prot_seqs[chrM_idx] <- translate(cds_seqs[chrM_idx], genetic.code=SGC1,
                               if.fuzzy.codon="solve")

```

---

extractUpstreamSeqs     *Extract sequences upstream of a set of genes or transcripts*

---

## Description

extractUpstreamSeqs is a generic function for extracting sequences upstream of a supplied set of genes or transcripts.

**Usage**

```
extractUpstreamSeqs(x, genes, width=1000, ...)

## Dispatch is on the 2nd argument!

## S4 method for signature 'GenomicRanges'
extractUpstreamSeqs(x, genes, width=1000)

## S4 method for signature 'TxDb'
extractUpstreamSeqs(x, genes, width=1000, exclude.seqlevels=NULL)
```

**Arguments**

x	An object containing the chromosome sequences from which to extract the upstream sequences. It can be a <a href="#">BSgenome</a> , <a href="#">TwoBitFile</a> , or <a href="#">FaFile</a> object, or any <i>genome sequence container</i> . More formally, x must be an object for which <a href="#">seqinfo</a> and <a href="#">getSeq</a> are defined.
genes	An object containing the locations (i.e. chromosome name, start, end, and strand) of the genes or transcripts with respect to the reference genome. Only <a href="#">GenomicRanges</a> and <a href="#">TxDb</a> objects are supported at the moment. If the latter, the gene locations are obtained by calling the <a href="#">genes</a> function on the <a href="#">TxDb</a> object internally.
width	How many bases to extract upstream of each TSS (transcription start site).
...	Additional arguments, for use in specific methods.
exclude.seqlevels	A character vector containing the chromosome names (a.k.a. sequence levels) to exclude when the genes are obtained from a <a href="#">TxDb</a> object.

**Value**

A [DNAStringSet](#) object containing one upstream sequence per gene (or per transcript if genes is a [GenomicRanges](#) object containing transcript ranges).

More precisely, if genes is a [GenomicRanges](#) object, the returned object is *parallel* to it, that is, the i-th element in the returned object is the upstream sequence corresponding to the i-th gene (or transcript) in genes. Also the names on the [GenomicRanges](#) object are propagated to the returned object.

If genes is a [TxDb](#) object, the names on the returned object are the gene IDs found in the [TxDb](#) object. To see the type of gene IDs (i.e. Entrez gene ID or Ensembl gene ID or ...), you can display genes with `show(genes)`.

In addition, the returned object has the following metadata columns (accessible with [mcols](#)) that provide some information about the gene (or transcript) corresponding to each upstream sequence:

- `gene_seqnames`: the chromosome name of the gene (or transcript);
- `gene_strand`: the strand of the gene (or transcript);
- `gene_TSS`: the transcription start site of the gene (or transcript).

**Note**

**IMPORTANT:** Always make sure to use a [TxDb](#) package (or [TxDb](#) object) that contains a gene model compatible with the *genome sequence container* x, that is, a gene model based on the exact same reference genome as x.

See [http://bioconductor.org/packages/release/BiocViews.html#\\_\\_\\_TxDb](http://bioconductor.org/packages/release/BiocViews.html#___TxDb) for the list of TxDb packages available in the current release of Bioconductor. Note that you can make your own custom TxDb object from various annotation resources. See the `makeTxDbFromUCSC`, `makeTxDbFromBiomart`, and `makeTxDbFromGFF` functions for more information about this.

### Author(s)

H. Pages

### See Also

- The `available.genomes` function in the **BSgenome** package for checking availability of BSgenome data packages (and installing the desired one).
- The `makeTxDbFromUCSC`, `makeTxDbFromBiomart`, and `makeTxDbFromGFF` functions for making your own custom TxDb object from various annotation resources.
- The **BSgenome**, **TwoBitFile**, and **FaFile** classes, defined and documented in the **BSgenome**, **rtracklayer**, and **Rsamtools** packages, respectively.
- The TxDb class.
- The `genes` function for extracting gene ranges from a TxDb object.
- The **GenomicRanges** class defined and documented in the **GenomicRanges** package.
- The **DNAStringSet** class defined and documented in the **Biostrings** package.
- The `seqinfo` getter defined and documented in the **GenomeInfoDb** package.
- The `getSeq` function for extracting subsequences from a sequence container.

### Examples

```
## Load a genome:
library(BSgenome.Dmelanogaster.UCSC.dm3)
genome <- BSgenome.Dmelanogaster.UCSC.dm3
genome

## Use a TxDb object:
library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
txdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
txdb # contains Ensembl gene IDs

## Because the chrU and chrUextra sequences are made of concatenated
## scaffolds (see http://genome.ucsc.edu/cgi-bin/hgGateway?db=dm3),
## extracting the upstream sequences for genes located on these
## scaffolds is not reliable. So we exclude them:
exclude <- c("chrU", "chrUextra")
up1000seqs <- extractUpstreamSeqs(genome, txdb, width=1000,
                                exclude.seqlevels=exclude)
up1000seqs # the names are Ensembl gene IDs
mcols(up1000seqs)

## Upstream sequences for genes close to the chromosome bounds can be
## shorter than 1000 (note that this does not happen for circular
## chromosomes like chrM):
table(width(up1000seqs))
mcols(up1000seqs)[width(up1000seqs) != 1000, ]
```

---

FeatureDb-class      *FeatureDb objects*

---

### Description

The FeatureDb class is a generic container for storing genomic locations of an arbitrary type of genomic features.

See [?TxDb](#) for a container for storing transcript annotations.

See [?makeFeatureDbFromUCSC](#) for a convenient way to make FeatureDb objects from BioMart online resources.

### Methods

In the code snippets below, *x* is a FeatureDb object.

`metadata(x)`: Return *x*'s metadata in a data frame.

### Author(s)

Marc Carlson

### See Also

- The [TxDb](#) class for storing transcript annotations.
- [makeFeatureDbFromUCSC](#) for a convenient way to make a FeatureDb object from UCSC online resources.
- [saveDb](#) and [loadDb](#) for saving and loading the database content of a FeatureDb object.
- [features](#) for how to extract genomic features from a FeatureDb object.

### Examples

```
fdb_file <- system.file("extdata", "FeatureDb.sqlite",
                       package="GenomicFeatures")
fdb <- loadDb(fdb_file)
fdb
```

---

features      *Extract simple features from a FeatureDb object*

---

### Description

Generic function to extract genomic features from a FeatureDb object.

### Usage

```
features(x)
## S4 method for signature 'FeatureDb'
features(x)
```

**Arguments**

x                    A [FeatureDb](#) object.

**Value**

a GRanges object

**Author(s)**

M. Carlson

**See Also**

[FeatureDb](#)

**Examples**

```
fdb <- loadDb(system.file("extdata", "FeatureDb.sqlite",
                          package="GenomicFeatures"))
features(fdb)
```

---

getPromoterSeq

*Get gene promoter sequences*

---

**Description**

Extract sequences for the genes or transcripts specified in the query (a [GRanges](#) or [GRangesList](#) object) from a [BSgenome](#) object or an [FaFile](#).

**Usage**

```
## S4 method for signature 'GRangesList'
getPromoterSeq(query, subject, upstream=2000, downstream=200, ...)
## S4 method for signature 'GRangesList'
getPromoterSeq(query, subject, upstream=2000, downstream=200, ...)
## S4 method for signature 'GRanges'
getPromoterSeq(query, subject, upstream=2000, downstream=200, ...)
```

**Arguments**

query                A [GRanges](#) or [GRangesList](#) object containing genes grouped by transcript.

subject              A [BSgenome](#) object or a [FaFile](#) from which the sequences will be taken.

upstream             The number of DNA bases to include upstream of the TSS (transcription start site)

downstream          The number of DNA bases to include downstream of the TSS (transcription start site)

...                    Additional arguments

**Details**

getPromoterSeq is an overloaded method dispatching on query, which is either a GRanges or a GRangesList. It is a wrapper for the promoters and getSeq functions. The purpose is to allow sequence extraction from either a [BSgenome](#) or [FaFile](#).

Default values for upstream and downstream were chosen based on our current understanding of gene regulation. On average, promoter regions in the mammalian genome are 5000 bp upstream and downstream of the transcription start site.

**Value**

A [DNAStringSet](#) or [DNAStringSetList](#) instance corresponding to the GRanges or GRangesList supplied in the query.

**Author(s)**

Paul Shannon

**See Also**

[intra-range-methods](#) ## promoters methods for Ranges objects [intra-range-methods](#) ## promoters methods for GRanges objects [getSeq](#)

**Examples**

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
library(BSgenome.Hsapiens.UCSC.hg19)

e2f3 <- "1871" # entrez geneID for a cell cycle control transcription
             # factor, chr6 on the plus strand

transcriptCoordsByGene.GRangesList <-
  transcriptsBy (TxDb.Hsapiens.UCSC.hg19.knownGene, by = "gene") [e2f3]
  # a GrangesList of length one, describing three transcripts

promoter.seqs <- getPromoterSeq (transcriptCoordsByGene.GRangesList,
                                Hsapiens, upstream=10, downstream=0)
  # DNAStringSetList of length 1
  # [["1871"]] GCTTCCTGGA GCTTCCTGGA CGGAGCCAGG
```

---

id2name

*Map internal ids to external names for a given feature type*

---

**Description**

Utility function for retrieving the mapping from the internal ids to the external names of a given feature type.

**Usage**

```
id2name(txdb, feature.type=c("tx", "exon", "cds"))
```



## Arguments

<code>txdb</code>	A <a href="#">TxDb</a> object.
<code>feature.type</code>	The feature type for which the mapping must be retrieved.

## Details

Transcripts, exons and CDS in a [TxDb](#) object are stored in separate tables where the primary key is an integer called *feature internal id*. This id is stored in the "tx\_id" column for transcripts, in the "exon\_id" column for exons, and in the "cds\_id" column for CDS. Unlike other commonly used ids like Entrez Gene IDs or Ensembl IDs, this internal id was generated at the time the [TxDb](#) object was created and has no meaning outside the scope of this object.

The `id2name` function can be used to translate this internal id into a more informative id or name called *feature external name*. This name is stored in the "tx\_name" column for transcripts, in the "exon\_name" column for exons, and in the "cds\_name" column for CDS.

Note that, unlike the feature internal id, the feature external name is not guaranteed to be unique or even defined (the column can contain NAs).

## Value

A named character vector where the names are the internal ids and the values the external names.

## Author(s)

H. Pages

## See Also

- [transcripts](#), [transcriptsBy](#), and [transcriptsByOverlaps](#), for how to extract genomic features from a [TxDb](#) object.
- The [TxDb](#) class.

## Examples

```
txdb1_file <- system.file("extdata", "hg19_knownGene_sample.sqlite",
                          package="GenomicFeatures")
txdb1 <- loadDb(txdb1_file)
id2name(txdb1, feature.type="tx")[1:4]
id2name(txdb1, feature.type="exon")[1:4]
id2name(txdb1, feature.type="cds")[1:4]

txdb2_file <- system.file("extdata", "Biomart_Ensembl_sample.sqlite",
                          package="GenomicFeatures")
txdb2 <- loadDb(txdb2_file)
id2name(txdb2, feature.type="tx")[1:4]
id2name(txdb2, feature.type="exon")[1:4]
id2name(txdb2, feature.type="cds")[1:4]
```

---

makeFeatureDbFromUCSC *Making a FeatureDb object from annotations available at the UCSC Genome Browser*

---

## Description

The makeFeatureDbFromUCSC function allows the user to make a [FeatureDb](#) object from simple annotation tracks at UCSC. The tracks in question must (at a minimum) have a start, end and a chromosome affiliation in order to be made into a [FeatureDb](#). This function requires a precise declaration of its first three arguments to indicate which genome, track and table wish to be imported. There are discovery functions provided to make this process go smoothly.

## Usage

```
supportedUCSCFeatureDbTracks(genome)
```

```
supportedUCSCFeatureDbTables(genome, track)
```

```
UCSCFeatureDbTableSchema(genome,
                           track,
                           tablename)
```

```
makeFeatureDbFromUCSC(
  genome,
  track,
  tablename,
  columns = UCSCFeatureDbTableSchema(genome, track, tablename),
  url="http://genome.ucsc.edu/cgi-bin/",
  goldenPath_url="http://hgdownload.cse.ucsc.edu/goldenPath",
  chromCol,
  chromStartCol,
  chromEndCol,
  taxonomyId=NA)
```

## Arguments

**genome** genome abbreviation used by UCSC and obtained by `ucscGenomes()` [ , "db"]. For example: "hg18".

**track** name of the UCSC track. Use `supportedUCSCFeatureDbTracks` to get the list of available tracks for a particular genome

**tablename** name of the UCSC table containing the annotations to retrieve. Use the `supportedUCSCFeatureDbTables` utility function to get the list of supported tables for a track.

**columns** a named character vector to list out the names and types of the other columns that the downloaded track should have. Use `UCSCFeatureDbTableSchema` to retrieve this information for a particular table.

**url, goldenPath\_url** use to specify the location of an alternate UCSC Genome Browser.

**chromCol** If the schema comes back and the 'chrom' column has been labeled something other than 'chrom', use this argument to indicate what that column has been labeled as so we can properly designate it. This could happen (for example)

with the knownGene track tables, which has no 'chromStart' or 'chromEnd' columns, but which DOES have columns that could reasonably substitute for these columns under particular circumstances. Therefore we allow these three columns to have arguments so that their definition can be re-specified

chromStartCol Same thing as chromCol, but for renames of 'chromStart'  
 chromEndCol Same thing as chromCol, but for renames of 'chromEnd'  
 taxonomyId By default this value is NA and the organism inferred will be used to look up the correct value for this. But you can use this argument to override that and supply your own valid taxId here.

## Details

makeFeatureDbFromUCSC is a convenience function that builds a tiny database from one of the UCSC track tables. supportedUCSCFeatureDbTracks a convenience function that returns potential track names that could be used to make FeatureDb objects supportedUCSCFeatureDbTables a convenience function that returns potential table names for FeatureDb objects (table names go with a track name) UCSCFeatureDbTableSchema A convenience function that creates a named vector of types for all the fields that can potentially be supported for a given track. By default, this will be called on your specified tablename to include all of the fields in a track.

## Value

A [FeatureDb](#) object for makeFeatureDbFromUCSC. Or in the case of supportedUCSCFeatureDbTracks and UCSCFeatureDbTableSchema a named character vector

## Author(s)

M. Carlson and H. Pages

## See Also

[ucscGenomes](#),

## Examples

```
## Display the list of genomes available at UCSC:
library(GenomicFeatures)
library(rtracklayer)
ucscGenomes()[ , "db"]

## Display the list of Tracks supported by makeFeatureDbFromUCSC():
# supportedUCSCFeatureDbTracks("mm9")

## Display the list of tables supported by your track:
supportedUCSCFeatureDbTables(genome="mm9",
                             track="oreganno")

## Display fields that could be passed in to colnames:
UCSCFeatureDbTableSchema(genome="mm9",
                         track="oreganno",
                         tablename="oreganno")

## Retrieving a full transcript dataset for Yeast from UCSC:
fdb <- makeFeatureDbFromUCSC(genome="mm9",
```

```

                                track="oreganno",
                                tablename="oreganno")
fdb

```

---

makeTxDb

*Making a TxDb object from user supplied annotations*


---

## Description

makeTxDb is a low-level constructor for making a [TxDb](#) object from user supplied transcript annotations. See [?makeTxDbFromUCSC](#) and [?makeTxDbFromBiomart](#) for higher-level functions that feed data from the UCSC or BioMart sources to makeTxDb.

## Usage

```

makeTxDb(transcripts, splicings,
          genes=NULL, chrominfo=NULL, metadata=NULL,
          reassign.ids=FALSE)

```

## Arguments

transcripts	data frame containing the genomic locations of a set of transcripts
spl icings	data frame containing the exon and cds locations of a set of transcripts
genes	data frame containing the genes associated to a set of transcripts
chrominfo	data frame containing information about the chromosomes hosting the set of transcripts
metadata	2-column data frame containing meta information about this set of transcripts like organism, genome, UCSC table, etc... The names of the columns must be "name" and "value" and their type must be character.
reassign.ids	controls how internal ids should be assigned for each type of feature i.e. for transcripts, exons, and cds. For each type, if reassign.ids is FALSE and if the ids are supplied, then they are used as the internal ids, otherwise the internal ids are assigned in a way that is compatible with the order defined by ordering the features first by chromosome, then by strand, then by start, and finally by end.

## Details

The transcripts (required), splicings (required) and genes (optional) arguments must be data frames that describe a set of transcripts and the genomic features related to them (exons, cds and genes at the moment). The chrominfo (optional) argument must be a data frame containing chromosome information like the length of each chromosome.

transcripts must have 1 row per transcript and the following columns:

- tx\_id: Transcript ID. Integer vector. No NAs. No duplicates.
- tx\_name: [optional] Transcript name. Character vector (or factor). NAs and/or duplicates are ok.
- tx\_type: [optional] Transcript type (e.g. mRNA, ncRNA, snoRNA, etc...). Character vector (or factor). NAs and/or duplicates are ok.

- `tx_chrom`: Transcript chromosome. Character vector (or factor) with no NAs.
- `tx_strand`: Transcript strand. Character vector (or factor) with no NAs where each element is either "+" or "-".
- `tx_start`, `tx_end`: Transcript start and end. Integer vectors with no NAs.

Other columns, if any, are ignored (with a warning).

`splicings` must have N rows per transcript, where N is the nb of exons in the transcript. Each row describes an exon plus, optionally, the cds contained in this exon. Its columns must be:

- `tx_id`: Foreign key that links each row in the `splicings` data frame to a unique row in the `transcripts` data frame. Note that more than 1 row in `splicings` can be linked to the same row in `transcripts` (many-to-one relationship). Same type as `transcripts$tx_id` (integer vector). No NAs. All the values in this column must be present in `transcripts$tx_id`.
- `exon_rank`: The rank of the exon in the transcript. Integer vector with no NAs. (`tx_id`, `exon_rank`) pairs must be unique.
- `exon_id`: [optional] Exon ID. Integer vector with no NAs.
- `exon_name`: [optional] Exon name. Character vector (or factor). NAs and/or duplicates are ok.
- `exon_chrom`: [optional] Exon chromosome. Character vector (or factor) with no NAs. If missing then `transcripts$tx_chrom` is used. If present then `exon_strand` must also be present.
- `exon_strand`: [optional] Exon strand. Character vector (or factor) with no NAs. If missing then `transcripts$tx_strand` is used and `exon_chrom` must also be missing.
- `exon_start`, `exon_end`: Exon start and end. Integer vectors with no NAs.
- `cds_id`: [optional] cds ID. Integer vector. If present then `cds_start` and `cds_end` must also be present. NAs are allowed and must match NAs in `cds_start` and `cds_end`.
- `cds_name`: [optional] cds name. Character vector (or factor). If present then `cds_start` and `cds_end` must also be present. NAs and/or duplicates are ok. Must be NA if corresponding `cds_start` and `cds_end` are NAs.
- `cds_start`, `cds_end`: [optional] cds start and end. Integer vectors. If one of the 2 columns is missing then all `cds_*` columns must be missing. NAs are allowed and must occur at the same positions in `cds_start` and `cds_end`.

Other columns, if any, are ignored (with a warning).

`genes` must have N rows per transcript, where N is the nb of genes linked to the transcript (N will be 1 most of the time). Its columns must be:

- `tx_id`: [optional] `genes` must have either a `tx_id` or a `tx_name` column but not both. Like `splicings$tx_id`, this is a foreign key that links each row in the `genes` data frame to a unique row in the `transcripts` data frame.
- `tx_name`: [optional] Can be used as an alternative to the `genes$tx_id` foreign key.
- `gene_id`: Gene ID. Character vector (or factor). No NAs.

Other columns, if any, are ignored (with a warning).

`chrominfo` must have 1 row per chromosome and the following columns:

- `chrom`: Chromosome name. Character vector (or factor) with no NAs and no duplicates.
- `length`: Chromosome length. Integer vector with either all NAs or no NAs.
- `is_circular`: [optional] Chromosome circularity flag. Logical vector. NAs are ok.

Other columns, if any, are ignored (with a warning).

**Value**

A [TxDb](#) object.

**Author(s)**

H. Pages

**See Also**

- [makeTxDbFromUCSC](#), [makeTxDbFromBiomart](#), [makeTxDbFromGRanges](#), and [makeTxDbFromGFF](#), for convenient ways to make a [TxDb](#) object from UCSC or BioMart online resources, or from a [GRanges](#) object, or from a GFF or GTF file.
- The [TxDb](#) class.
- [saveDb](#) and [loadDb](#) in the **AnnotationDbi** package for saving and loading a [TxDb](#) object as an SQLite file.

**Examples**

```
transcripts <- data.frame(
  tx_id=1:3,
  tx_chrom="chr1",
  tx_strand=c("-", "+", "+"),
  tx_start=c(1, 2001, 2001),
  tx_end=c(999, 2199, 2199))
splittings <- data.frame(
  tx_id=c(1L, 2L, 2L, 2L, 3L, 3L),
  exon_rank=c(1, 1, 2, 3, 1, 2),
  exon_start=c(1, 2001, 2101, 2131, 2001, 2131),
  exon_end=c(999, 2085, 2144, 2199, 2085, 2199),
  cds_start=c(1, 2022, 2101, 2131, NA, NA),
  cds_end=c(999, 2085, 2144, 2193, NA, NA))

txdb <- makeTxDb(transcripts, splittings)
```

---

`makeTxDbFromBiomart`    *Make a TxDb object from annotations available on a BioMart database*

---

**Description**

The `makeTxDbFromBiomart` function allows the user to make a [TxDb](#) object from transcript annotations available on a BioMart database.

**Usage**

```
makeTxDbFromBiomart(biomart="ensembl",
  dataset="hsapiens_gene_ensembl",
  transcript_ids=NULL,
  circ_seqs=DEFAULT_CIRC_SEQS,
  filters="",
  id_prefix="ensembl_",
  host="www.biomart.org",
```

```

        port=80,
        taxonomyId=NA,
        miRBaseBuild=NA)

getChromInfoFromBiomart(biomart="ensembl",
                        dataset="hsapiens_gene_ensembl",
                        id_prefix="ensembl_",
                        host="www.biomart.org",
                        port=80)

```

## Arguments

biomart	which BioMart database to use. Get the list of all available BioMart databases with the <a href="#">listMarts</a> function from the <code>biomaRt</code> package. See the details section below for a list of BioMart databases with compatible transcript annotations.
dataset	which dataset from BioMart. For example: "hsapiens_gene_ensembl", "mmusculus_gene_ensembl", "dmelanogaster_gene_ensembl", "celegans_gene_ensembl", "scerevisiae_gene_ensembl", etc in the ensembl database. See the examples section below for how to discover which datasets are available in a given BioMart database.
transcript_ids	optionally, only retrieve transcript annotation data for the specified set of transcript ids. If this is used, then the meta information displayed for the resulting <a href="#">TxDb</a> object will say 'Full dataset: no'. Otherwise it will say 'Full dataset: yes'.
circ_seqs	a character vector to list out which chromosomes should be marked as circular.
filters	Additional filters to use in the BioMart query. Must be a named list. An example is <code>filters=list(source="entrez")</code>
id_prefix	Specifies the prefix used in BioMart attributes. For example, some BioMarts may have an attribute specified as "ensembl_transcript_id" whereas others have the same attribute specified as "transcript_id". Defaults to "ensembl_".
host	The host URL of the BioMart. Defaults to <code>www.biomart.org</code> .
port	The port to use in the HTTP communication with the host.
taxonomyId	By default this value is NA and the dataset selected will be used to look up the correct value for this. But you can use this argument to override that and supply your own taxId here (which will be independently checked to make sure its a real taxonomy id). Normally you should never need to use this.
miRBaseBuild	specify the string for the appropriate build Information from <code>mirbase.db</code> to use for microRNAs. This can be learned by calling <code>supportedMiRBaseBuildValues</code> . By default, this value will be set to NA, which will inactivate the microRNAs accessor.

## Details

`makeTxDbFromBiomart` is a convenience function that feeds data from a BioMart database to the lower level `makeTxDb` function. See `?makeTxDbFromUCSC` for a similar function that feeds data from the UCSC source.

The `listMarts` function from the **biomaRt** package can be used to list all public BioMart databases. Not all databases returned by this function contain datasets that are compatible with (i.e. understood by) `makeTxDbFromBiomart`. Here is a list of datasets known to be compatible (updated on Sep 24, 2014):

- All the datasets in the main Ensembl database: use `biomart="ensembl"`.

- All the datasets in the Ensembl Fungi database: use `biomart="fungi_mart_XX"` where `XX` is the release version of the database e.g. `"fungi_mart_22"`.
- All the datasets in the Ensembl Metazoa database: use `biomart="metazoa_mart_XX"` where `XX` is the release version of the database e.g. `"metazoa_mart_22"`.
- All the datasets in the Ensembl Plants database: use `biomart="plants_mart_XX"` where `XX` is the release version of the database e.g. `"plants_mart_22"`.
- All the datasets in the Ensembl Protists database: use `biomart="protists_mart_XX"` where `XX` is the release version of the database e.g. `"protists_mart_22"`.
- All the datasets in the Gramene Mart: use `biomart="ENSEMBL_MART_PLANT"`.

Not all these datasets have CDS information.

### Value

A `TxDb` object for `makeTxDbFromBiomart`.

A data frame with 1 row per chromosome (or scaffold) and with columns `chrom` and `length` for `getChromInfoFromBiomart`.

### Author(s)

M. Carlson and H. Pages

### See Also

- `makeTxDbFromUCSC`, `makeTxDbFromGRanges`, and `makeTxDbFromGFF`, for convenient ways to make a `TxDb` object from UCSC online resources, or from a `GRanges` object, or from a GFF or GTF file.
- The `listMarts`, `useMart`, `listDatasets`, and `listFilters` functions in the **biomaRt** package.
- `DEFAULT_CIRC_SEQS`.
- The `supportedMiRBaseBuildValues` function for listing all the possible values for the `miRBaseBuild` argument.
- The `TxDb` class.
- `makeTxDb` for the low-level function used by the `makeTxDbFrom*` functions to make the `TxDb` object returned to the user.

### Examples

```
## -----
## A. BASIC USAGE
## -----

## We can use listDatasets() from the biomaRt package to list the
## datasets available in the "ensembl" BioMart database:
library(biomaRt)
head(listDatasets(useMart("ensembl")))

## Retrieve the full transcript dataset for Worm:
txdb1 <- makeTxDbFromBiomart(dataset="celegans_gene_ensembl")
txdb1

## Retrieve an incomplete transcript dataset for Human:
```



```

transcript_ids <- c(
  "ENST00000013894",
  "ENST000000268655",
  "ENST000000313243",
  "ENST000000435657",
  "ENST000000384428",
  "ENST000000478783"
)
txdb2 <- makeTxDbFromBiomart(dataset="hsapiens_gene_ensembl",
  transcript_ids=transcript_ids)
txdb2 # note that these annotations match the GRCh38 genome assembly

## -----
## B. USING A HOST OTHER THAN www.biomart.org
## -----

## A typical use case is to access the "ensembl" BioMart database on a
## mirror e.g. on uswest.ensembl.org. A gotcha when doing this is that
## the name of the database on the mirror can be different! We can check
## this with listMarts() from the biomaRt package:
listMarts(host="useast.ensembl.org")

## Therefore, in addition to setting 'host' to "uswest.ensembl.org" we
## must also change the name passed to the 'biomart' argument:
txdb3 <- makeTxDbFromBiomart(biomart="ENSEMBL_MART_ENSEMBL",
  dataset="hsapiens_gene_ensembl",
  transcript_ids=transcript_ids,
  host="useast.ensembl.org")
txdb3

## -----
## C. USING FILTERS
## -----

## We can use listFilters() from the biomaRt package to get valid filter
## names:
mart <- useMart("ensembl", dataset="hsapiens_gene_ensembl")
head(listFilters(mart))

## Retrieve transcript dataset for Ensembl gene ENSG00000011198:
my_filter <- list(ensembl_gene_id="ENSG00000011198")
txdb4 <- makeTxDbFromBiomart(dataset="hsapiens_gene_ensembl",
  filters=my_filter)
txdb4
transcripts(txdb4, columns=c("tx_id", "tx_name", "gene_id"))
transcriptLengths(txdb4)

## -----
## D. RETRIEVING CHROMOSOME INFORMATION ONLY
## -----

chrominfo <- getChromInfoFromBiomart(dataset="celegans_gene_ensembl")
chrominfo

```

---

makeTxDbFromGFF      *Make a TxDb object from annotations available as a GFF3 or GTF file*

---

## Description

The makeTxDbFromGFF function allows the user to make a [TxDb](#) object from transcript annotations available as a GFF3 or GTF file.

## Usage

```
makeTxDbFromGFF(file,
                 format=c("auto", "gff3", "gtf"),
                 dataSource=NA,
                 organism=NA,
                 taxonomyId=NA,
                 circ_seqs=DEFAULT_CIRC_SEQS,
                 chrominfo=NULL,
                 mirBaseBuild=NA,
                 dbxrefTag,
                 exonRankAttributeName=NA,
                 gffGeneIdAttributeName=NA,
                 useGenesAsTranscripts=FALSE,
                 gffTxName="mRNA",
                 species=NA)
```

## Arguments

file	Input GFF3 or GTF file. Can be a path to a file, or an URL, or a connection object, or a <a href="#">GFF3File</a> or <a href="#">GTFFile</a> object.
format	Format of the input file. Accepted values are: "auto" (the default) for auto-detection of the format, "gff3", or "gtf". Use "gff3" or "gtf" only if auto-detection failed.
dataSource	A single string describing the origin of the data file. Please be as specific as possible.
organism	What is the Genus and species of this organism. Please use proper scientific nomenclature for example: "Homo sapiens" or "Canis familiaris" and not "human" or "my fuzzy buddy". If properly written, this information may be used by the software to help you out later.
taxonomyId	By default this value is NA and the organism provided will be used to look up the correct value for this. But you can use this argument to override that and supply your own taxonomy id here (which will be separately validated). Since providing a valid taxonomy id will not require us to look up one based on your organism: this is one way that you can loosen the restrictions about what is and isn't a valid value for the organism.
circ_seqs	A character vector to list out which chromosomes should be marked as circular.
chrominfo	Data frame containing information about the chromosomes. Will be passed to the internal call to <a href="#">makeTxDb</a> . See <a href="#">?makeTxDb</a> for more information. Alternatively, can be a <a href="#">Seqinfo</a> object.

miRBaseBuild	Specify the string for the appropriate build Information from mirbase.db to use for microRNAs. This can be learned by calling <code>supportedMiRBaseBuildValues</code> . By default, this value will be set to NA, which will inactivate the microRNAs accessor.
dbxrefTag	If not missing, the values in the Dbxref attribute with the specified tag (like "GeneID") are used for the feature names.
exonRankAttributeName	this argument is defunct
gffGeneIdAttributeName	this argument is defunct
useGenesAsTranscripts	this argument is defunct
gffTxName	this argument is defunct
species	this argument was replaced with the <code>organism</code> argument and is now defunct

### Details

`makeTxDbFromGFF` is a convenience function that feeds data from the parsed file to the [makeTxDbFromGRanges](#) function.

### Value

A [TxDb](#) object.

### Author(s)

M. Carlson and H. Pages

### See Also

- [makeTxDbFromGRanges](#), which `makeTxDbFromGFF` is based on, for making a [TxDb](#) object from a [GRanges](#) object.
- The `import` function in the **rtracklayer** package (also used by `makeTxDbFromGFF` internally).
- [makeTxDbFromUCSC](#) and [makeTxDbFromBiomart](#) for convenient ways to make a [TxDb](#) object from UCSC or BioMart online resources.
- `DEFAULT_CIRC_SEQS`.
- The [supportedMiRBaseBuildValues](#) function for listing all the possible values for the `miRBaseBuild` argument.
- The [TxDb](#) class.
- [makeTxDb](#) for the low-level function used by the `makeTxDbFrom*` functions to make the [TxDb](#) object returned to the user.

### Examples

```
## TESTING GFF3
gfffile <- system.file("extdata", "GFF3_files", "a.gff3", package="GenomicFeatures")
txdb <- makeTxDbFromGFF(file=gfffile,
  dataSource="partial gtf file for Tomatoes for testing",
  organism="Solanum lycopersicum")

## TESTING GTF, this time specifying the chrominfo
```

```
gtffFile <- system.file("extdata", "GTF_files", "Aedes_aegypti.partial.gtf",
                        package="GenomicFeatures")
chrominfo <- data.frame(chrom = c('supercont1.1', 'supercont1.2'),
                       length=c(5220442, 5300000),
                       is_circular=c(FALSE, FALSE))
txdb2 <- makeTxDbFromGFF(file=gtffFile,
                        chrominfo=chrominfo,
                        dataSource=paste("ftp://ftp.ensemblgenomes.org/pub/metazoa/",
                                        "release-13/gtf/aedes_aegypti/", sep=""),
                        organism="Aedes aegypti")
```

---

makeTxDbFromGRanges     *Make a TxDb object from a GRanges object*

---

## Description

The `makeTxDbFromGRanges` function allows the user to extract gene, transcript, exon, and CDS information from a [GRanges](#) object structured as GFF3 or GTF, and to return that information in a [TxDb](#) object.

## Usage

```
makeTxDbFromGRanges(gr, drop.stop.codons=FALSE, metadata=NULL, taxonomyId=NA)
```

## Arguments

<code>gr</code>	A <a href="#">GRanges</a> object structured as GFF3 or GTF, typically obtained with <code>rtracklayer::import()</code> .
<code>drop.stop.codons</code>	TRUE or FALSE. If TRUE, then features of type <code>stop_codon</code> are ignored. Otherwise (the default) the stop codons are considered to be part of the CDS and merged to them.
<code>metadata</code>	A 2-column data frame containing meta information to be included in the <a href="#">TxDb</a> object. This data frame is just passed to <code>makeTxDb</code> , which <code>makeTxDbFromGRanges</code> calls at the end to make the <a href="#">TxDb</a> object from the information extracted from <code>gr</code> . See <code>?makeTxDb</code> for more information about the format of metadata.
<code>taxonomyId</code>	By default this value is NA which will result in an NA field since there is no reliable way to infer this from a <a href="#">GRanges</a> object. But you can use this argument to supply your own valid taxId here and if you do, then the Organism can be filled in as well

## Value

A [TxDb](#) object.

## Author(s)

H. Pages

**See Also**

- [makeTxDbFromUCSC](#), [makeTxDbFromBiomart](#), and [makeTxDbFromGFF](#), for convenient ways to make a [TxDb](#) object from UCSC or BioMart online resources, or directly from a GFF or GTF file.
- The [import](#) function in the [rtracklayer](#) package.
- The [asGFF](#) method for [TxDb](#) objects ([asGFF,TxDb-method](#)) for the reverse of [makeTxDbFromGRanges](#), that is, for turning a [TxDb](#) object into a [GRanges](#) object structured as GFF.
- The [TxDb](#) class.
- [makeTxDb](#) for the low-level function used by the [makeTxDbFrom\\*](#) functions to make the [TxDb](#) object returned to the user.

**Examples**

```
library(rtracklayer) # for the import() function

## -----
## WITH A GRanges OBJECT STRUCTURED AS GFF3
## -----
GFF3_files <- system.file("extdata", "GFF3_files",
                          package="GenomicFeatures")

path <- file.path(GFF3_files, "a.gff3")
gr <- import(path)
txdb <- makeTxDbFromGRanges(gr)
txdb

## Reverse operation:
gr2 <- asGFF(txdb)

## Sanity check:
stopifnot(identical(as.list(txdb), as.list(makeTxDbFromGRanges(gr2))))

## -----
## WITH A GRanges OBJECT STRUCTURED AS GTF
## -----
GTF_files <- system.file("extdata", "GTF_files", package="GenomicFeatures")

## test1.gtf was grabbed from http://mblab.wustl.edu/GTF22.html (5 exon
## gene with 3 translated exons):
path <- file.path(GTF_files, "test1.gtf")
gr <- import(path)
txdb <- makeTxDbFromGRanges(gr)
txdb

path <- file.path(GTF_files, "Aedes_aegypti.partial.gtf")
gr <- import(path)
txdb <- makeTxDbFromGRanges(gr)
txdb
```

## Description

The `makeTxDbFromUCSC` function allows the user to make a `TxDb` object from transcript annotations available at the UCSC Genome Browser.

## Usage

```
supportedUCSCTables()

makeTxDbFromUCSC(
  genome="hg19",
  tablename="knownGene",
  transcript_ids=NULL,
  circ_seqs=DEFAULT_CIRC_SEQS,
  url="http://genome.ucsc.edu/cgi-bin/",
  goldenPath_url="http://hgdownload.cse.ucsc.edu/goldenPath",
  taxonomyId=NA,
  mirBaseBuild=NA)

getChromInfoFromUCSC(
  genome,
  goldenPath_url="http://hgdownload.cse.ucsc.edu/goldenPath")
```

## Arguments

<code>genome</code>	genome abbreviation used by UCSC and obtained by <code>ucscGenomes()[ , "db"]</code> . For example: "hg19".
<code>tablename</code>	name of the UCSC table containing the transcript annotations to retrieve. Use the <code>supportedUCSCTables</code> utility function to get the list of supported tables. Note that not all tables are available for all genomes.
<code>transcript_ids</code>	optionally, only retrieve transcript annotation data for the specified set of transcript ids. If this is used, then the meta information displayed for the resulting <code>TxDb</code> object will say 'Full dataset: no'. Otherwise it will say 'Full dataset: yes'.
<code>circ_seqs</code>	a character vector to list out which chromosomes should be marked as circular.
<code>url, goldenPath_url</code>	use to specify the location of an alternate UCSC Genome Browser.
<code>taxonomyId</code>	By default this value is NA and the organism inferred will be used to look up the correct value for this. But you can use this argument to supply your own valid taxId here.
<code>mirBaseBuild</code>	specify the string for the appropriate build Information from mirbase.db to use for microRNAs. This can be learned by calling <code>supportedMirBaseBuildValues</code> . By default, this value will be set to NA, which will inactivate the microRNAs accessor.

## Details

`makeTxDbFromUCSC` is a convenience function that feeds data from the UCSC source to the lower level `makeTxDb` function. See `?makeTxDbFromBiomart` for a similar function that feeds data from a BioMart database.



```

                                circ_seqs="chrM")
txdb2

## -----
## B. RETRIEVING CHROMOSOME INFORMATION ONLY
## -----

chrominfo <- getChromInfoFromUCSC(genome="hg38")
chrominfo

```

---

makeTxDbPackage	<i>Making a TxDb package from annotations available at the UCSC Genome Browser, biomaRt or from another source.</i>
-----------------	---

---

## Description

A [TxDb](#) package is an annotation package containing a [TxDb](#) object.

The `makeTxDbPackageFromUCSC` function allows the user to make a [TxDb](#) package from transcript annotations available at the UCSC Genome Browser.

The `makeTxDbPackageFromBiomaRt` function allows the user to do the same thing as `makeTxDbPackageFromUCSC` except that the annotations originate from `biomaRt`.

Finally, the `makeTxDbPackage` function allows the user to make a [TxDb](#) package directly from a [TxDb](#) object.

## Usage

```

makeTxDbPackageFromUCSC(
  version=,
  maintainer,
  author,
  destDir=".",
  license="Artistic-2.0",
  genome="hg19",
  tablename="knownGene",
  transcript_ids=NULL,
  circ_seqs=DEFAULT_CIRC_SEQS,
  url="http://genome.ucsc.edu/cgi-bin/",
  goldenPath_url="http://hgdownload.cse.ucsc.edu/goldenPath",
  taxonomyId=NA,
  miRBaseBuild=NA)

makeFDbPackageFromUCSC(
  version,
  maintainer,
  author,
  destDir=".",
  license="Artistic-2.0",
  genome="hg19",
  track="tRNAs",
  tablename="tRNAs",

```



```

columns = UCSCFeatureDbTableSchema(genome, track, tablename),
url="http://genome.ucsc.edu/cgi-bin/",
goldenPath_url="http://hgdownload.cse.ucsc.edu/goldenPath",
chromCol=NULL,
chromStartCol=NULL,
chromEndCol=NULL,
taxonomyId=NA)

makeTxDbPackageFromBiomart(
  version,
  maintainer,
  author,
  destDir=".",
  license="Artistic-2.0",
  biomart="ensembl",
  dataset="hsapiens_gene_ensembl",
  transcript_ids=NULL,
  circ_seqs=DEFAULT_CIRC_SEQS,
  filters="",
  id_prefix="ensembl_",
  host="www.biomart.org",
  port=80,
  taxonomyId=NA,
  miRBaseBuild=NA)

makeTxDbPackage(txdb,
  version,
  maintainer,
  author,
  destDir=".",
  license="Artistic-2.0",
  pkgname=NULL)

supportedMiRBaseBuildValues()

```

## Arguments

version	What is the version number for this package?
maintainer	Who is the package maintainer? (must include email to be valid). Should be a <a href="#">person</a> object, or something coercible to one, like a string. May be omitted if the author argument is a person containing someone with the maintainer role.
author	Who is the creator of this package? Should be a <a href="#">person</a> object, or something coercible to one, like a character vector of names. The maintainer argument will be merged into this list.
destDir	A path where the package source should be assembled.
license	What is the license (and it's version)
biomart	which BioMart database to use. Get the list of all available BioMart databases with the <a href="#">listMarts</a> function from the <a href="#">biomaRt</a> package. See the details section below for a list of BioMart databases with compatible transcript annotations.
dataset	which dataset from BioMart. For example: "hsapiens_gene_ensembl", "mmusculus_gene_ensembl", "dmelanogaster_gene_ensembl", "celegans_gene_ensembl", "scerevisiae_gene_ensembl",

	etc in the ensembl database. See the examples section below for how to discover which datasets are available in a given BioMart database.
genome	genome abbreviation used by UCSC and obtained by <code>ucscGenomes()[ , "db"]</code> . For example: "hg18".
track	name of the UCSC track. Use <code>supportedUCSCFeatureDbTracks</code> to get the list of available tracks for a particular genome
tablename	name of the UCSC table containing the transcript annotations to retrieve. Use the <code>supportedUCSCTables</code> utility function to get the list of supported tables. Note that not all tables are available for all genomes.
transcript_ids	optionally, only retrieve transcript annotation data for the specified set of transcript ids. If this is used, then the meta information displayed for the resulting <code>TxDb</code> object will say 'Full dataset: no'. Otherwise it will say 'Full dataset: yes'.
circ_seqs	a character vector to list out which chromosomes should be marked as circular.
filters	Additional filters to use in the BioMart query. Must be a named list. An example is <code>filters=as.list(c(source="entrez"))</code>
host	The host URL of the BioMart. Defaults to <code>www.biomart.org</code> .
port	The port to use in the HTTP communication with the host.
id_prefix	Specifies the prefix used in BioMart attributes. For example, some BioMarts may have an attribute specified as "ensembl_transcript_id" whereas others have the same attribute specified as "transcript_id". Defaults to "ensembl_".
columns	a named character vector to list out the names and types of the other columns that the downloaded track should have. Use <code>UCSCFeatureDbTableSchema</code> to retrieve this information for a particular table.
url, goldenPath_url	use to specify the location of an alternate UCSC Genome Browser.
chromCol	If the schema comes back and the 'chrom' column has been labeled something other than 'chrom', use this argument to indicate what that column has been labeled as so we can properly designate it. This could happen (for example) with the <code>knownGene</code> track tables, which has no 'chromStart' or 'chromEnd' columns, but which DOES have columns that could reasonably substitute for these columns under particular circumstances. Therefore we allow these three columns to have arguments so that their definition can be re-specified
chromStartCol	Same thing as <code>chromCol</code> , but for renames of 'chromStart'
chromEndCol	Same thing as <code>chromCol</code> , but for renames of 'chromEnd'
txdb	A <code>TxDb</code> object that represents a handle to a transcript database. This object type is what is returned by <code>makeTxDbFromUCSC</code> , <code>makeTxDbFromUCSC</code> or <code>makeTxDb</code>
taxonomyId	By default this value is NA and the organism provided (or inferred) will be used to look up the correct value for this. But you can use this argument to override that and supply your own valid taxId here
miRBaseBuild	specify the string for the appropriate build Information from <code>mirbase.db</code> to use for microRNAs. This can be learned by calling <code>supportedMiRBaseBuildValues</code> . By default, this value will be set to NA, which will inactivate the microRNAs accessor.
pkgname	By default this value is NULL and does not need to be filled in (a package name will be generated for you). But if you override this value, then the package and it's object will be instead named after this value. Be aware that the standard rules for package names will apply, (so don't include spaces, underscores or dashes)

## Details

makeTxDbPackageFromUCSC is a convenience function that calls both the [makeTxDbFromUCSC](#) and the [makeTxDbPackage](#) functions. The [makeTxDbPackageFromBiomart](#) follows a similar pattern and calls the [makeTxDbFromBiomart](#) and [makeTxDbPackage](#) functions. [supportedMiRBaseBuildValues](#) is a convenience function that will list all the possible values for the `miRBaseBuild` argument.

## Value

A [TxDb](#) object.

## Author(s)

M. Carlson

## See Also

[makeTxDbFromUCSC](#), [makeTxDbFromBiomart](#), [makeTxDb](#), [ucscGenomes](#), [DEFAULT\\_CIRC\\_SEQS](#)

## Examples

```
## First consider relevant helper/discovery functions:
## Display the list of tables supported by makeTxDbPackageFromUCSC():
supportedUCSCTables()

## Can also list all the possible values for the miRBaseBuild argument:
supportedMiRBaseBuildValues()

## Next are examples of actually building a package:
## Not run:
## Makes a transcript package for Yeast from the ensGene table at UCSC:
makeTxDbPackageFromUCSC(version="0.01",
                        maintainer="Some One <so@someplace.org>",
                        author="Some One <so@someplace.com>",
                        genome="sacCer2",
                        tablename="ensGene")

## Makes a transcript package from Human by using biomart and limited to a
## small subset of the transcripts.
transcript_ids <- c(
  "ENST00000400839",
  "ENST00000400840",
  "ENST00000478783",
  "ENST00000435657",
  "ENST00000268655",
  "ENST00000313243",
  "ENST00000341724")

makeTxDbPackageFromBiomart(version="0.01",
                          maintainer="Some One <so@someplace.org>",
                          author="Some One <so@someplace.com>",
                          transcript_ids=transcript_ids)

## End(Not run)
```

---

mapToTranscripts      *Map range coordinates between transcripts and genome space*

---

### Description

Map range coordinates between features in the transcriptome and genome (reference) space.

See [?mapToAlignments](#) in the **GenomicAlignments** package for mapping coordinates between reads (local) and genome (reference) space using a CIGAR alignment.

### Usage

```
## mapping to transcripts
## S4 method for signature 'GenomicRanges,GRangesList'
mapToTranscripts(x, transcripts,
  ignore.strand = FALSE)
## S4 method for signature 'ANY,TxDb'
mapToTranscripts(x, transcripts, ignore.strand = FALSE,
  extractor.fun = GenomicFeatures::transcripts, ...)
## S4 method for signature 'GenomicRanges,GRangesList'
pmapToTranscripts(x, transcripts,
  ignore.strand = FALSE)

## mapping from transcripts
## S4 method for signature 'GenomicRanges,GRangesList'
mapFromTranscripts(x, transcripts,
  ignore.strand = FALSE)
## S4 method for signature 'GenomicRanges,GRangesList'
pmapFromTranscripts(x, transcripts,
  ignore.strand = FALSE)
## S4 method for signature 'Ranges,GRangesList'
pmapFromTranscripts(x, transcripts)
```

### Arguments

- |               |   |
|---------------|---|
| x             | <a href="#">GenomicRanges</a> object of positions to be mapped. The seqnames of x are used in <code>mapFromTranscripts</code> , i.e., when mapping from transcripts to the genome. In the case of <code>pmapFromTranscripts</code> , x can be a <code>Ranges</code> object.   |
| transcripts   | A named <a href="#">GenomicRanges</a> or <a href="#">GRangesList</a> object used to map between x and the result. The ranges can be any feature in the transcriptome extracted from a <code>TxDb</code> (e.g., introns, exons, cds regions). See <a href="#">?transcripts</a> and <a href="#">?transcriptsBy</a> for a list of extractor functions.<br><br>The <code>transcripts</code> object must have names. When mapping from transcripts to the genome, they are used to determine mapping pairs; in the reverse direction they become the seqlevels of the output object. |
| ignore.strand | When <code>ignore.strand</code> is <code>TRUE</code> , strand is ignored in overlaps operations (i.e., all strands are considered "+") and the strand in the output is <code>'*'</code> .<br><br>When <code>ignore.strand</code> is <code>FALSE</code> strand in the output is taken from the <code>transcripts</code> argument. When <code>transcripts</code> is a <code>GRangesList</code> , all inner list elements of a common list element must have the same strand or an error is thrown.  |

Mapped position is computed by counting from the transcription start site (TSS) and is not affected by the value of `ignore.strand`.

`extractor.fun` Function to extract genomic features from a `TxDb` object. This argument is only applicable to `mapToTranscripts` when `transcripts` is a `TxDb` object. The extractor should be the name of a function (not a character()) described on the `?transcripts`, `?transcriptsBy`, or `?microRNAs` man page. Valid extractor functions:

- `transcripts ## default`
- `exons`
- `cds`
- `genes`
- `promoters`
- `disjointExons`
- `transcriptsBy`
- `exonsBy`
- `cdsBy`
- `intronsByTranscript`
- `fiveUTRsByTranscript`
- `threeUTRsByTranscript`
- `microRNAs`
- `tRNAs`

... Additional arguments passed to `extractor.fun` functions.

## Details

In `GenomicFeatures`  $\geq$  1.21.10, the default for `ignore.strand` was changed to `FALSE` for consistency with other methods in `GenomicRanges` and `GenomicAlignments`. Additionally, the mapped position is computed from the TSS and does not depend on the `ignore.strand` argument. See the section on `ignore.strand` for details.

- `mapToTranscripts`, `pmapToTranscripts` The genomic range in `x` is mapped to the local position in the `transcripts` ranges. A successful mapping occurs when `x` is completely within the `transcripts` range, equivalent to:

```
findOverlaps(..., type="within")
```

Transcriptome-based coordinates start counting at 1 at the beginning of the `transcripts` range and return positions where `x` was aligned. The `seqlevels` of the return object are taken from the `transcripts` object and should be transcript names. In this direction, mapping is attempted between all elements of `x` and all elements of `transcripts`.

`mapToTranscripts` uses `findOverlaps` to map ranges in `x` to ranges in `transcripts`. This method does not return unmapped ranges.

`pmapToTranscripts` maps the *i*-th range in `x` to the *i*-th range in `transcripts`. Recycling is supported for both `x` and `transcripts` when either is `length == 1L`; otherwise the lengths must match. Ranges in `x` that do not map (out of bounds or strand mismatch) are returned as zero-width ranges starting at 0. These ranges are given the `seqname` of "UNMAPPED".

- `mapFromTranscripts`, `pmapFromTranscripts` The transcript-based position in `x` is mapped to genomic coordinates using the ranges in `transcripts`. A successful mapping occurs when the following is `TRUE`:

```
width(transcripts) >= start(x) + width(x)
```

`x` is aligned to `transcripts` by moving in `start(x)` positions in from the beginning of the `transcripts` range. The `seqlevels` of the return object are chromosome names.

`mapFromTranscripts` uses the `seqname` of `x` and the names of `transcripts` to determine mapping pairs (vs attempting to match all possible pairs). Name matching is motivated by use cases such as differentially expressed regions where the expressed regions in `x` would only be related to a subset of regions in `transcripts`. This method does not return unmapped ranges.

`pmapFromTranscripts` maps the *i*-th range in `x` to the *i*-th range in `transcripts` and therefore does not use name matching. Recycling is supported in `pmapFromTranscripts` when either `x` or `transcripts` is `length == 1L`; otherwise the lengths must match. Ranges in `x` that do not map (out of bounds or strand mismatch) are returned as zero-width ranges starting at 0. These ranges are given the `seqname` of "UNMAPPED".

### Value

`pmapToTranscripts` returns a `GRanges` the same length as `x`.

`pmapFromTranscripts` returns a `GRanges` when `transcripts` is a `GRanges` and a `GRangesList` when `transcripts` is a `GRangesList`. In both cases the return object is the same length as `x`. The rationale for returning the `GRangesList` is to preserve exon structure; ranges in a list element that are not overlapped by `x` are returned as a zero-width range. The `GRangesList` return object will have no `seqlevels` called "UNMAPPED"; those will only occur when a `GRanges` is returned.

`mapToTranscripts` and `mapFromTranscripts` return `GRanges` objects that vary in length similar to a `Hits` object. The result contains mapped records only; strand mismatch and out of bound ranges are not returned. `xHits` and `transcriptsHits` metadata columns (similar to the `queryHits` and `subjectHits` of a `Hits` object) indicate elements of `x` and `transcripts` used in the mapping.

When mapping to transcript coordinates, `seqlevels` of the output are the names on the `transcripts` object and most often these will be transcript names. When mapping to the genome, `seqlevels` of the output are the `seqlevels` of `transcripts` which are usually chromosome names.

### Author(s)

V. Obenchain, M. Lawrence and H. Pages

### See Also

- [?mapToAlignments](#) in the **GenomicAlignments** package for methods mapping between reads and genome space using a CIGAR alignment.

### Examples

```
## -----
## A. Basic Use
## -----

## -----
## (i) Map from genome to transcript:

## The seqnames of the output are the transcript names, not chromosomes. For
## this reason 'transcripts' must be named.
x <- GRanges("A", IRanges(16, 18))
gr1 <- GRanges("A", IRanges(1, 10, names="tx_a"))
```

```

gr2 <- GRanges("A", IRanges(15, 20, names="tx_b"))

## 'transcripts' as GRanges:
mapToTranscripts(x, gr2)

## 'transcripts' as GRangesList:
mapToTranscripts(x, GRangesList("tx_c" = c(gr1, gr2)))

## Round trip from genomic -> transcript -> genomic coordinates:
tx_coord <- mapToTranscripts(x, gr2)
mapFromTranscripts(tx_coord, gr2)

## -----
## (ii) Map from transcript to genome:

## A prerequisite for mapping from transcript -> genome is that the seqname
## of the range in 'x' match the name of the range in 'transcripts'. Here
## the seqname of 'x' is "TX_1" and mapping is only attempted with the second
## range in 'gr':
x <- GRanges("TX_1", IRanges(5, 10))
gr <- GRanges("chr3", IRanges(c(1, 1), width=50, names=c("TX_2", "TX_1")))
mapFromTranscripts(x, gr)

## -----
## (iii) Element-wise versions:

## Recycling is supported when length(transcripts) == 1; otherwise the
## lengths of 'x' and 'transcripts' must be the same.
x <- GRanges("A", IRanges(c(1, 5, 10), width=1))
transcripts <- GRanges("A", IRanges(4, 7))
pmapToTranscripts(x, transcripts)

## -----
## B. Map local sequence locations to the genome
## -----

## NAGNAG alternative splicing plays an essential role in biological processes
## and represents a highly adaptable system for posttranslational regulation
## of gene function. The majority of NAGNAG studies largely focus on messenger
## RNA. A study by Sun, Lin, and Yan
## (http://www.hindawi.com/journals/bmri/2014/736798/) demonstrated that
## NAGNAG splicing is also operative in large intergenic noncoding RNA
## (lincRNA).

## One finding of interest was that linc-POLR3G-10 exhibited two NAGNAG
## acceptors located in two distinct transcripts: TCONS_00010012 and
## TCONS_00010010.

## Extract the exon coordinates of TCONS_00010012 and TCONS_00010010:
lincrna <- c("TCONS_00010012", "TCONS_00010010")
library(TxDb.Hsapiens.UCSC.hg19.lincRNAsTranscripts)
txdb <- TxDb.Hsapiens.UCSC.hg19.lincRNAsTranscripts
exons <- exonsBy(txdb, by="tx", use.names=TRUE)[lincrna]
exons

## The two NAGNAG acceptors were identified in the upstream region of

```

```

## the fourth and fifth exons located in TCONS_00010012.
## Extract the sequences for transcript TCONS_00010012:
library(BSgenome.Hsapiens.UCSC.hg19)
genome <- BSgenome.Hsapiens.UCSC.hg19
exons_seq <- getSeq(genome, exons[[1]])

## TCONS_00010012 has 4 exons:
exons_seq

## The most common triplet among the lincRNA sequences was CAG. Identify
## the location of this pattern in all exons.
cag_loc <- vmatchPattern("CAG", exons_seq)

## Convert the first occurrence of CAG in each exon back to genome coordinates.
first_loc <- do.call(c, sapply(cag_loc, "[", 1, simplify=TRUE))
pmapFromTranscripts(first_loc, exons[[1]])

## -----
## C. Map 3'UTR variants to genome coordinates
## -----

## A study by Skeeles et. al (PLoS ONE 8(3): e58609. doi:
## 10.1371/journal.pone.0058609) investigated the impact of 3'UTR variants
## on the expression of cancer susceptibility genes.

## 8 candidate miRNA genes on chromosome 12 were used to test for
## differential luciferase expression in mice. In Table 2 of the manuscript
## variant locations are given as nucleotide position within the gene.
geneNames <- c("Bcap29", "Dgkb", "Etv1", "Hbp1", "Hbp1", "Ifrd1",
              "Ifrd1", "Pik3cg", "Pik3cg", "Tspan13", "Twistnb")
starts <- c(1409, 3170, 3132, 2437, 2626, 3239, 3261, 4947, 4979, 958, 1489)
snps <- GRanges(geneNames, IRanges(starts, width=1))

## To map these transcript-space coordinates to the genome we need gene ranges
## in genome space.
library(org.Mm.eg.db)
geneid <- select(org.Mm.eg.db, unique(geneNames), "ENTREZID", "SYMBOL")
geneid

## Extract the gene regions:
library(TxDb.Mmusculus.UCSC.mm10.knownGene)
txdb <- TxDb.Mmusculus.UCSC.mm10.knownGene
genes <- genes(txdb)[geneid$ENTREZID]

## A prerequisite of the mapping from transcript space to genome space
## is that seqnames in 'x' match names in 'transcripts'. Rename
## 'genes' with the appropriate gene symbol.
names(genes) <- geneid$SYMBOL

## The xHits and transcriptsHits metadta columns indicate which ranges in
## 'snps' and 'genes' were involved in the mapping.
mapFromTranscripts(snps, genes)

## -----
## D. Map dbSNP variants to cds or cDNA coordinates

```



```

## -----

## The GIPR gene encodes a G-protein coupled receptor for gastric inhibitory
## polypeptide (GIP). Originally GIP was identified to inhibited gastric acid
## secretion and gastrin release but was later demonstrated to stimulate
## insulin release in the presence of elevated glucose.

## In this example 5 SNPs located in the GIPR gene are mapped to cDNA
## coordinates. A list of SNPs in GIPR can be downloaded from dbSNP or NCBI.
rsids <- c("rs4803846", "rs139322374", "rs7250736", "rs7250754", "rs9749185")

## Extract genomic coordinates with a SNPlocs package.
library(SNPlocs.Hsapiens.dbSNP141.GRCh38)
snps <- snpid2grange(SNPlocs.Hsapiens.dbSNP141.GRCh38, rsids)

## Gene regions of GIPR can be extracted from a TxDb package of compatible
## build. The TxDb package uses Entrez gene identifiers and GIPR is a gene
## symbol. Conversion between gene symbols and Entrez gene IDs is done by
## calling select() on an organism db package.
library(org.Hs.eg.db)
geneid <- select(org.Hs.eg.db, "GIPR", "ENTREZID", "SYMBOL")

## The transcriptsBy() extractor returns a range for each transcript that
## includes the UTR and exon regions (i.e., cDNA).
library(TxDb.Hsapiens.UCSC.hg38.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg38.knownGene
txbygene <- transcriptsBy(txdb, "gene")
cDNA <- txbygene[geneid$ENTREZID]
cDNA

## Before mapping, the chromosome names (seqlevels) in the two objects must
## be harmonized. The style for 'snps' is dbSNP and 'cDNA' is UCSC.
seqlevelsStyle(snps)
seqlevelsStyle(cDNA)

## Modify the style and genome in 'snps' to match 'cDNA'.
seqlevelsStyle(snps) <- seqlevelsStyle(cDNA)
genome(snps) <- genome(cDNA)

## The 'cDNA' object is a GRangesList of length 1. This single list element
## contains the cDNA range for 4 different transcripts. To map to each
## transcript individually 'cDNA' must be unlisted before mapping.

## Map all 5 SNPS to all 4 transcripts:
mapToTranscripts(snps, unlist(cDNA))

## Map the first SNP to transcript uc002pct.1 and the second to uc002pcu.1.
pmapToTranscripts(snps[1:2], unlist(cDNA)[1:2])

## The cdsBy() extractor returns coding regions by gene or by transcript.
## Extract the coding regions for transcript uc002pct.1.
cds <- cdsBy(txdb, "tx", use.names=TRUE)["uc002pct.1"]
cds

## The 'cds' object is a GRangesList of length 1 containing all cds ranges
## for the single transcript uc002pct.1.

```

```

## To map to the concatenated group of ranges leave 'cds' as a GRangesList.
mapToTranscripts(snps, cds)

## Only the second SNP could be mapped. Unlisting the 'cds' object maps the
## SNPs to the individual cds ranges (vs the concatenated range).
mapToTranscripts(snps[2], unlist(cds))

## The location is the same because the SNP hit the first cds range. If the
## transcript were on the "-" strand the difference in concatenated vs
## non-concatenated position would be more obvious.

## Change the strand of 'cds':
strand(cds) <- "-"

## Re-map using 'ignore.strand'. The 'ignore.strand' argument is used
## in overlaps operations but does not affect the mapped position.

## Map to concatenated group of cds regions:
mapToTranscripts(snps[2], cds, ignore.strand=TRUE)

## Map to individual cds regions:
mapToTranscripts(snps[2], unlist(cds), ignore.strand=TRUE)

```

---

microRNAs

*Extract microRNA or tRNA genomic ranges from an object*

---

## Description

Generic functions to extract microRNA or tRNA genomic ranges from an object. This page documents the methods for [TxDb](#) objects only.

## Usage

```

microRNAs(x)
## S4 method for signature 'TxDb'
microRNAs(x)

tRNAs(x)
## S4 method for signature 'TxDb'
tRNAs(x)

```

## Arguments

x                    A [TxDb](#) object.

## Value

A [GRanges](#) object.

## Author(s)

M. Carlson

**See Also**

- [transcripts](#), [transcriptsBy](#), and [transcriptsByOverlaps](#) for the core genomic features extractors.
- The [TxDb](#) class.

**Examples**

```
## Not run: library(TxDb.Hsapiens.UCSC.hg19.knownGene)
library(mirbase.db)
microRNAs(TxDb.Hsapiens.UCSC.hg19.knownGene)

## End(Not run)
```

nearest-methods

*Finding the nearest genomic range neighbor in a TxDb***Description**

The distance methods for TxDb objects and subclasses.

**Usage**

```
## S4 method for signature 'GenomicRanges,TxDb'
distance(x, y, ignore.strand=FALSE,
        ..., id, type=c("gene", "tx", "exon", "cds"))
```

**Arguments**

x	The query <a href="#">GenomicRanges</a> instance.
y	For distance, a <a href="#">TxDb</a> instance. The id is used to extract ranges from the <a href="#">TxDb</a> which are then used to compute the distance from x.
id	A character vector the same length as x. The id must be identifiers in the <a href="#">TxDb</a> object. type indicates what type of identifier id is.
type	A character(1) describing the id. Must be one of 'gene', 'tx', 'exon' or 'cds'.
ignore.strand	A logical indicating if the strand of the ranges should be ignored. When TRUE, strand is set to '+'.
...	Additional arguments for methods.

**Details**

- distance: Returns the distance for each range in x to the range extracted from the [TxDb](#) object y. Values in id are matched to one of 'gene\_id', 'tx\_id', 'exon\_id' or 'cds\_id' identifiers in the [TxDb](#) and the corresponding ranges are extracted. The type argument specifies which identifier is represented in id. The extracted ranges are used in the distance calculation with the ranges in x.

The behavior of distance has changed in Bioconductor 2.12. See the man page ?distance in IRanges for details.

**Value**

For distance, an integer vector of distances between the ranges in x and y.

**Author(s)**

Valerie Obenchain <[vobencha@fhcrc.org](mailto:vobencha@fhcrc.org)>

**See Also**

- [nearest-methods](#) man page in IRanges.
- [nearest-methods](#) man page in GenomicRanges.

**Examples**

```
## -----
## distance()
## -----

library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
txdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
gr <- GRanges(c("chr2L", "chr2R"),
              IRanges(c(100000, 200000), width=100))
distance(gr, txdb, id=c("FBgn0259717", "FBgn0261501"), type="gene")
distance(gr, txdb, id=c("10000", "23000"), type="cds")

## The id's must be in the appropriate order with respect to 'x'.
distance(gr, txdb, id=c("4", "4097"), type="tx")

## 'id' "4" is on chr2L and "4097" is on chr2R.
transcripts(txdb, list(tx_id=c("4", "4097")))

## If we reverse the 'id' the chromosomes are incompatible with gr.
distance(gr, txdb, id=c("4097", "4"), type="tx")

## distance() compares each 'x' to the corresponding 'y'.
## If an 'id' is not found in the TxDb 'y' will not
## be the same length as 'x' and an error is thrown.
## Not run:
distance(gr, txdb, id=c("FBgn0000008", "INVALID"), type="gene") ## will fail

## End(Not run)
```

---

select-methods

*Using the "select" interface on TxDb objects*

---

**Description**

select, columns and keys can be used together to extract data from a [TxDb](#) object.

## Details

In the code snippets below, `x` is a `TxDB` object.

`keytypes(x)`: allows the user to discover which keytypes can be passed in to `select` or `keys` and the `keytype` argument.

`keys(x, keytype, pattern, column, fuzzy)`: Return keys for the database contained in the `TxDB` object .

The `keytype` argument specifies the kind of keys that will be returned. By default keys will return the "GENEID" keys for the database.

If `keys` is used with `pattern`, it will pattern match on the `keytype`.

But if the `column` argument is also provided along with the `pattern` argument, then `pattern` will be matched against the values in `column` instead.

And if `keys` is called with `column` and no `pattern` argument, then it will return all keys that have corresponding values in the `column` argument.

Thus, the behavior of `keys` all depends on how many arguments are specified.

Use of the `fuzzy` argument will toggle fuzzy matching to `TRUE` or `FALSE`. If `pattern` is not used, `fuzzy` is ignored.

`columns(x)`: Show which kinds of data can be returned for the `TxDB` object.

`select(x, keys, columns, keytype)`: When all the appropriate arguments are specified `select` will retrieve the matching data as a `data.frame` based on parameters for selected keys and columns and `keytype` arguments.

## Author(s)

Marc Carlson

## See Also

- [AnnotationDb-class](#) for more descriptions of methods `select`, `keytypes`, `keys` and `columns`.
- [transcripts](#), [transcriptsBy](#), and [transcriptsByOverlaps](#), for other ways to extract genomic features from a `TxDB` object.
- The `TxDB` class.

## Examples

```
txdb_file <- system.file("extdata", "Biomart_Ensembl_sample.sqlite",
                        package="GenomicFeatures")
txdb <- loadDb(txdb_file)
txdb

## find key types
keytypes(txdb)

## list IDs that can be used to filter
head(keys(txdb, "GENEID"))
head(keys(txdb, "TXID"))
head(keys(txdb, "TXNAME"))

## list columns that can be returned by select
columns(txdb)

## call select
```

```
res <- select(txdb, head(keys(txdb, "GENEID")),
             columns=c("GENEID", "TXNAME"),
             keytype="GENEID")
head(res)
```

---

transcriptLengths      *Extract the transcript lengths from a TxDb object*

---

## Description

The transcriptLengths function extracts the transcript lengths from a [TxDb](#) object. It also returns the CDS and UTR lengths for each transcript if the user requests them.

## Usage

```
transcriptLengths(txdb, with.cds_len=FALSE,
                  with.utr5_len=FALSE, with.utr3_len=FALSE)
```

## Arguments

txdb                    A [TxDb](#) object.  
with.cds\_len, with.utr5\_len, with.utr3\_len  
TRUE or FALSE. Whether or not to also extract and return the CDS, 5' UTR, and 3' UTR lengths for each transcript.

## Details

All the lengths are counted in number of nucleotides.

The length of a processed transcript is just the sum of the lengths of its exons. This should not be confounded with the length of the stretch of DNA transcribed into RNA (a.k.a. transcription unit), which can be obtained with `width(transcripts(txdb))`.

## Value

A data frame with 1 row per transcript. The rows are guaranteed to be in the same order as the elements of the [GRanges](#) object returned by `transcripts(txdb)`. The data frame has between 5 and 8 columns, depending on what the user requested via the `with.cds_len`, `with.utr5_len`, and `with.utr3_len` arguments.

The first 3 columns are the same as the metadata columns of the object returned by

```
transcripts(txdb, columns=c("tx_id", "tx_name", "gene_id"))
```

that is:

- `tx_id`: The internal transcript ID. This ID is unique within the scope of the [TxDb](#) object. It is not an official or public ID (like an Ensembl or FlyBase ID) or an Accession number, so it cannot be used to lookup the transcript in public data bases or in other [TxDb](#) objects. Furthermore, this ID could change when re-running the code that was used to make the [TxDb](#) object.
- `tx_name`: An official/public transcript name or ID that can be used to lookup the transcript in public data bases or in other [TxDb](#) objects. This column is not guaranteed to contain unique values and it can contain NAs.

- `gene_id`: The official/public ID of the gene that the transcript belongs to. Can be NA if the gene is unknown or if the transcript is not considered to belong to a gene.

The other columns are quantitative:

- `nexon`: The number of exons in the transcript.
- `tx_len`: The length of the processed transcript.
- `cds_len`: [optional] The length of the CDS region of the processed transcript.
- `utr5_len`: [optional] The length of the 5' UTR region of the processed transcript.
- `utr3_len`: [optional] The length of the 3' UTR region of the processed transcript.

### Author(s)

H. Pages

### See Also

- [transcripts](#), [transcriptsBy](#), and [transcriptsByOverlaps](#), for how to extract the genomic locations of features from a [TxDb](#) object.
- [extractTranscriptSeqs](#) for extracting transcript (or CDS) sequences from chromosome sequences.
- [coverageByTranscript](#) for computing coverage by transcript (or CDS) of a set of ranges.
- [makeTxDbFromUCSC](#) and [makeTxDbFromBiomart](#) for convenient ways to make [TxDb](#) objects from UCSC or BioMart online resources.
- The [TxDb](#) class.

### Examples

```
library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
txdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
dm3_txlens <- transcriptLengths(txdb)
head(dm3_txlens)

dm3_txlens <- transcriptLengths(txdb, with.cds_len=TRUE,
                               with.utr5_len=TRUE,
                               with.utr3_len=TRUE)
head(dm3_txlens)

## When cds_len is 0 (non-coding transcript), utr5_len and utr3_len
## must also be 0:
non_coding <- dm3_txlens[dm3_txlens$cds_len == 0, ]
stopifnot(all(non_coding[6:8] == 0))

## When cds_len is not 0 (coding transcript), cds_len + utr5_len +
## utr3_len must be equal to tx_len:
coding <- dm3_txlens[dm3_txlens$cds_len != 0, ]
stopifnot(all(rowSums(coding[6:8]) == coding[[5]]))

## A sanity check:
stopifnot(identical(dm3_txlens$tx_id, mcols(transcripts(txdb))$tx_id))
```

---

 transcriptLocs2refLocs

*Converting transcript-based locations into reference-based locations*


---

### Description

transcriptLocs2refLocs converts transcript-based locations into reference-based (aka chromosome-based or genomic) locations.

transcriptWidths computes the lengths of the transcripts (called the "widths" in this context) based on the boundaries of their exons.

### Usage

```
transcriptLocs2refLocs(tlocs,
  exonStarts=list(), exonEnds=list(), strand=character(0),
  decreasing.rank.on.minus.strand=FALSE, error.if.out.of.bounds=TRUE)

transcriptWidths(exonStarts=list(), exonEnds=list())
```

### Arguments

**tlocs** A list of integer vectors of the same length as exonStarts and exonEnds. Each element in tlocs must contain transcript-based locations.

**exonStarts, exonEnds** The starts and ends of the exons, respectively. Each argument can be a list of integer vectors, an [IntegerList](#) object, or a character vector where each element is a comma-separated list of integers. In addition, the lists represented by exonStarts and exonEnds must have the same shape i.e. have the same lengths and have elements of the same lengths. The length of exonStarts and exonEnds is the number of transcripts.

**strand** A character vector of the same length as exonStarts and exonEnds specifying the strand ("+" or "-") from which the transcript is coming.

**decreasing.rank.on.minus.strand** TRUE or FALSE. Describes the order of exons in transcripts located on the minus strand: are they ordered by increasing (default) or decreasing rank?

**error.if.out.of.bounds** TRUE or FALSE. Controls how out of bound tlocs are handled: an error is thrown (default) or NA is returned.

### Value

For transcriptLocs2refLocs: A list of integer vectors of the same shape as tlocs.

For transcriptWidths: An integer vector with one element per transcript.

### Author(s)

H. Pages



**See Also**

- [extractTranscriptSeqs](#) for extracting transcript (or CDS) sequences from chromosomes.
- [coverageByTranscript](#) for computing coverage by transcript (or CDS) of a set of ranges.

**Examples**

```
## -----
## GOING FROM TRANSCRIPT-BASED TO REFERENCE-BASED LOCATIONS
## -----
library(BSgenome.Hsapiens.UCSC.hg19) # load the genome
genome <- BSgenome.Hsapiens.UCSC.hg19
txdb_file <- system.file("extdata", "hg19_knownGene_sample.sqlite",
                        package="GenomicFeatures")
txdb <- loadDb(txdb_file)
transcripts <- exonsBy(txdb, by="tx", use.names=TRUE)
tx_seqs <- extractTranscriptSeqs(genome, transcripts)

## Get the reference-based locations of the first 4 (5' end)
## and last 4 (3' end) nucleotides in each transcript:
tlocs <- lapply(width(tx_seqs), function(w) c(1:4, (w-3):w))
tx_strand <- sapply(strand(transcripts), runValue)
## Note that, because of how we made them, 'tlocs', 'start(exbytx)',
## 'end(exbytx)' and 'tx_strand' have the same length, and, for any
## valid positional index, elements at this position are corresponding
## to each other. This is how transcriptLocs2refLocs() expects them
## to be!
rlocs <- transcriptLocs2refLocs(tlocs,
                              start(transcripts), end(transcripts),
                              tx_strand, decreasing.rank.on.minus.strand=TRUE)

## -----
## EXTRACTING WORM TRANSCRIPTS ZC101.3 AND F37B1.1
## -----
## Transcript ZC101.3 (is on + strand):
## Exons starts/ends relative to transcript:
rstarts1 <- c(1, 488, 654, 996, 1365, 1712, 2163, 2453)
rends1 <- c(137, 578, 889, 1277, 1662, 1870, 2410, 2561)
## Exons starts/ends relative to chromosome:
starts1 <- 14678410 + rstarts1
ends1 <- 14678410 + rends1

## Transcript F37B1.1 (is on - strand):
## Exons starts/ends relative to transcript:
rstarts2 <- c(1, 325)
rends2 <- c(139, 815)
## Exons starts/ends relative to chromosome:
starts2 <- 13611188 - rends2
ends2 <- 13611188 - rstarts2

exon_starts <- list(as.integer(starts1), as.integer(starts2))
exon_ends <- list(as.integer(ends1), as.integer(ends2))
transcripts <- IRangesList(start=exon_starts, end=exon_ends)

library(BSgenome.Celegans.UCSC.ce2)
## Both transcripts are on chrII:
chrII <- Celegans$chrII
```

```

tx_seqs <- extractTranscriptSeqs(chrII, transcripts, strand=c("+","-"))

## Same as 'width(tx_seqs)':
transcriptWidths(exonStarts=exon_starts, exonEnds=exon_ends)

transcriptLocs2refLocs(list(c(1:6, 135:140, 1555:1560),
                             c(1:6, 137:142, 625:630)),
                        exonStarts=exon_starts,
                        exonEnds=exon_ends,
                        strand=c("+","-"))

## A sanity check:
ref_locs <- transcriptLocs2refLocs(list(1:1560, 1:630),
                                    exonStarts=exon_starts,
                                    exonEnds=exon_ends,
                                    strand=c("+","-"))
stopifnot(chrII[ref_locs[[1]]] == tx_seqs[[1]])
stopifnot(complement(chrII)[ref_locs[[2]]] == tx_seqs[[2]])

```

---

transcripts

---

*Extract genomic features from an object*


---

## Description

Generic functions to extract genomic features from an object. This page documents the methods for [TxDb](#) objects only.

## Usage

```

transcripts(x, ...)
## S4 method for signature 'TxDb'
transcripts(x, vals=NULL, columns=c("tx_id", "tx_name"))

exons(x, ...)
## S4 method for signature 'TxDb'
exons(x, vals=NULL, columns="exon_id")

cds(x, ...)
## S4 method for signature 'TxDb'
cds(x, vals=NULL, columns="cds_id")

genes(x, ...)
## S4 method for signature 'TxDb'
genes(x, vals=NULL, columns="gene_id", single.strand.genes.only=TRUE)

## S4 method for signature 'TxDb'
promoters(x, upstream=2000, downstream=200, ...)

```

## Arguments

x                    A [TxDb](#) object.

...	For the transcripts, exons, cds, and genes generic functions: arguments to be passed to methods. For the promoters method for <a href="#">TxDb</a> objects: arguments to be passed to the internal call to transcripts.
vals	Either NULL or a named list of vectors to be used to restrict the output. Valid names for this list are: "gene_id", "tx_id", "tx_name", "tx_chrom", "tx_strand", "exon_id", "exon_name", "exon_chrom", "exon_strand", "cds_id", "cds_name", "cds_chrom", "cds_strand" and "exon_rank".
columns	Columns to include in the output. Must be NULL or a character vector as given by the columns method. With the following restrictions: <ul style="list-style-type: none"> <li>• "TXCHROM" and "TXSTRAND" are not allowed for transcripts.</li> <li>• "EXONCHROM" and "EXONSTRAND" are not allowed for exons.</li> <li>• "CDSCHROM" and "CDSSTRAND" are not allowed for cds.</li> </ul> <p>If the vector is named, those names are used for the corresponding column in the element metadata of the returned object.</p>
single.strand.genes.only	TRUE or FALSE. If TRUE (the default), then genes that have exons located on both strands of the same chromosome or on two different chromosomes are dropped. In that case, the genes are returned in a <a href="#">GRanges</a> object. Otherwise, all genes are returned in a <a href="#">GRangesList</a> object with the columns specified thru the columns argument set as <i>top level</i> metadata columns. (Please keep in mind that the <i>top level</i> metadata columns of a <a href="#">GRangesList</a> object are not displayed by the show method.)
upstream	For promoters : An integer(1) value indicating the number of bases upstream from the transcription start site. For additional details see <code>?promoters,GRanges-method`</code> .
downstream	For promoters : An integer(1) value indicating the number of bases downstream from the transcription start site. For additional details see <code>?promoters,GRanges-method`</code> .

## Details

These are the main functions for extracting transcript information from a [TxDb](#) object. These methods can restrict the output based on categorical information. To restrict the output based on interval information, use the [transcriptsByOverlaps](#), [exonsByOverlaps](#), and [cdsByOverlaps](#) functions.

The promoters function computes user-defined promoter regions for the transcripts in a [TxDb](#) object. The return object is a [GRanges](#) of promoter regions around the transcription start site the span of which is defined by upstream and downstream. For additional details on how the promoter range is computed and the handling of + and - strands see `?promoters,GRanges-method``.

## Value

A [GRanges](#) object. The only exception being when genes is used with `single.strand.genes.only=FALSE`, in which case a [GRangesList](#) object is returned.

## Author(s)

M. Carlson, P. Aboyoun and H. Pages

**See Also**

- [transcriptsBy](#) and [transcriptsByOverlaps](#) for more ways to extract genomic features from a [TxDb](#) object.
- [transcriptLengths](#) for extracting the transcript lengths from a [TxDb](#) object.
- [extractTranscriptSeqs](#) for extracting transcript (or CDS) sequences from chromosome sequences.
- [coverageByTranscript](#) for computing coverage by transcript (or CDS) of a set of ranges.
- [disjointExons](#) for extracting the non-overlapping exon parts from a [TxDb](#) object.
- [select-methods](#) for how to use the simple "select" interface to extract information from a [TxDb](#) object.
- [microRNAs](#) and [tRNAs](#) for extracting microRNA or tRNA genomic ranges from a [TxDb](#) object.
- [id2name](#) for mapping [TxDb](#) internal ids to external names for a given feature type.
- The [TxDb](#) class.

**Examples**

```
txdb_file <- system.file("extdata", "hg19_knownGene_sample.sqlite",
                        package="GenomicFeatures")
txdb <- loadDb(txdb_file)

## -----
## transcripts()
## -----

tx <- transcripts(txdb)
tx

## A sanity check:
stopifnot(identical(mcols(tx)$tx_id, seq_along(tx)))

vals <- list(tx_chrom = c("chr3", "chr5"), tx_strand = "+")
transcripts(txdb, vals)

## -----
## exons()
## -----

exons(txdb, vals=list(exon_id=1), columns=c("EXONID", "TXNAME"))
exons(txdb, vals=list(tx_name="uc009vip.1"), columns=c("EXONID",
  "TXNAME"))

## -----
## genes()
## -----

genes(txdb) # a GRanges object
cols <- c("tx_id", "tx_chrom", "tx_strand",
         "exon_id", "exon_chrom", "exon_strand")
single_strand_genes <- genes(txdb, columns=cols)

## Because we've returned single strand genes only, the "tx_chrom"
## and "exon_chrom" metadata columns are guaranteed to match
## 'seqnames(single_strand_genes)':
```

```

stopifnot(identical(as.character(seqnames(single_strand_genes)),
                    as.character(mcols(single_strand_genes)$tx_chrom)))
stopifnot(identical(as.character(seqnames(single_strand_genes)),
                    as.character(mcols(single_strand_genes)$exon_chrom)))
## and also the "tx_strand" and "exon_strand" metadata columns are
## guaranteed to match 'strand(single_strand_genes)':
stopifnot(identical(as.character(strand(single_strand_genes)),
                    as.character(mcols(single_strand_genes)$tx_strand)))
stopifnot(identical(as.character(strand(single_strand_genes)),
                    as.character(mcols(single_strand_genes)$exon_strand)))

all_genes <- genes(txdb, columns=cols, single.strand.genes.only=FALSE)
all_genes # a GRangesList object
multiple_strand_genes <- all_genes[elementLengths(all_genes) >= 2]
multiple_strand_genes
mcols(multiple_strand_genes)

## -----
## promoters()
## -----

## This:
promoters(txdb, upstream=100, downstream=50)
## is equivalent to:
promoters(transcripts(txdb), upstream=100, downstream=50)

## Extra arguments are passed to transcripts(). So this:
promoters(txdb, upstream=100, downstream=50,
          columns=c("tx_name", "gene_id"))
## is equivalent to:
promoters(transcripts(txdb, columns=c("tx_name", "gene_id")),
          upstream=100, downstream=50)

```

---

transcriptsBy

*Extract and group genomic features of a given type*


---

## Description

Generic functions to extract genomic features of a given type grouped based on another type of genomic feature. This page documents the methods for [TxDb](#) objects only.

## Usage

```

transcriptsBy(x, by=c("gene", "exon", "cds"), ...)
## S4 method for signature 'TxDb'
transcriptsBy(x, by=c("gene", "exon", "cds"), use.names=FALSE)

exonsBy(x, by=c("tx", "gene"), ...)
## S4 method for signature 'TxDb'
exonsBy(x, by=c("tx", "gene"), use.names=FALSE)

cdsBy(x, by=c("tx", "gene"), ...)
## S4 method for signature 'TxDb'
cdsBy(x, by=c("tx", "gene"), use.names=FALSE)

```

```

intronsByTranscript(x, ...)
## S4 method for signature 'TxDb'
intronsByTranscript(x, use.names=FALSE)

fiveUTRsByTranscript(x, ...)
## S4 method for signature 'TxDb'
fiveUTRsByTranscript(x, use.names=FALSE)

threeUTRsByTranscript(x, ...)
## S4 method for signature 'TxDb'
threeUTRsByTranscript(x, use.names=FALSE)

```

### Arguments

x	A <a href="#">TxDb</a> object.
...	Arguments to be passed to or from methods.
by	One of "gene", "exon", "cds" or "tx". Determines the grouping.
use.names	Controls how to set the names of the returned <a href="#">GRangesList</a> object. These functions return all the features of a given type (e.g. all the exons) grouped by another feature type (e.g. grouped by transcript) in a <a href="#">GRangesList</a> object. By default (i.e. if use.names is FALSE), the names of this <a href="#">GRangesList</a> object (aka the group names) are the internal ids of the features used for grouping (aka the grouping features), which are guaranteed to be unique. If use.names is TRUE, then the names of the grouping features are used instead of their internal ids. For example, when grouping by transcript (by="tx"), the default group names are the transcript internal ids ("tx_id"). But, if use.names=TRUE, the group names are the transcript names ("tx_name"). Note that, unlike the feature ids, the feature names are not guaranteed to be unique or even defined (they could be all NAs). A warning is issued when this happens. See <a href="#">?id2name</a> for more information about feature internal ids and feature external names and how to map the formers to the latters.  Finally, use.names=TRUE cannot be used when grouping by gene by="gene". This is because, unlike for the other features, the gene ids are external ids (e.g. Entrez Gene or Ensembl ids) so the db doesn't have a "gene_name" column for storing alternate gene names.

### Details

These functions return a [GRangesList](#) object where the ranges within each of the elements are ordered according to the following rule:

When using exonsBy or cdsBy with by = "tx", the returned exons or CDS are ordered by ascending rank for each transcript, that is, by their position in the transcript. In all other cases, the ranges will be ordered by chromosome, strand, start, and end values.

### Value

A [GRangesList](#) object.

### Author(s)

M. Carlson, P. Aboyoun and H. Pages

**See Also**

- [transcripts](#) and [transcriptsByOverlaps](#) for more ways to extract genomic features from a [TxDb](#) object.
- [transcriptLengths](#) for extracting the transcript lengths from a [TxDb](#) object.
- [extractTranscriptSeqs](#) for extracting transcript (or CDS) sequences from chromosome sequences.
- [coverageByTranscript](#) for computing coverage by transcript (or CDS) of a set of ranges.
- [select-methods](#) for how to use the simple "select" interface to extract information from a [TxDb](#) object.
- [id2name](#) for mapping [TxDb](#) internal ids to external names for a given feature type.
- The [TxDb](#) class.

**Examples**

```
txdb_file <- system.file("extdata", "hg19_knownGene_sample.sqlite",
                        package="GenomicFeatures")
txdb <- loadDb(txdb_file)

## Get the transcripts grouped by gene:
transcriptsBy(txdb, "gene")

## Get the exons grouped by gene:
exonsBy(txdb, "gene")

## Get the CDS grouped by transcript:
cds_by_tx0 <- cdsBy(txdb, "tx")
## With more informative group names:
cds_by_tx1 <- cdsBy(txdb, "tx", use.names=TRUE)
## Note that 'cds_by_tx1' can also be obtained with:
names(cds_by_tx0) <- id2name(txdb, feature.type="tx")[names(cds_by_tx0)]
stopifnot(identical(cds_by_tx0, cds_by_tx1))

## Get the introns grouped by transcript:
intronsByTranscript(txdb)

## Get the 5' UTRs grouped by transcript:
fiveUTRsByTranscript(txdb)
fiveUTRsByTranscript(txdb, use.names=TRUE) # more informative group names
```

---

`transcriptsByOverlaps` *Extract genomic features from an object based on their by genomic location*

---

**Description**

Generic functions to extract genomic features for specified genomic locations. This page documents the methods for [TxDb](#) objects only.

**Usage**

```

transcriptsByOverlaps(x, ranges,
                      maxgap = 0L, minoverlap = 1L,
                      type = c("any", "start", "end"), ...)
## S4 method for signature 'TxDb'
transcriptsByOverlaps(x, ranges,
                      maxgap = 0L, minoverlap = 1L,
                      type = c("any", "start", "end"),
                      columns = c("tx_id", "tx_name"))

exonsByOverlaps(x, ranges,
                maxgap = 0L, minoverlap = 1L,
                type = c("any", "start", "end"), ...)
## S4 method for signature 'TxDb'
exonsByOverlaps(x, ranges,
                maxgap = 0L, minoverlap = 1L,
                type = c("any", "start", "end"),
                columns = "exon_id")

cdsByOverlaps(x, ranges,
              maxgap = 0L, minoverlap = 1L,
              type = c("any", "start", "end"), ...)
## S4 method for signature 'TxDb'
cdsByOverlaps(x, ranges,
              maxgap = 0L, minoverlap = 1L,
              type = c("any", "start", "end"),
              columns = "cds_id")

```

**Arguments**

x	A <a href="#">TxDb</a> object.
...	Arguments to be passed to or from methods.
ranges	A <a href="#">GRanges</a> object to restrict the output.
type	How to perform the interval overlap operations of the ranges. See the <a href="#">findOverlaps</a> manual page in the <a href="#">GRanges</a> package for more information.
maxgap	A non-negative integer representing the maximum distance between a query interval and a subject interval.
minoverlap	Ignored.
columns	Columns to include in the output. See <a href="#">?transcripts</a> for the possible values.

**Details**

These functions subset the results of [transcripts](#), [exons](#), and [cds](#) function calls with using the results of [findOverlaps](#) calls based on the specified ranges.

**Value**

a [GRanges](#) object

**Author(s)**

P. Aboyoun



**See Also**

- [transcripts](#) and [transcriptsBy](#) for more ways to extract genomic features from a [TxDb](#) object.
- [select-methods](#) for how to use the simple "select" interface to extract information from a [TxDb](#) object.
- [id2name](#) for mapping [TxDb](#) internal ids to external names for a given feature type.
- The [TxDb](#) class.

**Examples**

```
txdb <- loadDb(system.file("extdata", "hg19_knownGene_sample.sqlite",
                          package="GenomicFeatures"))
gr <- GRanges(seqnames = rep("chr1",2),
              ranges = IRanges(start=c(500,10500), end=c(10000,30000)),
              strand = strand(rep("-",2)))
transcriptsByOverlaps(txdb, gr)
```

TxDb-class

*TxDb objects***Description**

The TxDb class is a container for storing transcript annotations.

See [?FeatureDb](#) for a more generic container for storing genomic locations of an arbitrary type of genomic features.

See [?makeTxDbFromUCSC](#) and [?makeTxDbFromBiomart](#) for convenient ways to make TxDb objects from UCSC or BioMart online resources.

See [?makeTxDbFromGFF](#) for making a TxDb object from annotations available as a GFF3 or GTF file.

**Methods**

In the code snippets below, x is a TxDb object.

`metadata(x)`: Return x's metadata in a data frame.

`seqlevels0(x)`: Get the *sequence levels* originally in x. This ignores any change the user might have made to the *sequence levels* with the `seqlevels` setter.

`seqlevels(x), seqlevels(x) <- value`: Get or set the *sequence levels* in x.

`seqinfo(x), seqinfo(x) <- value`: Get or set the information about the underlying sequences. Note that, for now, the setter only supports replacement of the sequence names, i.e., except for their sequence names (accessed with `seqnames(value)` and `seqnames(seqinfo(x))`, respectively), [Seqinfo](#) objects `value` (supplied) and `seqinfo(x)` (current) must be identical.

`isActiveSeq(x)`: Return the currently active sequences for this txdb object as a named logical vector. Only active sequences will be tapped when using the supplied accessor methods. Inactive sequences will be ignored. By default, all available sequences will be active.

`isActiveSeq(x) <- value`: Allows the user to change which sequences will be actively accessed by the accessor methods by altering the contents of this named logical vector.

`seqlevelsStyle(x)`, `seqlevelsStyle(x) <- value`: Get or set the seqname style for `x`. See the [seqlevelsStyle](#) generic getter and setter in the **GenomeInfoDb** package for more information.

`as.list(x)`: Dump the entire db into a list of data frames, say `txdb_dump`, that can then be used to recreate the original db with `do.call(makeTxDb, txdb_dump)` with no loss of information (except possibly for some of the metadata). Note that the transcripts are dumped in the same order in all the data frames.

### Author(s)

H. Pages, Marc Carlson

### See Also

- [makeTxDbFromUCSC](#), [makeTxDbFromBiomart](#), [makeTxDbFromGRanges](#), and [makeTxDbFromGFF](#), for convenient ways to make a **TxDb** object from UCSC or BioMart online resources, or from a **GRanges** object, or from a GFF or GTF file.
- [saveDb](#) and [loadDb](#) in the **AnnotationDbi** package for saving and loading a **TxDb** object as an SQLite file.
- [transcripts](#), [transcriptsBy](#), and [transcriptsByOverlaps](#), for how to extract genomic features from a **TxDb** object.
- [transcriptLengths](#) for extracting the transcript lengths from a **TxDb** object.
- [select-methods](#) for how to use the simple "select" interface to extract information from a **TxDb** object.
- The **FeatureDb** class for storing genomic locations of an arbitrary type of genomic features.
- The **Seqinfo** class in the **GenomeInfoDb** package.

### Examples

```
txdb_file <- system.file("extdata", "Biomart_Ensembl_sample.sqlite",
                        package="GenomicFeatures")
txdb <- loadDb(txdb_file)
txdb

## Use of seqinfo():
seqlevelsStyle(txdb)
seqinfo(txdb)
seqlevels(txdb)
seqlengths(txdb) # shortcut for 'seqlengths(seqinfo(txdb))'
isCircular(txdb) # shortcut for 'isCircular(seqinfo(txdb))'
names(which(isCircular(txdb)))

## You can set user-supplied seqlevels on 'txdb' to restrict any further
## operations to a subset of chromosomes:
seqlevels(txdb) <- c("Y", "6")
## Then you can restore the seqlevels stored in the db:
seqlevels(txdb) <- seqlevels0(txdb)

## Use of as.list():
txdb_dump <- as.list(txdb)
txdb_dump
txdb1 <- do.call(makeTxDb, txdb_dump)
stopifnot(identical(as.list(txdb1), txdb_dump))
```

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