Package 'GenomicFeatures'

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Title Tools for making and manipulating transcript centric annotations

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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 (>= 1.13.10), GenomicRanges (>= 1.7.17), AnnotationDbi (>= 1.15.39)

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

Suggests rtracklayer, biomaRt, org.Mm.eg.db, Biostrings, BSgenome,BSgenome.Hsapiens.UCSC.hg18 (>= 1.3.14),BSgenome.C base.db, FDb.UCSC.tRNAs, RUnit,TxDb.Hsapiens.UCSC.hg18.knownGene

Collate AllClasses.R AllGenerics.R utils.R Ensembl.utils.R TranscriptDb-class.R FeatureDb-class.R makeTranscriptDb.R makeTranscriptDbFromUCSC.R makeTranscriptDbFromBiomart.R makeFeatureDbFromUCSC.R transcripts.R transcriptsByOverlaps.R transcriptsBy.R regions.R features.R extractTranscriptsFromGenome.R makeTxDbPackage.R methods-select.R test_GenomicFeatures_package.R spliceGraph_utils.R spliceGraph.R

biocViews Genetics, Infrastructure, Annotation,HighThroughputSequencing

R topics documented:

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

Description

These functions coerce a `TranscriptDb` object to a `GRanges` object with `values` 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 <- loadFeatures(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 us 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 BSgenome object. See the available.genomes function in the BSgenome package for how to install a genome.
txdb	A TranscriptDb object or a GRangesList 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 sortExonsByRank), this argument describes the input. For sortExonsByRank, it describes how exons should be ordered in the output.
use.names	TRUE or FALSE. Ignored if txdb is not a TranscriptDb 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 DNAString or MaskedDNAString object for `extractTranscripts`.

A GRangesList object for `sortExonsByRank`, typically coming from `exonsBy(... , by="tx")`.

`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.

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

Value

For `extractTranscriptsFromGenome`: A named DNAStringSet 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 DNAStringSet 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 <- loadFeatures(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:
tlocs <- 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, '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(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)))
```

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

`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 seperate 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 `NA`s).

Value

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

Author(s)

H. Pages

See Also

TranscriptDb, `transcripts`, `transcriptsBy`

Examples

```
txdb1_file <- system.file("extdata", "UCSC_knownGene_sample.sqlite",
                          package="GenomicFeatures")
txdb1 <- loadFeatures(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 <- loadFeatures(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 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 supportedUCSCFeatureDbTa 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'

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():
## This method works but may take a long time to run.
# 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
```

---

makeTranscriptDb *Making a TranscriptDb object from user supplied annotations*

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, ...)
```

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.
...	ignored for now

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).
- tx_chrom: Transcript chromosome. Character vector (or factor) with no NAs.
- tx_strand: Transcript strand. Character vector (or factor) 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$tx_chrom is used. If present then exon_strand must be present too.
- exon_strand: [optional] Exon strand. Character vector (or factor) with no NAs. If missing then transcripts$tx_strand is used and exon_chrom must be missing too.
- 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 be too. 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 be too. 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.
- 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

TranscriptDb, makeTranscriptDbFromUCSC, makeTranscriptDbFromBiomart

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))
splicings <-  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, splicings)
```

---

makeTranscriptDbFromBiomart

Making 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 = NULL)
```

Arguments

biomart	which BioMart database to use. Get the list of all available BioMart databases with the listMarts function from the biomaRt 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_ensemb "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 TranscriptDb 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 filters=as.list(c(source="entrez"))
host	The host URL of the BioMart. Defaults to www.biomart.org.
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 mirbase.db to use for microRNAs. This can be learned by calling supportedMiRBaseBuildValues. By default, this value will be NULL, 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 fungal_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, makeTranscriptDb
supportedMiRBaseBuildValues

Examples

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

---

makeTranscriptDbFromUCSC *Making 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 = NULL)
```

Arguments

`genome`	genome abbreviation used by UCSC and obtained by `ucscGenomes()[ , "db"]`. For example: `"hg18"`.
`tablename`	name of the UCSC table containing the transcript annotations to retrieve. Use the `supportedUCSCtables` 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 TranscriptDb 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 `supportedMiRBaseBuildValues`. By default, this value will be NULL, 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, makeTranscriptDb supportedMiRBaseBuildV

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 = NULL)

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 = NULL)

  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 listMarts function from the biomaRt 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_ensemb "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 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 transcript annotations to retrieve. Use the supportedUCSCtables 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 TranscriptDb 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 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'
txdb	A TranscriptDb object that represents a handle to a transcript database. This object type is what is returned by makeTranscriptDbFromUCSC, makeTranscriptDbFromUCSC or makeTranscriptDb
miRBaseBuild	specify the string for the appropriate build Information from mirbase.db to use for microRNAs. This can be learned by calling supportedMiRBaseBuildValues. By default, this value will be NULL, 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)
```

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 deprecated. 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 Transcript Object.*

Description

These methods provide a way to dump a TranscriptDb object to an SQLite file, and to recreate that object the saved file.

Usage

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

Arguments

x	a transcripts object, which contains a connection to a DB.
file	A SQLite Database filename.

Value

For loadFeatures only, a TranscriptDb object is returned.

Author(s)

M. Carlson

See Also

TranscriptDb

Examples

```
txdb <-
  loadFeatures(system.file("extdata", "UCSC_knownGene_sample.sqlite",
                           package = "GenomicFeatures"))
txdb
```

spliceGraph *Create a splicing graph from an TranscriptDb object*

Description

Extracts the edges of a splicing graph structure which is generated based on a given TranscriptDb object.

Usage

```
spliceGraph(txdb, ...)
## S4 method for signature 'TranscriptDb'
spliceGraph(txdb, genes=getGH(txdb), ...)
```

Arguments

txdb	A TranscriptDb object.
genes	A character vector representing the ENTREZ gene ids used for creating the splicing graph. If no genes are specified all genes in the TranscriptDb object are used.
...	Arguments to be passed to or from methods.

Details

This is the main function for creating a splicing graph structure based on a provided TranscriptDb object. Splicing graphs in general are efficient representations of gene structures and associated alternative splicing information. The main elements of a splicing graph are called vertices and edges. Vertices (or nodes) basically represent potential splicing events and the edges mimic the corresponding introns and exons of all known transcipt variants. Since not all splice sites are alternative splice sites the graph can be simplified by collapsing edges and the vertices where no evidence for alternative splicing is present. Finally the function provides a GRangesList object containing the collapsed edges and their associated exons. Each edge contains at least one exon. Keep in mind that the exons per edges in the GRangesList are not the original exons defined within the TranscriptDb object. The original exons, the genes and the new exons can be rerieved from the resulting GRangesList object. See the example code below.

Value

Returns a GRangesList object containing the collapsed edges of the splicing graph. This object contains the new disjoint exons, the gene ids as well as the original exon ids.

Author(s)

M. Carlson, M. Morgan, D. Bindreither

References

Heber, S., Alekseyev, M., Sze, S., Tang, H., and Pevzner, P. A. *Splicing graphs and EST assembly problem* Bioinformatics Date: Jul 2002 Vol: 18 Pages: S181-S188

Sammeth, M. (2009) *Complete alternative splicing events are bubbles in splicing graphs* J. Comput. Biol. Date: Aug 2009 Vol: 16 Pages: 1117-1140

See Also

TranscriptDb, GRangesList

Examples

```
if(interactive()) {
  library(TxDb.Hsapiens.UCSC.hg18.knownGene)
  txdb <- TxDb.Hsapiens.UCSC.hg18.knownGene

  ## creates the splice graph structure and retrieves the exons
  ## associated with the individual edges
  exonsByEdges <- spliceGraph(txdb, genes=c("1", "10"))
  exonsByEdges

  ## get the new exon ids
```

```
  values(unlist(exonsByEdges))[["disJ_exon_id"]]

  ## get the gene ids
  values(exonsByEdges)[["gene_id"]]

  ## get the original exon ids
  values(unlist(exonsByEdges))[["exon_ids"]]
}
```

`TranscriptDb-class` *TranscriptDb objects*

Description

The TranscriptDb class is a container for storing transcript annotations. The FeatureDb class is a container for storing more generic GenomicFeature annotations.

See ?`makeTranscriptDbFromUCSC` and ?`makeTranscriptDbFromBiomart` for making a TranscriptDb object from the UCSC or BioMart sources.

See ?`makeFeatureDbFromUCSC` for making a FeatureDb object from the UCSC or BioMart sources.

See ?`saveDb` and ?`loadDb` for saving and loading the database contents of a TranscriptDb or FeatureDb object.

`select`, `cols` and `keys` are used together to extract data from an `TranscriptDb` object.

Methods

In the code snippets below, `x` is a TranscriptDb object. For the metadata and show methods, there is also support for FeatureDb objects.

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

`seqinfo(x)`: Gets the information about the underlying sequences as a Seqinfo object. Note that there is no `seqinfo` setter for TranscriptDb objects (this information is stored in the SQLite db, and, in normal use, this db is accessed in read-only mode).

`as.list(x)`: Dumps the entire db into a list of data frames `txdump` that can be used in `do.call(makeTranscriptDb, t` 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.

`asGFF(x)`: Dumps the transcript information from the db into a GRanges object formatted like a GFF file.

`asBED(x)`: Dumps the transcript information from the db into a GRanges object formatted like a bed file.

`isActiveSeq(x)`: Returns 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.

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

`keys(x, keytype)`: returns keys for the database contained in the `TranscriptDb` object . By default it will return the "TXNAME" keys for the database, but if used with the `keytype` argument, it will return the keys from that keytype.

`cols(x)`: shows which kinds of data can be returned for the `TranscriptDb` object.

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

See ?transcripts, ?transcriptsByOverlaps, ?id2name and ?transcriptsBy for other useful operations on TranscriptDb objects.

Author(s)

H. Pages, Marc Carlson

See Also

Seqinfo-class, makeTranscriptDbFromUCSC, makeTranscriptDbFromBiomart, loadFeatures, transcripts, transcriptsByOverlaps, id2name, transcriptsBy

Examples

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

## Examples on how to change which sequences are active
## Set chr1 and chr3 to be inactive:
isActiveSeq(txdb) <- c("1"=FALSE, "3"=FALSE)
## Set ALL of the chromsomed to be inactive
isActiveSeq(txdb)[seqlevels(txdb)] <- FALSE
## Now set only chr1 and chr5 to be active
isActiveSeq(txdb) <- c("1"=TRUE, "5"=TRUE)

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

## Use of select and supporting methods
## 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
cols(txdb)
## call select
res = select(txdb, head(keys(txdb, "GENEID")),
```

```
             cols = c("GENEID","TXNAME"),
             keytype="GENEID")
head(res)
```

`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")

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

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

Arguments

`x`	A TranscriptDb 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 with values in the above list of valid names. With the following restrictions: • `"tx_chrom"` and `"tx_strand"` are not allowed for `transcripts`. • `"exon_chrom"` and `"exon_strand"` are not allowed for `exons`. • `"cds_chrom"` and `"cds_strand"` are not allowed for `cds`. If the vector is named, those names are used for the corresponding column in the element metadata of the returned object.

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.

Value

a GRanges object

Author(s)

M. Carlson, P. Aboyoun and H. Pages

See Also

TranscriptDb, id2name, transcriptsBy, transcriptsByOverlaps

Examples

```
txdb <- loadFeatures(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("exon_id", "tx_name"))
exons(txdb, vals=list(tx_name="uc009vip.1"), columns=c("exon_id",
"tx_name"))
```

---

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 TranscriptDb 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 GRangesList 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 GRangesList object. By default (i.e. if use.names is FALSE), the names of this GRangesList 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 ?id2name 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 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

TranscriptDb, transcripts, id2name, transcriptsByOverlaps

Examples

```
txdb_file <- system.file("extdata", "UCSC_knownGene_sample.sqlite",
                         package="GenomicFeatures")
txdb <- loadFeatures(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 TranscriptDb object.
...	Arguments to be passed to or from methods.
ranges	A GRanges object to restrict the output.
type	How to perform the interval overlap operations of the ranges. See the findOverlaps manual page in the GRanges 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 ?transcripts 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

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See Also

TranscriptDb, transcripts

Examples

```
txdb <- loadFeatures(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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