

# 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), IRanges (>= 1.17.13), GenomicRanges (>= 1.13.16), AnnotationDbi (>= 1.23.14)

**Imports** methods, DBI (>= 0.2-5), RSQLite (>= 0.8-1), BiocGenerics, IRanges, GenomicRanges, Biostrings (>= 2.23.2), rtracklayer (>= 1.15.1), biomaRt (>= 2.17.1), RCurl, utils, Biobase (>= 2.15.1)

## Suggests

rtracklayer, biomaRt, org.Mm.eg.db, Biostrings, BSgenome, BSgenome.Hsapiens.UCSC.hg18 (>= 1.3.14), BSgenome.Hsapiens.UCSC.hg19, mirbase.db, FDb.UCSC.tRNAs, TxDb.Hsapiens.UCSC.hg18.knownGene, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Dmelanogaster.UCSC.knownGene, tools, pasillaBamSubset (>= 0.0.5), seqnames.db, RUnit

**Collate** utils.R Ensembl.utils.R TranscriptDb-class.R FeatureDb-class.R  
makeTranscriptDb.R makeTranscriptDbFromUCSC.R  
makeTranscriptDbFromBiomart.R makeTranscriptDbFromGFF.R  
makeFeatureDbFromUCSC.R saveFeatures.R id2name.R transcripts.R  
transcriptsByOverlaps.R transcriptsBy.R regions.R features.R  
extractTranscriptsFromGenome.R makeTxDbPackage.R  
seqnames-methods.R select-methods.R nearest-methods.R  
getPromoterSeq-methods.R test\_GenomicFeatures\_package.R

**biocViews** Genetics, Infrastructure, Annotation, HighThroughputSequencing

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|                   |   |
|-------------------|---|
| as-format-methods | <i>Coerce to file format structures</i> |
|-------------------|---|

---

### Description

These functions coerce a [TranscriptDb](#) 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 [TranscriptDb](#) is passed to [export](#), when targeting a BED or GFF file, this coercion occurs automatically.

### Usage

```
## S4 method for signature TranscriptDb
asBED(x)
## S4 method for signature TranscriptDb
asGFF(x)
```

**Arguments**

x                    A TranscriptDb 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", "UCSC_knownGene_sample.sqlite",
                        package="GenomicFeatures")
txdb <- loadDb(txdb_file)

asBED(txdb)
asGFF(txdb)
```

---

DEFAULT\_CIRC\_SEQS            *character vector: strings that are usually circular chromosomes*

---

**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**

[makeTranscriptDbFromUCSC](#), [makeTranscriptDbFromBiomart](#)

**Examples**

```
DEFAULT_CIRC_SEQS
```

---

```
extractTranscriptsFromGenome
```

*Tools for extracting transcript sequences*

---

**Description**

extractTranscriptsFromGenome extracts the transcript sequences from a BSgenome data package using the transcript information (exon boundaries) stored in a [TranscriptDb](#) or [GRangesList](#) object.

extractTranscripts extracts a set of transcripts from a single DNA sequence.

Related utilities:

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

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

sortExonsByRank orders (or reorders) by rank the exons stored in a [GRangesList](#) object containing exons grouped by transcript.

**Usage**

```
extractTranscriptsFromGenome(genome, txdb,
                             decreasing.rank.on.minus.strand=FALSE,
                             use.names=TRUE)
```

```
extractTranscripts(x,
                  exonStarts=list(), exonEnds=list(), strand=character(0),
                  decreasing.rank.on.minus.strand=FALSE)
```

## Related utilities:

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

```
transcriptLocs2refLocs(tlocs,
                      exonStarts=list(), exonEnds=list(), strand=character(0),
                      decreasing.rank.on.minus.strand=FALSE)
```

```
sortExonsByRank(x, decreasing.rank.on.minus.strand=FALSE)
```

**Arguments**

|                                 |  |
|---------------------------------|--|
| genome                          | A <a href="#">BSgenome</a> object. See the <a href="#">available.genomes</a> function in the BSgenome package for how to install a genome.   |
| txdb                            | A <a href="#">TranscriptDb</a> object or a <a href="#">GRangesList</a> object.   |
| 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? For all the functions described in this man page (except <code>sortExonsByRank</code> ), this argument describes the input. For <code>sortExonsByRank</code> , it describes how exons should be ordered in the output.  |
| use.names                       | TRUE or FALSE. Ignored if txdb is not a <a href="#">TranscriptDb</a> object. If TRUE (the default), the returned sequences are named with the transcript names. If FALSE, they are named with the transcript internal ids. Note that, unlike the transcript internal ids, the transcript names are not guaranteed to be unique or even defined (they could be all NAs). A warning is issued when this happens.   |
| x                               | A <a href="#">DNAStrng</a> or <a href="#">MaskedDNAStrng</a> object for <code>extractTranscripts</code> .<br>A <a href="#">GRangesList</a> object for <code>sortExonsByRank</code> , typically coming from <code>exonsBy(..., by="tx")</code> .  |
| exonStarts, exonEnds            | The starts and ends of the exons, respectively.<br>Each argument can be a list of integer vectors, an <a href="#">IntegerList</a> object, or a character vector where each element is a comma-separated list of integers. In addition, the lists represented by <code>exonStarts</code> and <code>exonEnds</code> must have the same shape i.e. have the same lengths and have elements of the same lengths. The length of <code>exonStarts</code> and <code>exonEnds</code> is the number of transcripts. |
| strand                          | A character vector of the same length as <code>exonStarts</code> and <code>exonEnds</code> specifying the strand ("+" or "-") from which the transcript is coming.   |
| tlocs                           | A list of integer vectors of the same length as <code>exonStarts</code> and <code>exonEnds</code> . Each element in <code>tlocs</code> must contain transcript-based locations.  |

**Value**

For `extractTranscriptsFromGenome`: A named [DNAStrngSet](#) object with one element per transcript. When txdb is a [GRangesList](#) object, elements in the output align with elements in the input (txdb), and they have the same names.

For `extractTranscripts`: A [DNAStrngSet](#) object with one element per transcript.

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

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

For `sortExonsByRank`: A [GRangesList](#) object with one top-level element per transcript. More precisely, the returned object has the same "shape" (i.e. same length and same number of elements per top-level element) as the input [GRangesList](#) object x.

**Author(s)**

H. Pages

**See Also**

[available.genomes](#), [TranscriptDb-class](#), [exonsBy](#), [GRangesList-class](#), [DNAStringSet-class](#), [translate](#)

**Examples**

```

library(BSgenome.Hsapiens.UCSC.hg18) # load the genome

## -----
## A. USING extractTranscriptsFromGenome() WITH A TranscriptDb OBJECT
## -----
txdb_file <- system.file("extdata", "UCSC_knownGene_sample.sqlite",
                        package="GenomicFeatures")
txdb <- loadDb(txdb_file)
tx_seqs1 <- extractTranscriptsFromGenome(Hsapiens, txdb)
tx_seqs1

## -----
## B. USING extractTranscriptsFromGenome() WITH A GRangesList OBJECT
## -----

## A GRangesList object containing exons grouped by transcripts gives
## the same result as above:
exbytx <- exonsBy(txdb, by="tx", use.names=TRUE)
tx_seqs2 <- extractTranscriptsFromGenome(Hsapiens, exbytx)
stopifnot(identical(as.character(tx_seqs2), as.character(tx_seqs1)))

## A sanity check:
stopifnot(identical(unname(sapply(width(exbytx), sum)), width(tx_seqs2)))

## CDSs grouped by transcripts (this extracts only the translated parts
## of the transcripts):
cds_seqs <- extractTranscriptsFromGenome(Hsapiens, cdsBy(txdb, by="tx"))
translate(cds_seqs)

## -----
## C. GOING FROM TRANSCRIPT-BASED TO REFERENCE-BASED LOCATIONS
## -----
## Get the reference-based locations of the first 4 (5' end)
## and last 4 (3' end) nucleotides in each transcript:
tllocs <- lapply(width(tx_seqs2), function(w) c(1:4, (w-3):w))
tx_strand <- sapply(strand(exbytx), runValue)
## Note that, because of how we made them, tllocs, 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(tllocs, start(exbytx), end(exbytx),
                              tx_strand, decreasing.rank.on.minus.strand=TRUE)

## -----
## D. 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))

library(BSgenome.Celegans.UCSC.ce2)
## Both transcripts are on chrII:
chrII <- Celegans$chrII
tx_seqs <- extractTranscripts(chrII,
                              exonStarts=exon_starts,
                              exonEnds=exon_ends,
                              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]])

## -----
## E. sortExonsByRank()
## -----
## Typically used to reorder by decreasing rank the exons in transcripts
## located on the minus strand:
exbytx3 <- sortExonsByRank(exbytx, decreasing.rank.on.minus.strand=TRUE)
exbytx3
tx_seqs3 <- extractTranscriptsFromGenome(Hsapiens, exbytx3,

```

```
decreasing.rank.on.minus.strand=TRUE)  
stopifnot(identical(as.character(tx_seqs3), as.character(tx_seqs1)))
```

---

FeatureDb-class

*FeatureDb objects*

---

## Description

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

See [?TranscriptDb](#) 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 [TranscriptDb](#) 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 | <i>Extract simple features from a FeatureDb object</i> |
|----------|--|

---

**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)
```

---

GenomicFeatures-deprecated

*Deprecated Functions in package **GenomicFeatures***

---

**Description**

The functions or variables listed here have been deprecated and should no longer be used.

**See Also**

[Deprecated](#)

---

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 <a href="#">GRanges</a> or <a href="#">GRangesList</a> object containing genes grouped by transcript. |
| subject    | A <a href="#">BSgenome</a> object or a <a href="#">FaFile</a> 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**

`txdb`            A [TranscriptDb](#) object.

`feature.type`    The feature type for which the mapping must be retrieved.

**Details**

Transcripts, exons and CDS in a [TranscriptDb](#) 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 [TranscriptDb](#) 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 [TranscriptDb](#) object.
- The [TranscriptDb](#) class.

### Examples

```
txdb1_file <- system.file("extdata", "UCSC_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)

```

**Arguments**

|                     |  |
|---------------------|--|
| genome              | genome abbreviation used by UCSC and obtained by <code>ucscGenomes()</code> [ , "db"]. 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 annotations to retrieve. Use the <code>supportedUCSCFeatureDbTables</code> 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 <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'  |

**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



---

|                  |  |
|------------------|--|
| makeTranscriptDb | <i>Making a TranscriptDb object from user supplied annotations</i> |
|------------------|--|

---

### Description

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

### Usage

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

### Arguments

|              |  |
|--------------|--|
| transcripts  | data frame containing the genomic locations of a set of transcripts  |
| splicings    | 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 species, 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\_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).
- `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 are allowed and must match NAs in `cds_start` and `cds_end`.
- `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. Either all NAs or an integer vector with no NAs.
- `is_circular`: [optional] Chromosome circularity flag. Either all NAs or a logical vector with no NAs.

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



**Value**

A [TranscriptDb](#) object.

**Author(s)**

H. Pages

**See Also**

- [makeTranscriptDbFromUCSC](#) and [makeTranscriptDbFromBiomart](#) for convenient ways to make [TranscriptDb](#) objects from UCSC or BioMart online resources.
- [makeTranscriptDbFromGFF](#) for making a [TranscriptDb](#) object from annotations available as a GFF3 or GTF file.
- The [TranscriptDb](#) class.

**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 <- makeTranscriptDb(transcripts, splittings)
```

---

makeTranscriptDbFromBiomart

*Make a TranscriptDb object from annotations available on a BioMart database*

---

**Description**

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

**Usage**

```

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

makeTranscriptDbFromBiomart(biomart="ensembl",
                             dataset="hsapiens_gene_ensembl",
                             transcript_ids=NULL,
                             circ_seqs=DEFAULT_CIRC_SEQS,
                             filters="",
                             id_prefix="ensembl_",
                             host="www.biomart.org",
                             port=80,
                             miRBaseBuild=NA)

```

**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="#">TranscriptDb</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=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_".  |
| 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**

`makeTranscriptDbFromBiomart` is a convenience function that feeds data from a BioMart database

to the lower level `makeTranscriptDb` function. See `?makeTranscriptDbFromUCSC` for a similar function that feeds data from the UCSC source.

BioMart databases that are known to have compatible transcript annotations are:

- the most recent `ensembl`: ENSEMBL GENES (SANGER UK)
- the most recent `bacterial_mart`: ENSEMBL BACTERIA (EBI UK)
- the most recent `fungus_mart`: ENSEMBL FUNGAL (EBI UK)
- the most recent `metazoa_mart`: ENSEMBL METAZOA (EBI UK)
- the most recent `plant_mart`: ENSEMBL PLANT (EBI UK)
- the most recent `protist_mart`: ENSEMBL PROTISTS (EBI UK)
- the most recent `ensembl_expressionmart`: EURATMART (EBI UK)

Not all annotations will have CDS information.

### Value

A `TranscriptDb` object.

### Author(s)

M. Carlson and H. Pages

### See Also

`listMarts`, `useMart`, `listDatasets`, `DEFAULT_CIRC_SEQS`, `makeTranscriptDbFromUCSC`, `makeTranscriptDbFromGFF`, `makeTranscriptDb`, `supportedMirBaseBuildValues`

### Examples

```
## Discover which datasets are available in the "ensembl" BioMart
## database:
library("biomaRt")
head(listDatasets(useMart("ensembl")))

## Retrieving an incomplete transcript dataset for Human from the
## "ensembl" BioMart database:
transcript_ids <- c(
  "ENST00000268655",
  "ENST00000313243",
  "ENST00000341724",
  "ENST00000400839",
  "ENST00000435657",
  "ENST00000478783"
)
txdb <- makeTranscriptDbFromBiomart(transcript_ids=transcript_ids)
txdb # note that these annotations match the GRCh37 genome assembly

## Now what if we want to use another mirror? We might make use of the
## new host argument. But wait! If we use biomaRt, we can see that
## this host has named the mart differently!
```

```
listMarts(host="uswest.ensembl.org")
## Therefore we must also change the name passed into the "mart"
## argument thusly:
try(
txdb <- makeTranscriptDbFromBiomart(biomart="ENSEMBL_MART_ENSEMBL",
                                   transcript_ids=transcript_ids,
                                   host="uswest.ensembl.org")
)
txdb
```

---

```
makeTranscriptDbFromGFF
```

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

---

## Description

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

## Usage

```
makeTranscriptDbFromGFF(file,
                        format=c("gff3", "gtf"),
                        exonRankAttributeName=NA,
                        gffGeneIdAttributeName=NA,
                        chrominfo=NA,
                        dataSource=NA,
                        species=NA,
                        circ_seqs=DEFAULT_CIRC_SEQS,
                        miRBaseBuild=NA,
                        useGenesAsTranscripts=FALSE)
```

## Arguments

|                        |   |
|------------------------|---|
| file                   | path/file to be processed   |
| format                 | "gff3" or "gtf" depending on which file format you have to process  |
| exonRankAttributeName  | character(1) name of the attribute that defines the exon rank information, or NA to indicate that exon ranks are inferred from order of occurrence in the GFF.  |
| gffGeneIdAttributeName | an optional argument that can be used for gff style files ONLY. If the gff file lacks rows to specify gene IDs but the mRNA rows of the gff file specify the gene IDs via a named attribute, then passing the name of the attribute for this argument can allow the file to still extract gene IDs that map to these transcripts. If left blank, then the parser will try and extract rows that are named 'gene' for gene to transcript mappings when parsing a gff3 file. For gtf files this argument is ignored entirely. |

|                       |   |
|-----------------------|---|
| chrominfo             | data frame containing information about the chromosomes. Will be passed to the internal call to <a href="#">makeTranscriptDb</a> . See <a href="#">?makeTranscriptDb</a> for the details.   |
| dataSource            | Where did this data file originate? Please be as specific as possible.  |
| species               | 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.                                       |
| circ_seqs             | a character vector to list out which chromosomes should be marked as circular.  |
| miRBaseBuild          | specify the string for the appropriate build Information from mirbase.db to use for microRNAs. This can be learned by calling <a href="#">supportedMiRBaseBuildValues</a> . By default, this value will be set to NA, which will inactivate the microRNAs accessor.   |
| useGenesAsTranscripts | This flag is normally off, but if enabled it will try to salvage a file that has no RNA features by assuming that you can use the ranges available for the Gene features in their place. Obviously, this is something you won't want to do unless you are dealing with something very simple like a prokaryote. |

## Details

`makeTranscriptDbFromGFF` is a convenience function that feeds data from the parsed file to the lower level [makeTranscriptDb](#) function.

There are some real deficiencies in the gtf and the gff3 file formats to bear in mind when making use of them. For gtf files the length of the transcripts is not normally encoded and so it has to be inferred from the exon ranges presented. That's not a horrible problem, but it bears mentioning for the sake of full disclosure. And for gff3 files the situation is typically even worse since they usually don't encode any information about the exon rank within a transcript. This is a serious oversight and so if you have an alternative to using this kind of data, you should really do so.

Some files will have an attribute defined to indicate the exon rank information. For GTF files this is usually given as "exon\_number", however you still must specify this argument if you don't want the code to try and infer the exon rank information. For gff3 files, we have not seen any examples of this information encoded anywhere, but if you have a file with an attribute, you can still specify this to avoid the inference.

## Value

A [TranscriptDb](#) object.

## Author(s)

M. Carlson

## See Also

[DEFAULT\\_CIRC\\_SEQS](#), [makeTranscriptDbFromUCSC](#), [makeTranscriptDbFromBiomart](#), [makeTranscriptDb](#), [supportedMiRBaseBuildValues](#)

**Examples**

```
## TESTING GFF3
gffFile <- system.file("extdata","a.gff3",package="GenomicFeatures")
txdb <- makeTranscriptDbFromGFF(file=gffFile,
  format="gff3",
  exonRankAttributeName=NA,
  dataSource="partial gtf file for Tomatoes for testing",
  species="Solanum lycopersicum")
if(interactive()) {
  saveDb(txdb,file="TESTGFF.sqlite")
}

## TESTING GTF, this time specifying the chrominfo
gtfFile <- system.file("extdata","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 <- makeTranscriptDbFromGFF(file=gtfFile,
  format="gtf",
  exonRankAttributeName="exon_number",
  chrominfo=chrominfo,
  dataSource=paste("ftp://ftp.ensemblgenomes.org/pub/metazoa/",
    "release-13/gtf/aedes_aegypti/",sep=""),
  species="Aedes aegypti")
if(interactive()) {
  saveDb(txdb2,file="TESTGTF.sqlite")
}
```

---

makeTranscriptDbFromUCSC

*Make a TranscriptDb object from annotations available at the UCSC  
Genome Browser*

---

**Description**

The makeTranscriptDbFromUCSC function allows the user to make a [TranscriptDb](#) object from transcript annotations available at the UCSC Genome Browser.

**Usage**

```
supportedUCSCtables()

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

makeTranscriptDbFromUCSC(
  genome="hg18",
```

```

    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",
    miRBaseBuild=NA)

```

## Arguments

|                     |   |
|---------------------|---|
| genome              | genome abbreviation used by UCSC and obtained by <code>ucscGenomes()</code> [ , "db"]. For example: "hg18".   |
| 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>TranscriptDb</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.  |
| url, goldenPath_url | use to specify the location of an alternate UCSC Genome Browser.  |
| 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.              |

## Details

`makeTranscriptDbFromUCSC` is a convenience function that feeds data from the UCSC source to the lower level `makeTranscriptDb` function. See `?makeTranscriptDbFromBiomart` for a similar function that feeds data from a BioMart database.

## Value

A `TranscriptDb` object.

## Author(s)

M. Carlson and H. Pages

## See Also

`ucscGenomes`, `DEFAULT_CIRC_SEQS`, `makeTranscriptDbFromBiomart`, `makeTranscriptDbFromGFF`, `makeTranscriptDb`, `supportedMiRBaseBuildValues`

**Examples**

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

## Display the list of tables supported by makeTranscriptDbFromUCSC():
supportedUCSCTables()

## Not run:
## Retrieving a full transcript dataset for Yeast from UCSC:
txdb1 <- makeTranscriptDbFromUCSC(genome="sacCer2", tablename="ensGene")

## End(Not run)

## Retrieving an incomplete transcript dataset for Mouse from UCSC
## (only transcripts linked to Entrez Gene ID 22290):
transcript_ids <- c(
  "uc009uzf.1",
  "uc009uzg.1",
  "uc009uzh.1",
  "uc009uzi.1",
  "uc009uzj.1"
)

txdb2 <- makeTranscriptDbFromUCSC(genome="mm9", tablename="knownGene",
                                transcript_ids=transcript_ids)

txdb2
```

---

makeTxDbPackage

*Making a TranscriptDb packages from annotations available at the UCSC Genome Browser, biomaRt or from another source.*

---

**Description**

The `makeTxDbPackageFromUCSC` function allows the user to make a [TranscriptDb](#) object 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 [TranscriptDb](#) object from transcript annotations that are in a custom transcript Database, such as could be produced using `makeTranscriptDb`.

**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",
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)

```

```

makeTxDbPackageFromBiomart(
  version,
  maintainer,
  author,
  destDir=".",
  license="Artistic-2.0",
  biomart="ensembl",
  dataset="hsapiens_gene_ensembl",
  transcript_ids=NULL,
  circ_seqs=DEFAULT_CIRC_SEQS,
  miRBaseBuild=NA)

```

```

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

```

```
supportedMiRBaseBuildValues()
```

## Arguments

version            What is the version number for this package?

|                     |  |
|---------------------|--|
| maintainer          | Who is the package maintainer? (must include email to be valid)  |
| author              | Who is the creator of this package?  |
| 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 <code>listMarts</code> 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.   |
| genome              | genome abbreviation used by UCSC and obtained by <code>ucscGenomes()</code> [ , "db"]. 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>TranscriptDb</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.   |
| 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>TranscriptDb</code> object that represents a handle to a transcript database. This object type is what is returned by <code>makeTranscriptDbFromUCSC</code> , <code>makeTranscriptDbFromUCSC</code> or <code>makeTranscriptDb</code>   |
| 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**

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

**Value**

A [TranscriptDb](#) object.

**Author(s)**

M. Carlson

**See Also**

[ucscGenomes](#), [DEFAULT\\_CIRC\\_SEQS](#), [makeTranscriptDbFromUCSC](#), [makeTranscriptDbFromBiomart](#), [makeTranscriptDb](#) [supportedUCSCtables](#) [getChromInfoFromUCSC](#) [getChromInfoFromBiomart](#)

**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)

```

---

nearest-methods

*Finding the nearest genomic range neighbor in a TranscriptDb*


---

## Description

The distance methods for TranscriptDb objects and subclasses.

## Usage

```

## S4 method for signature GenomicRanges,TranscriptDb
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="#">TranscriptDb</a> instance. The id is used to extract ranges from the <a href="#">TranscriptDb</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 TranscriptDb 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 TranscriptDb object y. Values in id are matched to one of 'gene\_id', 'tx\_id', 'exon\_id' or 'cds\_id' identifiers in the TranscriptDb 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 ids 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 TranscriptDb 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)
```

---

regions

*Functions that compute genomic regions of interest.*

---

**Description**

Functions that compute genomic regions of interest such as promotor, upstream regions etc, from the genomic locations provided in a UCSC-style data frame.

WARNING: All the functions described in this man page are now defunct!

Please use [transcripts](#), [exons](#) or [intronsByTranscript](#) on a [TranscriptDb](#) object instead.

**Usage**

```
transcripts_deprecated(genes, proximal = 500, distal = 10000)
exons_deprecated(genes)
introns_deprecated(genes)
```

**Arguments**

|          |   |
|----------|---|
| genes    | A UCSC-style data frame i.e. a data frame with 1 row per transcript and at least the following columns: "name", "chrom", "strand", "txStart", "txEnd", "exonCount", "exonStarts", "exonEnds", "intronStarts" and "intronEnds". A value in any of the last 4 columns must be a comma-separated list of integers. Note that unlike what UCSC does the start values here must be 1-based, not 0-based. |
| proximal | The number of bases on either side of TSS and 3'-end for the promoter and end region, respectively.   |
| distal   | The number of bases on either side for upstream/downstream, i.e. enhancer/silencer regions.   |

**Details**

The assumption made for introns is that there must be more than one exon, and that the introns are between the end of one exon and before the start of the next exon.

**Value**

All of these functions return a [RangedData](#) object with a gene column with the UCSC ID of the gene. For `transcripts_deprecated`, each element corresponds to a transcript, and there are columns for each type of region (promoter, threeprime, upstream, and downstream). For `exons_deprecated`, each element corresponds to an exon. For `introns_deprecated`, each element corresponds to an intron.

**Author(s)**

M. Lawrence.

**See Also**

[transcripts](#), [exons](#), [intronsByTranscript](#), [TranscriptDb-class](#)

---

saveFeatures

*Methods to save and load the database contents for a TranscriptDb or FeatureDb object.*

---

## Description

These methods provide a way to dump a [TranscriptDb](#) or [FeatureDb](#) object to an SQLite file, and to recreate that object from the saved file.

However, these methods are now deprecated and have been replaced by [saveDb](#) and [loadDb](#).

Users are encouraged to switch to those other methods as the methods documented here will soon be defunct.

## Usage

```
saveFeatures(x, file)
loadFeatures(file)
```

## Arguments

|      |   |
|------|---|
| x    | A <a href="#">TranscriptDb</a> or <a href="#">FeatureDb</a> object. |
| file | An SQLite Database filename.  |

## Value

For loadFeatures only, a [TranscriptDb](#) or [FeatureDb](#) object is returned.

## Author(s)

M. Carlson

## See Also

[saveDb](#), [TranscriptDb](#), [FeatureDb](#)

## Examples

```
## Not run:
txdb <-
  loadFeatures(system.file("extdata", "UCSC_knownGene_sample.sqlite",
                           package = "GenomicFeatures"))
txdb

## End(Not run)
```

## Description

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

## Details

In the code snippets below, x is a [TranscriptDb](#) 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 [TranscriptDb](#) 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 [TranscriptDb](#) 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 description of methods select,keytypes,keys and columns.
- [transcripts](#), [transcriptsBy](#), and [transcriptsByOverlaps](#), for other ways to extract genomic features from a [TranscriptDb](#) object.
- The [TranscriptDb](#) 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)
```

---

TranscriptDb-class      *TranscriptDb* objects

---

**Description**

The TranscriptDb 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 [?makeTranscriptDbFromUCSC](#) and [?makeTranscriptDbFromBiomart](#) for convenient ways to make TranscriptDb objects from UCSC or BioMart online resources.

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

**Methods**

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

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

`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.

`seqnameStyle(x)`: List the matching seqname styles for `x`. `seqnameStyle(x)` is equivalent to `seqnameStyle(seqinfo(x))`. Note that this information is not stored in `x` but inferred by looking up `seqlevels(x)` against a seqname style database stored in the `seqnames.db` meta-data package (required).

`determineDefaultSeqnameStyle(x)`: Determine the default seqname style for the database in `x`.

`as.list(x)`: Dumps the entire db into a list of data frames `txdump` that can be used in `do.call(makeTranscriptDb, txdump)` to make the db again with no loss of information. Note that the transcripts are dumped in the same order in all the data frames.

### Author(s)

H. Pages, Marc Carlson

### See Also

- The [FeatureDb](#) class for storing genomic locations of an arbitrary type of genomic features.
- [makeTranscriptDbFromUCSC](#) and [makeTranscriptDbFromBiomart](#) for convenient ways to make `TranscriptDb` objects from UCSC or BioMart online resources.
- [makeTranscriptDbFromGFF](#) for making a `TranscriptDb` object from annotations available as a GFF3 or GTF file.
- [saveDb](#) and [loadDb](#) for saving and loading the database content of a `TranscriptDb` object.
- [transcripts](#), [transcriptsBy](#), and [transcriptsByOverlaps](#), for how to extract genomic features from a `TranscriptDb` object.
- [select-methods](#) for how to use the simple "select" interface to extract information from a `TranscriptDb` object.
- The [Seqinfo](#) class in the `GenomicRanges` package.

### Examples

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

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

## Can set txdb so that only chr1 and chr2 are used by using the seqlevels
seqlevels(txdb, force=TRUE) <- c("1", "2")
## And then you can restore the default seqlevels
txdb <- restoreSeqlevels(txdb)
```

```
## Use of as.list
txdump <- as.list(txdb)
txdump
txdb1 <- do.call(makeTranscriptDb, txdump)
stopifnot(identical(as.list(txdb1), txdump))
```

---

transcripts

*Extract genomic features from an object*

---

## Description

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

## Usage

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

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

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

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

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

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

microRNAs(x)
## S4 method for signature TranscriptDb
microRNAs(x)

tRNAs(x)
```

```
## S4 method for signature TranscriptDb
tRNAs(x)
```

### Arguments

|                          |  |
|--------------------------|--|
| x                        | A <a href="#">TranscriptDb</a> object.   |
| ...                      | Arguments to be passed to or from methods.   |
| 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 ?promoters, GRanges-method.  |
| downstream               | For promoters : An integer(1) value indicating the number of bases downstream from the transcription start site. For additional details see ?promoters, GRanges-method.  |
| 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

These are the main functions for extracting transcript information from a [TranscriptDb](#) object. With the exception of `microRNAs`, 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 `TranscriptDb` 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`.

`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. 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. `disjointExons` was contributed by Mike Love and Alejandro Reyes.

### See Also

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

### Examples

```
## transcripts(), exons(), genes():
txdb <- loadDb(system.file("extdata", "UCSC_knownGene_sample.sqlite",
  package="GenomicFeatures"))
vals <- list(tx_chrom = c("chr3", "chr5"), tx_strand = "+")

transcripts(txdb, vals)

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

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 weve 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)

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

## End(Not run)

## promoters() :
head(promoters(txdb, 100, 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 [TranscriptDb](#) objects only.

## Usage

```

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

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

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

intronsByTranscript(x, ...)
## S4 method for signature TranscriptDb

```

```

intronsByTranscript(x, use.names=FALSE)

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

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

```

## Arguments

|           |   |
|-----------|---|
| x         | A <a href="#">TranscriptDb</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.<br>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 and cdsBy with by = "tx", the ranges are returned in the order they appear in the transcript, i.e. order by the splicing.exon\_rank field in x's internal database. 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 [TranscriptDb](#) object.
- [select-methods](#) for how to use the simple "select" interface to extract information from a [TranscriptDb](#) object.
- [id2name](#) for mapping [TranscriptDb](#) internal ids to external names for a given feature type.
- The [TranscriptDb](#) class.

**Examples**

```
txdb_file <- system.file("extdata", "UCSC_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 [TranscriptDb](#) objects only.



**Usage**

```

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

```

**Arguments**

|            |   |
|------------|---|
| x          | A <a href="#">TranscriptDb</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 [TranscriptDb](#) object.
- [select-methods](#) for how to use the simple "select" interface to extract information from a [TranscriptDb](#) object.
- [id2name](#) for mapping [TranscriptDb](#) internal ids to external names for a given feature type.
- The [TranscriptDb](#) class.

**Examples**

```
txdb <- loadDb(system.file("extdata", "UCSC_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)
```

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