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 (>= 1.15.35), GenomicRanges (>= 1.9.66), AnnotationDbi (>= 1.19.36)

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.H 1.3.17), mirbase.db, FDb.UCSC.tRNAs,TxDb.Hsapiens.UCSC.hg18.knownGene,TxDb.Hsapiens.UCSC.hg19.knownGene,TxDb. tools,pasillaBamSubset (>= 0.0.5), 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 getPromoterSeq-methods.R test_GenomicFeatures_package.R

biocViews Genetics, Infrastructure, Annotation,HighThroughputSequencing

R topics documented:

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

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 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 <- 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:
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)))
```

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 *Extract simple features from a FeatureDb object*

Description

Generic function to extract genomic features from a FeatureDb object.

Usage

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

Arguments

x	A FeatureDb object.

Value

a GRanges object

Author(s)

M. Carlson

See Also

FeatureDb

Examples

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

getPromoterSeq *Get gene promoter sequences*

Description

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

Usage

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

Arguments

query	A GRanges or GRangesList object containing genes grouped by transcript.
subject	A BSgenome object or a FaFile from which the sequences will be taken.
upstream	The number of DNA bases to include upstream of the TSS (transcription start site)
downstream	The number of DNA bases to include downstream of the TSS (transcription start site)
...	Additional arguments

Details

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

Value

A DNAStringSet or DNAStringSetList instance corresponding to the GRanges or GRangesList supplied in the query.

Author(s)

Paul Shannon

See Also

promoters 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 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 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 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 supportedUCSCFeatureDbT 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():
# 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,
                 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))
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

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 = 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_ense "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, makeTranscriptDbFromGFF, 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
```

---

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=NULL,
                        gffGeneIdAttributeName=NULL,
                        chrominfo,
                        dataSource,
                        species,
                        circ_seqs=DEFAULT_CIRC_SEQS,
                        miRBaseBuild=NULL)
```

Arguments

file	path/file to be processed
format	"gff3" or "gtf" depending on which file format you have to process
exonRankAttributeName	what is the name (if any) of the attribute that defines the exon rank information.
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. This data.frame has 3 columns: 'chrom', 'length' and 'is_circular'. The 'chrom' column contains the character names of the chromosome elements that are present, the 'length' is the integer length for each one and the 'is_circular' contains a logical value to indicate whether that element is a circularized (such as a mitochondria or a chloroplast). If this argument is left blank then there will not be any length information recorded for the different chromosomes since it is not possible to infer if from the transcript ranges alone.
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 supportedMiRBaseBuildValues. By default, this value will be NULL, which will inactivate the microRNAs accessor.

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",
          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 = 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, 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 = 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_ense "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 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 TranscriptDb or FeatureDb 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)
```

---

select-methods *Using the "select" interface on TranscriptDb objects*

Description

select, cols 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): Return 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): Show which kinds of data can be returned for the TranscriptDb object.

select(x, keys, cols, 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 cols and keytype arguments.

Author(s)

Marc Carlson

See Also

- 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
cols(txdb)

## call select
res <- select(txdb, head(keys(txdb, "GENEID")),
              cols=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 metadata 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, txdum 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)))

## 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))
```

---

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")

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

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

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

Arguments

x	A TranscriptDb object. For promoters(), x can be a TranscriptDb or a GRanges 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.

upstream — For promoters() : An integer(1) value indicating the number of bases upstream from the transcription start site. The upstream range extends from this value up to, but not including, the transcription start site. The upstream range is merged with the downstream range to form the full promoter region.

downstream — For promoters() : An integer(1) value indicating the number of bases downstream from the transcription start site. The downstream range extends from this value up to, and including, the transcription start site. The downstream range is merged with the upstream range to form the full promoter region.

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 or GRanges object. When a TranscriptDb is supplied the transcripts extractor is called; when a GRanges is supplied it is expected that these are transcript ranges. The return object is a GRanges of promoter regions around the transcription start site the span of which is defined by upstream and downstream. Ranges on the * strand are treated the same as those on the + strand. When no seqlengths are present in the TranscriptDb or GRanges (i.e., seqlength is NA) it is possible to have non-positive start values in the promoter ranges. This occurs when (TSS - upstream) < 1. In the equal but opposite case, the end values of the ranges may extend beyond the chromosome end when (TSS + downstream + 1) > 'chromosome end'. When seqlengths are not NA the promoter ranges are kept within the bounds of the defined seqlengths.

Value

a GRanges object

Author(s)

M. Carlson, P. Aboyoun and H. Pages

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

## 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))

## The promoter regions are defined around the transcription start
## sites. On the "+" strand this region surrounds the 'start'
## value in a GRanges. On the -" strand this region surrounds
## the 'end' value. Note the "*" ranges are treated as "+".
gr <- GRanges("chr1", IRanges(rep(10, 3), width=6), c("+", "-", "*"))
gr
promoters(gr, 2, 2)
```

---

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

- 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 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

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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