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>

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**R topics documented:**

makeTxDbFromGFF.R  makeFeatureDbFromUCSC.R  mapIdsToRanges.R
id2name.R  transcripts.R  transcriptsBy.R  transcriptsByOverlaps.R
extractTranscriptSeqs.R  extractUpstreamSeqs.R
getPromoterSeq-methods.R  makeTxDbPackage.R  select-methods.R
nearest-methods.R  transcriptLocs2refLocs.R
coordinate-mapping-methods.R  coverageByTranscript.R  zzz.R

**VignetteBuilder**  knitr

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

**NeedsCompilation**  no

**R topics documented:**

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Description

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

Usage

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

Arguments

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

Value

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

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

Author(s)

Michael Lawrence

Examples

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

txdb <- loadDb(txdb_file)

asBED(txdb)
asGFF(txdb)
```
Compute coverage by transcript (or CDS) of a set of ranges

**Description**

coverageByTranscript computes the transcript (or CDS) coverage of a set of ranges.

pcoverageByTranscript is a version of coverageByTranscript that operates element-wise.

**Usage**

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

**Arguments**

- **x**
  An object representing a set of ranges (typically aligned reads). GRanges, GRangesList, GAlignments, GAlignmentPairs, and GAlignmentsList objects are supported.
  More generally, for coverageByTranscript x can be any object for which seqinfo() and coverage() are supported (e.g. a BamFile object). Note that, for such objects, coverage() is expected to return an RleList object whose names are seqlevels(x)).
  More generally, for pcoverageByTranscript x can be any object for which grglist() is supported. It should have the length of transcripts or length 1. If the latter, it is recycled to the length of transcripts.

- **transcripts**
  A GRangesList object representing the exons of each transcript for which to compute coverage. For each transcript, the exons must be ordered by ascending rank, that is, by their position in the transcript. This means that, for a transcript located on the minus strand, the exons should typically be ordered by descending position on the reference genome. If transcripts was obtained with exonsBy, then the exons are guaranteed to be ordered by ascending rank. See ?exonsBy for more information.
  Alternatively transcripts can be any object for which exonsBy is implemented (e.g. a TxDb object), in which case it is replaced by the GRangesList object returned by exonsBy(transcripts, by="tx", use.names=TRUE).
  For pcoverageByTranscript, transcripts should have the length of x or length 1. If the latter, it is recycled to the length of x).

- **ignore.strand**
  TRUE or FALSE. If FALSE (the default) then the strand of a range in x and exon in transcripts must be the same in order for the range to contribute coverage to the exon. If TRUE then the strand is ignored.

- **...**
  Additional arguments passed to the internal call to grglist(). More precisely, when x is not a GRanges or GRangesList object, pcoverageByTranscript replace it by the GRangesList object returned by grglist(x, ...).

**Value**

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

Author(s)
Hervé Pagès

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

Examples

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

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

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

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

## We can also use pcoverageByTranscript() to compute 'tx_cvg'.
## For this we first create a GAlignmentsList object "parallel" to 'transcripts' where the i-th list element contains the aligned reads that overlap with the i-th transcript:
hits <- findOverlaps(reads, transcripts, ignore.strand=TRUE)

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

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

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

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

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

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

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

cds_cvg <- coverageByTranscript(reads, cds, ignore.strand=TRUE)
cds_cvg

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

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

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

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

utr5_width <- tx_lens$utr5_len
utr3_width <- tx_lens$utr3_len

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

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

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

Description

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

Usage

DEFAULT_CIRC_SEQS

See Also

makeTxDbFromUCSC, makeTxDbFromBiomart

Examples

DEFAULT_CIRC_SEQS

disjointExons

Extract non-overlapping exon parts from an object

Description

disjointExons extracts the non-overlapping exon parts from a TxDb object or any other supported object.

Usage

disjointExons(x, ...)

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

Arguments

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

Details

disjointExons creates a GRanges of non-overlapping exon parts with metadata columns of gene_id and exonic_part. Exon parts that overlap more than 1 gene can be dropped with aggregateGenes=FALSE. When includeTranscripts=TRUE a tx_name metadata column is included that lists all transcript names that overlap the exon fragment. This function replaces prepareAnnotationForDEXSeq in the DEXSeq package.
extractTranscriptSeqs

Value

A GRanges object.

Author(s)

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

See Also

- transcripts, transcriptsBy, and transcriptsByOverlaps for the core genomic features extractors.
- The TxDb class.

Examples

```r
## TODO
```

---

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

**Description**

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

**Usage**

```r
evaluateTranscriptSeqs(x, transcripts, ...)
```

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

## S4 method for signature 'ANY'
evaluateTranscriptSeqs(x, transcripts, ...)

**Arguments**

- **x**
  - An object representing a single chromosome or a collection of chromosomes. More precisely, x can be a DNAString object (single chromosome), or a BSgenome object (collection of chromosomes).
  - Other objects representing a collection of chromosomes are supported (e.g. FaFile objects in the Rsamtools package) as long as seqinfo and getSeq work on them.

- **transcripts**
  - An object representing the exon ranges of each transcript to extract. More precisely:
    - If x is a DNAString object, then transcripts must be a RangesList object.
• If x is a `BSgenome` object or any object representing a collection of chromosomes, then transcripts must be a `GRangesList` object or any object for which `exonsBy` is implemented (e.g. a `TxDb` object). If the latter, then it’s first turned into a `GRangesList` object with `exonsBy(transcripts, by="tx", ...)`. Note that, for each transcript, the exons must be ordered by ascending rank, that is, by ascending position in the transcript (when going in the 5’ to 3’ direction). This generally means (but not always) that they are also ordered from 5’ to 3’ on the reference genome. More precisely:

• For a transcript located on the plus strand, the exons will typically (but not necessarily) be ordered by ascending position on the reference genome.

• For a transcript located on the minus strand, the exons will typically (but not necessarily) be ordered by descending position on the reference genome.

If transcripts was obtained with `exonsBy` (see above), then the exons are guaranteed to be ordered by ascending rank. See `?exonsBy` for more information.

Additional arguments, for use in specific methods.

For the default method, additional arguments are allowed only when transcripts is not a `GRangesList` object, in which case they are passed to the internal call to `exonsBy` (see above).

`strand` Only supported when x is a `DNAString` object.

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

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

strand can only contain “+” and/or “-” values. “*” is not allowed.

Value

A `DNAStringSet` object parallel to transcripts, that is, the i-th element in it is the sequence of the i-th transcript in transcripts.

Author(s)

Hervé Pagès

See Also

• `coverageByTranscript` for computing coverage by transcript (or CDS) of a set of ranges.

• `transcriptLengths` for extracting the transcript lengths from a `TxDb` object.

• The `transcriptLocs2refLocs` function for converting transcript-based locations into reference-based locations.

• The `available.genomes` function in the `BSgenome` package for checking availability of BSgenome data packages (and installing the desired one).
• The `DNAString` and `DNASTringSet` classes defined and documented in the `Biostrings` package.
• The `translate` function in the `Biostrings` package for translating DNA or RNA sequences into amino acid sequences.
• The `GRangesList` class defined and documented in the `GenomicRanges` package.
• The `RangesList` class defined and documented in the `IRanges` package.
• The `exonsBy` function for extracting exon ranges grouped by transcript.
• The `TxDb` class.

**Examples**

```r
## ---------------------------------------------------------------------
## 1. A TOY EXAMPLE
## ---------------------------------------------------------------------
library(Biostrings)

## A chromosome of length 30:
x <- DNAString("ATTTAGGACACTCCCTGAGGACAAGACCCC")

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

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

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

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

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

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

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

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

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

```
txdb <- loadDb(txdb_file)

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

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

## Extract the transcript sequences from the genome:

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

## Note that 'tx_seqs' can also be obtained with:

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

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

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

## Note that, alternatively, the CDS sequences can be obtained from the
## transcript sequences by removing the 5' and 3' UTRs:
tx_lens <- transcriptLengths(txdb, with.utr5_len=TRUE, with.utr3_len=TRUE)
stopifnot(identical(tx_lens$tx_name, names(tx_seqs))) # sanity

## and put them in the same order as in 'cds_seqs':
m <- match(names(cds_seqs), names(tx_seqs))
tx_lens <- tx_lens[m,]
utr5_width <- tx_lens$utr5_len
utr3_width <- tx_lens$utr3_len
cds_seqs2 <- narrow(tx_seqs[m],
   start=utr5_width+1L, end=-(utr3_width+1L))
stopifnot(identical(as.character(cds_seqs2), as.character(cds_seqs)))

## 4. TRANSLATE THE CDS SEQUENCES

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

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

Extract sequences upstream of a set of genes or transcripts

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

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

## Dispatch is on the 2nd argument!

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

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

Arguments

x
An object containing the chromosome sequences from which to extract the upstream sequences. It can be a BSgenome, TwoBitFile, or FaFile object, or any genome sequence container. More formally, x must be an object for which seqinfo and getSeq are defined.

genes
An object containing the locations (i.e. chromosome name, start, end, and strand) of the genes or transcripts with respect to the reference genome. Only GenomicRanges and TxDb objects are supported at the moment. If the latter, the gene locations are obtained by calling the genes function on the TxDb object internally.

width
How many bases to extract upstream of each TSS (transcription start site).

... Additional arguments, for use in specific methods.

exclude.seqlevels
A character vector containing the chromosome names (a.k.a. sequence levels) to exclude when the genes are obtained from a TxDb object.

Value

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

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

If genes is a TxDb object, the names on the returned object are the gene IDs found in the TxDb object. To see the type of gene IDs (i.e. Entrez gene ID or Ensembl gene ID or ...), you can display genes with show(genes).
In addition, the returned object has the following metadata columns (accessible with `mcols`) that provide some information about the gene (or transcript) corresponding to each upstream sequence:

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

**Note**

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

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

**Author(s)**

Hervé Pagès

**See Also**

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

**Examples**

```r
eekUpstreamSeqs

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

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

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

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

FeatureDb-class

FeatureDb objects

Description

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

See ?TxDb for a container for storing transcript annotations.

See ?makeFeatureDbFromUCSC for a convenient way to make FeatureDb objects from BioMart
online resources.

Methods

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

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

Author(s)

Marc Carlson

See Also

• The TxDb class for storing transcript annotations.
• makeFeatureDbFromUCSC for a convenient way to make a FeatureDb object from UCSC on-
line 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=2000, downstream=200, ...)

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

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

Arguments

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

Details

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

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

Value

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

Author(s)

Paul Shannon

See Also

intra-range-methods ## promoters methods for Ranges objects intra-range-methods ## promoters methods for GRanges objects getSeq

Examples

```r
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"] GCTTCTGGA GCTTCTGGA 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 TxDb object.

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

Details

Transcripts, exons and CDS in a TxDb object are stored in separate tables where the primary key is an integer called feature internal id. This id is stored in the "tx_id" column for transcripts, in the "exon_id" column for exons, and in the "cds_id" column for CDS. Unlike other commonly used ids like Entrez Gene IDs or Ensembl IDs, this internal id was generated at the time the TxDb object was created and has no meaning outside the scope of this object.

The id2name function can be used to translate this internal id into a more informative id or name called feature external name. This name is stored in the "tx_name" column for transcripts, in the "exon_name" column for exons, and in the "cds_name" column for CDS.

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

Value

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

Author(s)

Hervé Pagès

See Also

- transcripts, transcriptsBy, and transcriptsByOverlaps, for how to extract genomic features from a TxDb object.
- The TxDb class.
makeFeatureDbFromUCSC

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

Description

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

Usage

supportedUCSCFeatureDbTracks(genome)

supportedUCSCFeatureDbTables(genome, track)

UCSCFeatureDbTableSchema(genome, track, tablename)

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

genome
 genome abbreviation used by UCSC and obtained by \texttt{ucscGenomes()[, "db"]}. For example: "hg18".

track
 name of the UCSC track. Use \texttt{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 \texttt{supportedUCSCFeatureDbTables} utility function to get the list of supported tables for a track.

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

url,goldenPath_url
 use to specify the location of an alternate UCSC Genome Browser.

chromCol
 If the schema comes back and the 'chrom' column has been labeled something other than 'chrom', use this argument to indicate what that column has been labeled as so we can properly designate it. This could happen (for example) with the knownGene track tables, which has no 'chromStart' or 'chromEnd' columns, but which DOES have columns that could reasonably substitute for these columns under particular circumstances. Therefore we allow these three columns to have arguments so that their definition can be re-specified

chromStartCol
 Same thing as chromCol, but for renames of 'chromStart'

chromEndCol
 Same thing as chromCol, but for renames of 'chromEnd'

taxonomyId
 By default this value is NA and the organism inferred will be used to look up the correct value for this. But you can use this argument to override that and supply your own valid taxId here.

Details

\texttt{makeFeatureDbFromUCSC} is a convenience function that builds a tiny database from one of the UCSC track tables. \texttt{supportedUCSCFeatureDbTracks} a convenience function that returns potential track names that could be used to make FeatureDb objects \texttt{supportedUCSCFeatureDbTables} a convenience function that returns potential table names for FeatureDb objects (table names go with a track name) \texttt{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 \texttt{FeatureDb} object for \texttt{makeFeatureDbFromUCSC}. Or in the case of \texttt{supportedUCSCFeatureDbTracks} and \texttt{UCSCFeatureDbTableSchema} a named character vector

Author(s)

M. Carlson

See Also

\texttt{ucscGenomes},
Examples

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

## Display the list of Tracks supported by makeFeatureDbFromUCSC():
# supportedUCSCFeatureDbTracks("mm10")

## Display the list of tables supported by your track:
supportedUCSCFeatureDbTables(genome="mm10",
   track="qPCR Primers")

## Display fields that could be passed in to colnames:
UCSCFeatureDbTableSchema(genome="mm10",
   track="qPCR Primers",
   tablename="qPcrPrimers")

## Retrieving a full transcript dataset for Mouse from UCSC:
fdb <- makeFeatureDbFromUCSC(genome="mm10",
   track="qPCR Primers",
   tablename="qPcrPrimers")

fdb
```

---

**makeTxDb**

*Making a TxDb object from user supplied annotations*

**Description**

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

**Usage**

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

**Arguments**

- **transcripts**: data frame containing the genomic locations of a set of transcripts
- **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 organism, genome, UCSC table, etc... The names of the columns must be "name" and "value" and their type must be character.
reassign.ids controls how internal ids should be assigned for each type of feature i.e. for transcripts, exons, and cds. For each type, if reassign.ids is FALSE and if the ids are supplied, then they are used as the internal ids, otherwise the internal ids are assigned in a way that is compatible with the order defined by ordering the features first by chromosome, then by strand, then by start, and finally by end.

**Details**

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

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

- **tx_id**: Transcript ID. Integer vector. No NAs. No duplicates.
- **tx_name**: [optional] Transcript name. Character vector (or factor). NAs and/or duplicates are ok.
- **tx_type**: [optional] Transcript type (e.g. mRNA, ncRNA, snoRNA, etc...). Character vector (or factor). NAs and/or duplicates are ok.
- **tx_chrom**: Transcript chromosome. Character vector (or factor) with no NAs.
- **tx_strand**: Transcript strand. Character vector (or factor) with no NAs where each element is either "+" or "-".
- **tx_start, tx_end**: Transcript start and end. Integer vectors with no NAs.

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

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

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

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

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

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

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

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

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

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

Value

A TxDb object.

Author(s)

Hervé Pagès

See Also

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

Examples

transcripts <- data.frame(
  tx_id=1:3,
  tx_chrom="chr1",
  tx_strand=c("-", "+", "+"),
  tx_start=c(1, 2001, 2001),
  tx_end=c(999, 2199, 2199))
splicings <- data.frame(
  tx_id=c(1L, 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),
makeTxDbFromBiomart

Make a TxDb object from annotations available on a BioMart database

Description

The makeTxDbFromBiomart function allows the user to make a TxDb object from transcript annotations available on a BioMart database.

Usage

makeTxDbFromBiomart(biomart="ENSEMBL_MART_ENSEMBL",
    dataset="hsapiens_gene_ensembl",
    transcript_ids=NULL,
    circ_seqs=DEFAULT_CIRC_SEQS,
    filter=NULL,
    id_prefix="ensembl_",
    host="www.ensembl.org",
    port=80,
    taxonomyId=NA,
    miRBaseBuild=NA)

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

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_ensembl", "dmelanogaster_gene_ensembl", "celegans_gene_ensembl", "scerevisiae_gene_ensembl", etc in the ensembl database. See the examples section below for how to discover which datasets are available in a given BioMart database.

transcript_ids optionally, only retrieve transcript annotation data for the specified set of transcript ids. If this is used, then the meta information displayed for the resulting TxDb 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.

filter Additional filters to use in the BioMart query. Must be a named list. An example is filter=list(source="entrez")

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_".

cds_end=c(999, 2085, 2144, 2193, NA, NA))

txdb <- makeTxDb(transcripts, splicings)
host

port
The port to use in the HTTP communication with the host.

taxonomyId
By default this value is NA and the dataset selected will be used to look up the correct value for this. But you can use this argument to override that and supply your own taxId here (which will be independently checked to make sure its a real taxonomy id). Normally you should never need to use this.

miRBaseBuild
specify the string for the appropriate build Information from mirbase.db to use for microRNAs. This can be learned by calling supportedMiRBaseBuildValues. By default, this value will be set to NA, which will inactivate the microRNAs accessor.

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

Here is a list of datasets known to be compatible with makeTxDbFromBiomart (updated on November 12, 2015):

- All the datasets in the main Ensembl database (list them with biomaRt::listDatasets(biomaRt::useMart(biomart="ENSEMBL\_MART\_ENSEMBL", host="www.ensembl.org"))).
- All the datasets in the Ensembl Fungi database (list them with biomaRt::listDatasets(biomaRt::useMart(biomart="fungal\_mart", host="fungi.ensembl.org"))).
- All the datasets in the Ensembl Metazoa database (list them with biomaRt::listDatasets(biomaRt::useMart(biomart="metazoa\_mart", host="metazoa.ensembl.org"))).
- All the datasets in the Ensembl Plants database (list them with biomaRt::listDatasets(biomaRt::useMart(biomart="plants\_mart", host="plants.ensembl.org"))).
- All the datasets in the Ensembl Protists database (list them with biomaRt::listDatasets(biomaRt::useMart(biomart="protist\_mart", host="protists.ensembl.org"))).
- All the datasets in the Gramene Mart (list them with biomaRt::listDatasets(biomaRt::useMart(biomart="ENSEMBL\_MART\_PLANT", host="ensembl.gramene.org"))).

Not all these datasets have CDS information.

Value
A TxDb object for makeTxDbFromBiomart.
A data frame with 1 row per chromosome (or scaffold) and with columns chrom and length for getChromInfoFromBiomart.

Author(s)
M. Carlson and H. Pagès

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

Examples

```r
## A. BASIC USAGE
## ---------------------------------------------------------------------
## We can use listDatasets() from the biomaRt package to list the
datasets available in the "ENSEMBL_MART_ENSEMBL" BioMart database:
library(biomaRt)
listMarts(host="www.ensembl.org")
datasets <- listDatasets(useMart(biomart="ENSEMBL_MART_ENSEMBL", host="www.ensembl.org"))
head(datasets)
subset(datasets, grepl("elegans", dataset, ignore.case=TRUE))

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

## Retrieve an incomplete transcript dataset for Human:
 transcript_ids <- c("ENST00000013894", "ENST00000268655", "ENST00000313243", "ENST00000435657", "ENST00000384428", "ENST00000478783")

if (interactive()) {
  txdb2 <- makeTxDbFromBiomart(dataset="hsapiens_gene_ensembl", transcript_ids=transcript_ids)
  txdb2 # note that these annotations match the GRCh38 genome assembly
}

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

## Therefore in addition to setting 'host' to "uswest.ensembl.org" we
## might also need to specify the 'biomart' argument:
if (interactive()) {
```
makeTxDbFromGFF

## Description

The `makeTxDbFromGFF` function allows the user to make a `TxDb` object from transcript annotations available as a GFF3 or GTF file.

## Usage

```r
makeTxDbFromGFF(file,
    format=c("auto", "gff3", "gtf"),
    dataSource=NA,
    organism=NA,
    taxonomyId=NA,
    circ_seqs=DEFAULT_CIRC_SEQS,
    chrominfo=NULL,
    
    txdb3 <- makeTxDbFromBiomart(biomart="ENSEMBL_MART_ENSEMBL",
                                  dataset="hsapiens_gene_ensembl",
                                  transcript_ids=transcript_ids,
                                  host="useast.ensembl.org")

    txdb3

## C. USING FILTERS

## We can use listFilters() from the biomaRt package to get valid filter
## names:

```
makeTxDbFromGFF

miRBaseBuild=NA,
dbxrefTag)

Arguments

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

Details

makeTxDbFromGFF is a convenience function that feeds data from the parsed file to the makeTxDbFromGRanges
function.

Value

A TxDb object.

Author(s)

M. Carlson and H. Pagès

See Also

- makeTxDbFromGRanges, which makeTxDbFromGFF is based on, for making a TxDb object
  from a GRanges object.
- The import function in the rtracklayer package (also used by makeTxDbFromGFF internally).
makeTxDbFromGRanges

Make a TxDb object from a GRanges object

Description

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

Usage

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

Arguments

gr          A GRanges object structured as GFF3 or GTF, typically obtained with rtracklayer::import().
drop.stop.codons
TRUE or FALSE. If TRUE, then features of type stop_codon are ignored. Otherwise (the default) the stop codons are considered to be part of the CDS and merged to them.
makeTxDbFromGRanges

metadata

A 2-column data frame containing meta information to be included in the TxDb object. This data frame is just passed to makeTxDb, which calls at the end to make the TxDb object from the information extracted from gr. See ?makeTxDb for more information about the format of metadata.

taxonomyId

By default this value is NA which will result in an NA field since there is no reliable way to infer this from a GRanges object. But you can use this argument to supply your own valid taxId here and if you do, then the Organism can be filled in as well

Value

A TxDb object.

Author(s)

Hervé Pagès

See Also

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

Examples

library(rtracklayer) # for the import() function

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

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

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

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

## WITH A GRanges OBJECT STRUCTURED AS GTF
GTF_files <- system.file("extdata", "GTF_files", package="GenomicFeatures")
## test1.gtf was grabbed from http://mblab.wustl.edu/GTF22.html (5 exon gene with 3 translated exons):

```r
path <- file.path(GTF_files, "test1.gtf")
gr <- import(path)
txdb <- makeTxDbFromGRanges(gr)
txdb

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

---

### makeTxDbFromUCSC

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

**Description**

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

**Usage**

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

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>genome</td>
<td>genome abbreviation used by UCSC and obtained by <code>ucscGenomes()[ , &quot;db&quot;]</code>. For example: &quot;hg19&quot;.</td>
</tr>
<tr>
<td>tablename</td>
<td>name of the UCSC table containing the transcript annotations to retrieve. Use the supportedUCSCtables utility function to get the list of tables known to work with <code>makeTxDbFromUCSC</code>.</td>
</tr>
</tbody>
</table>
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 TxDb object will say 'Full dataset: no'. Otherwise it will say 'Full dataset: yes'.

circ_segs  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.

taxonomyId  By default this value is NA and the organism inferred will be used to look up the correct value for this. But you can use this argument to supply your own valid taxId here.

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 set to NA, which will inactivate the microRNAs accessor.

Details

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

Value

For makeTxDbFromUCSC: A TxDb object.

For supportedUCSCtables: A data frame with 3 columns (tablename, track, and subtrack) and 1 row per table known to work with makeTxDbFromUCSC. IMPORTANT NOTE: In the returned data frame, the set of tables associated with a track with subtracks might contain tables that don’t exist for the specified genome.

For getChromInfoFromUCSC: A data frame with 1 row per chromosome (or scaffold) and with columns chrom and length.

Author(s)

M. Carlson and H. Pagès

See Also

- makeTxDbFromBiomart, makeTxDbFromGRanges, and makeTxDbFromGFF, for convenient ways to make a TxDb object from BioMart online resources, or from a GRanges object, or from a GFF or GTF file.
- ucscGenomes in the rtracklayer package.
- DEFAULT_CIRC_SEQS.
- The supportedMiRBaseBuildValues function for listing all the possible values for the miRBaseBuild argument.
- The TxDb class.
- makeTxDb for the low-level function used by the makeTxDbFrom* functions to make the TxDb object returned to the user.
Examples

```r
## A. BASIC USAGE
library(rtracklayer)
ucscGenomes()

## Display the list of tables known to work with makeTxDbFromUCSC():
supportedUCSCtables()

## Browse the UCSC track page for a given organism/table:
browseUCSCtrack(genome="sacCer3", tablename="ensGene")

## Retrieve a full transcript dataset for Yeast from UCSC:
txdb1 <- makeTxDbFromUCSC(genome="sacCer3", tablename="ensGene",
circ_seqs="chrM")

## Retrieve 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 <- makeTxDbFromUCSC(genome="mm10", tablename="knownGene",
transcript_ids=transcript_ids,
circ_seqs="chrM")

## B. IMPORTANT NOTE ABOUT supportedUCSCtables()

## In the data frame returned by supportedUCSCtables(), the set of tables associated with a track with subtracks might contain tables that don't exist for the specified genome:
supported_tables <- supportedUCSCtables("hg38")
browseUCSCtrack(genome="hg38", tablename="augustusHints")  # no such table

## C. RETRIEVING CHROMOSOME INFORMATION ONLY

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

makeTxDbPackage

Making a TxDb package from annotations available at the UCSC Genome Browser, biomaRt or from another source.

Description

A TxDb package is an annotation package containing a TxDb object.

The makeTxDbPackageFromUCSC function allows the user to make a TxDb package from transcript annotations available at the UCSC Genome Browser.

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

Finally, the makeTxDbPackage function allows the user to make a TxDb package directly from a TxDb object.

Usage

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

makeFDbPackageFromUCSC(
    version, maintainer, author, destDir=".", license="Artistic-2.0", genome="hg19", track="tRNAs", tablename="tRNAs", columns = UCSCFeatureDbTableSchema(genome, track, tablename), url="http://genome.ucsc.edu/cgi-bin/", goldenPath_url="http://hgdownload.cse.ucsc.edu/goldenPath", chromCol=NULL, chromStartCol=NULL, chromEndCol=NULL, taxonomyId=NA)

makeTxDbPackageFromBiomart(
    version,
makeTxDbPackage

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

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

supportedMiRBaseBuildValues()

Arguments

version  What is the version number for this package?
maintainer  Who is the package maintainer? (must include email to be valid). Should be a person object, or something coercible to one, like a string. May be omitted if the author argument is a person containing someone with the maintainer role.
author  Who is the creator of this package? Should be a person object, or something coercible to one, like a character vector of names. The maintainer argument will be merged into this list.
destDir  A path where the package source should be assembled.
license  What is the license (and it's version)
biomart  which BioMart database to use. Get the list of all available BioMart databases with the 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_ensembl", "dmelanogaster_gene_ensembl", "celegans_gene_ensembl", "scerevisiae_gene_ensembl", etc in the ensembl database. See the examples section below for how to discover which datasets are available in a given BioMart database.
genome  genome abbreviation used by UCSC and obtained by 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 tables known to work with makeTxDbFromUCSC.

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 TxDb object will say 'Full dataset: no'. Otherwise it will say 'Full dataset: yes'.

circ_segs

a character vector to list out which chromosomes should be marked as circular.

filter

Additional filters to use in the BioMart query. Must be a named list. An example is filter=as.list(c(source="entrez"))

host


port

The port to use in the HTTP communication with the host.

id_prefix

Specifies the prefix used in BioMart attributes. For example, some BioMarts may have an attribute specified as "ensembl_transcript_id" whereas others have the same attribute specified as "transcript_id". Defaults to "ensembl_".

columns

a named character vector to list out the names and types of the other columns that the downloaded track should have. Use 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 TxDb object that represents a handle to a transcript database. This object type is what is returned by makeTxDbFromUCSC, makeTxDbFromUCSC or makeTxDb

taxonomyId

By default this value is NA and the organism provided (or inferred) will be used to look up the correct value for this. But you can use this argument to override that and supply your own valid taxId here

miRBaseBuild

specify the string for the appropriate build Information from mirbase.db to use for microRNAs. This can be learned by calling supportedMiRBaseBuildValues. By default, this value will be set to NA, which will inactivate the microRNAs accessor.

pkgname

By default this value is NULL and does not need to be filled in (a package name will be generated for you). But if you override this value, then the package and it's object will be instead named after this value. Be aware that the standard rules for package names will apply, (so don't include spaces, underscores or dashes)

provider

If not given, a default is taken from the 'Data source' field of the metadata table.

providerVersion

If not given, a default is taken from one of 'UCSC table', 'BioMart version' or 'Data source' fields of the metadata table.
makeTxDbPackage

Details

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

Value

A TxDb object.

Author(s)

M. Carlson

See Also

makeTxDbFromUCSC, makeTxDbFromBiomart, makeTxDb, ucscGenomes, DEFAULT_CIRC_SEQS

Examples

```r
## First consider relevant helper/discovery functions:
## Get the list of tables known to work with makeTxDbPackageFromUCSC():
supportedUCSCtables(genome="hg19")

## 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)
```
mapIdsToRanges  

Map IDs to Genomic Ranges

Description

Map IDs to Genomic Ranges

Usage

mapIdsToRanges(x, ...)  

## S4 method for signature 'TxDb'
mapIdsToRanges(x, keys, type = c("cds", "exon", "tx", 
"gene"), columns = NULL)

Arguments

x  
Database to use for mapping

keys  
Values to lookup, passed to transcripts et. al.

type  
Types of feature to return

columns  
Additional metadata columns to include in the output

...  
Additional arguments passed to methods

Value

GRangesList corresponding to the keys

Methods (by class)

- TxDb: TxDb method

Examples

fl <- system.file(package = "GenomicFeatures", "extdata", "sample_ranges.rds")
txdb <- makeTxDbFromGRanges(readRDS(fl))

keys <- list(tx_name = c("ENST00000371582", "ENST00000371588", 
"ENST00000494752", "ENST00000614008", "ENST00000496771"))
mapIdsToRanges(txdb, keys = keys, type = "tx")
mapRangesToIds  Map Genomic Ranges to IDs

Description
Map Genomic Ranges to IDs

Usage
mapRangesToIds(x, ...)

## S4 method for signature 'TxDb'
mapRangesToIds(x, ranges, type = c("cds", "exon", "tx", "gene"), columns = NULL, ...)

Arguments
- x  Database to use for mapping
- ranges range object used to subset
- type of feature to return
- columns additional metadata columns to include in the output.
- ... Additional arguments passed to findOverlaps

Value
DataFrame of mcols from the database.

Methods (by class)
- TxDB: TxDB method

Examples
fl <- system.file(package = "GenomicFeatures", "extdata", "sample_ranges.rds")
taxdb <- makeTxDbFromGRanges(readRDS(fl))

keys <- list(tx_name = c("ENST00000371582", "ENST00000371588", "ENST00000494752", "ENST00000614008", "ENST00000496771"))
res <- mapIdsToRanges(txdb, keys = keys, type = "tx")
mapRangesToIds(txdb, res, "tx")
**mapToTranscripts**  
*Map range coordinates between transcripts and genome space*

**Description**

Map range coordinates between features in the transcriptome and genome (reference) space.  
See ?mapToAlignments in the GenomicAlignments package for mapping coordinates between reads (local) and genome (reference) space using a CIGAR alignment.

**Usage**

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

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

**Arguments**

- `x`  
  GenomicRanges object of positions to be mapped. The seqnames of x are used in mapFromTranscripts, i.e., when mapping from transcripts to the genome. In the case of pmapFromTranscripts, x can be a Ranges object.

- `transcripts`  
  A named GenomicRanges or GRangesList object used to map between x and the result. The ranges can be any feature in the transcriptome extracted from a TxDb (e.g., introns, exons, cds regions). See ?transcripts and ?transcriptsBy for a list of extractor functions.

  The transcripts object must have names. When mapping from transcripts to the genome, they are used to determine mapping pairs; in the reverse direction they become the seqlevels of the output object.

- `ignore.strand`  
  When ignore.strand is TRUE, strand is ignored in overlaps operations (i.e., all strands are considered "+") and the strand in the output is "*".

When `ignore.strand` is `FALSE` strand in the output is taken from the `transcripts` argument. When `transcripts` is a `GRangesList`, all inner list elements of a common list element must have the same strand or an error is thrown. Mapped position is computed by counting from the transcription start site (TSS) and is not affected by the value of `ignore.strand`.

### intronJunctions

Logical to indicate whether intronic ranges in `x` should be reported. Ranges in `x` that do not fall ‘within’ a range in `transcripts` are considered a non-hit and have no mapping. When `intronJunctions=TRUE` the non-hits that fall between 2 ranges in `transcripts` are reported as a zero-width range (start and end taken from the ranges they fall between). To be considered ‘intronic’, the `x` range must fall between ranges in `transcripts`. Those that ‘fall off’ either end or overlap the intron gap and a range in `transcripts` will not be mapped. This argument is only supported in `mapToTranscripts` when `transcripts` is a `GRangesList`.

### extractor.fun

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

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

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

### Details

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

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

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

\( \text{mapToTranscripts} \) uses \( \text{findOverlaps} \) to map ranges in \( x \) to ranges in transcripts. This method does not return unmapped ranges.

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

• \( \text{mapFromTranscripts}, \text{pmapFromTranscripts} \) The transcript-based position in \( x \) is mapped to genomic coordinates using the ranges in transcripts. A successful mapping occurs when the following is TRUE:

\[
\text{width(transcripts)} \geq \text{start}(x) + \text{width}(x)
\]

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

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

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

**Value**

\( \text{pmapToTranscripts} \) returns a \text{GRanges} the same length as \( x \).

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

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

When \text{intronJunctions} is \text{TRUE}, \text{mapToTranscripts} returns an extra metadata column named \text{intronic} to identify the intron ranges.

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

**Author(s)**

V. Obenchain, M. Lawrence and H. Pagès
mapToTranscripts

See Also

- ?mapToAlignments in the GenomicAlignments package for methods mapping between reads and genome space using a CIGAR alignment.

Examples

```r
## A. Basic Use
## ------------------------------------
## (i) Map from genome to transcript:
## The seqnames of the output are the transcript names, not chromosomes. For this reason 'transcripts' must be named.
x <- GRanges("A", IRanges(16, 18))
gr1 <- GRanges("A", IRanges(1, 10, names="tx_a"))
gr2 <- GRanges("A", IRanges(15, 20, names="tx_b"))
## 'transcripts' as GRanges:
mapToTranscripts(x, gr2)
## 'transcripts' as GRangesList:
mapToTranscripts(x, GRangesList("tx_c" = c(gr1, gr2)))
## Round trip from genomic -> transcript -> genomic coordinates:
tx_coord <- mapToTranscripts(x, gr2)
mapFromTranscripts(tx_coord, gr2)
## ------------------------------------
## (ii) Map from transcript to genome:
## A prerequisite for mapping from transcript -> genome is that the seqname of the range in 'x' match the name of the range in 'transcripts'. Here the seqname of 'x' is "TX_1" and mapping is only attempted with the second range in 'gr':
x <- GRanges("TX_1", IRanges(5, 10))
gr <- GRanges("chr3", IRanges(c(1, 1), width=50, names=c("TX_2", "TX_1")))
mapFromTranscripts(x, gr)
## ------------------------------------
## (iii) Element-wise versions:
## Recycling is supported when length(transcripts) == 1; otherwise the lengths of 'x' and 'transcripts' must be the same.
x <- GRanges("A", IRanges(c(1, 5, 10), width=1))
transcripts <- GRanges("A", IRanges(4, 7))
pmapToTranscripts(x, transcripts)
## B. Map local sequence locations to the genome
## ------------------------------------
## NAGNAG alternative splicing plays an essential role in biological processes
```
## and represents a highly adaptable system for posttranslational regulation of gene function. The majority of NAGNAG studies largely focus on messenger RNA. A study by Sun, Lin, and Yan (http://www.hindawi.com/journals/bmri/2014/736798/) demonstrated that NAGNAG splicing is also operative in large intergenic noncoding RNA (lincRNA).

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

Extract the exon coordinates of TCONS_00010012 and TCONS_00010010:

```r
lincrna <- c("TCONS_00010012", "TCONS_00010010")
library(TxDb.Hsapiens.UCSC.hg19.lincRNAsTranscripts)
txdb <- TxDb.Hsapiens.UCSC.hg19.lincRNAsTranscripts
exons <- exonsBy(txdb, by="tx", use.names=TRUE)[lincrna]
exons
```

The two NAGNAG acceptors were identified in the upstream region of the fourth and fifth exons located in TCONS_00010012.

Extract the sequences for transcript TCONS_00010012:

```r
library(BSgenome.Hsapiens.UCSC.hg19)
genome <- BSgenome.Hsapiens.UCSC.hg19
exons_seq <- getSeq(genome, exons[[1]])
exons_seq
```

The most common triplet among the lincRNA sequences was CAG. Identify the location of this pattern in all exons:

```r
cag_loc <- vmatchPattern("CAG", exons_seq)
```

Convert the first occurrence of CAG in each exon back to genome coordinates.

```r
first_loc <- do.call(c, sapply(cag_loc, "+", 1, simplify=TRUE))
pmapFromTranscripts(first_loc, exons[[1]])
```

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


8 candidate miRNA genes on chromosome 12 were used to test for differential luciferase expression in mice. In Table 2 of the manuscript variant locations are given as nucleotide position within the gene.

```r
geneNames <- c("Bcap29", "Dgkb", "Etv1", "Hbp1", "Hbp1", "Ifrd1", "Ifrd1", "Pik3cg", "Pik3cg", "Tspan13", "Twistnb")
starts <- c(1409, 3170, 3132, 2437, 2626, 3239, 3261, 4947, 4979, 958, 1489)
```

snps <- GRanges(geneNames, IRanges(starts, width=1))

To map these transcript-space coordinates to the genome we need gene ranges in genome space.

```r
library(org.Mm.eg.db)
geneid <- select(org.Mm.eg.db, unique(geneNames), "ENTREZID", "SYMBOL")
```
geneid

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

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

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

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

## In this example 5 SNPs located in the GIPR gene are mapped to cDNA
## coordinates. A list of SNPs in GIPR can be downloaded from dbSNP or NCBI.
rsids <- c("rs4803846", "rs139322374", "rs7258736", "rs7258754", "rs9749185")

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

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

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

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

## Modify the style and genome in 'snps' to match 'cDNA'.
seqlevelsStyle(snps) <- seqlevelsStyle(cDNA)
genome(snps) <- genome(cDNA)
## The 'cDNA' object is a GRangesList of length 1. This single list element contains the cDNA range for 4 different transcripts. To map to each transcript individually 'cDNA' must be unlisted before mapping.

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

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

## The cdsBy() extractor returns coding regions by gene or by transcript.
## Extract the coding regions for transcript uc002pct.2.
cds <- cdsBy(txdb, "tx", use.names=TRUE)["uc002pct.2"]
cds

## The 'cds' object is a GRangesList of length 1 containing all cds ranges for the single transcript uc002pct.2.

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

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

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

## Change strand:
strand(cds) <- strand(snps) <- "-"
mapToTranscripts(snps[2], unlist(cds))

---

**microRNAs**

*Extract microRNA or tRNA genomic ranges from an object*

### Description

Generic functions to extract microRNA or tRNA genomic ranges from an object. This page documents the methods for `TxDb` objects only.

### Usage

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

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

### Arguments

- `x` A `TxDb` object.
nearest-methods

Finding the nearest genomic range neighbor in a TxDb

Description
The distance methods for TxDb objects and subclasses.

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

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

Value
A GRanges object.

Author(s)
M. Carlson

See Also
• transcripts, transcriptsBy, and transcriptsByOverlaps for the core genomic features
extractors.
• The TxDb class.

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

- distance: Returns the distance for each range in x to the range extracted from the TxDb object y. Values in id are matched to one of 'gene_id', 'tx_id', 'exon_id' or 'cds_id' identifiers in the TxDb and the corresponding ranges are extracted. The type argument specifies which identifier is represented in id. The extracted ranges are used in the distance calculation with the ranges in x.

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

Value

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

Author(s)

Valerie Obenchain <vobencha@fhcrc.org>

See Also

- nearest-methods man page in IRanges.
- nearest-methods man page in GenomicRanges.

Examples

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

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

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

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

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

# End(Not run)
```
select-methods

Using the "select" interface on TxDb objects

Description

select, columns and keys can be used together to extract data from a TxDb object.

Details

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

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

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

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

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

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

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

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

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

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

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

Author(s)

Marc Carlson

See Also

- AnnotationDb-class for more description of methods select, keytypes, keys and columns.
- transcripts, transcriptsBy, and transcriptsByOverlaps, for other ways to extract genomic features from a TxDb object.
- The TxDb class.

Examples

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

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

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

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

---

transcriptLengths

Extract the transcript lengths from a TxDb object

### Description

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

### Usage

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

### Arguments

- **txdb**
  A `TxDb` object.

- **with.cds_len**, **with.utr5_len**, **with.utr3_len**
  TRUE or FALSE. Whether or not to also extract and return the CDS, 5' UTR, and 3' UTR lengths for each transcript.

- **...**
  Additional arguments used by `transcripts` and other accessor functions.

### Details

All the lengths are counted in number of nucleotides.

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

### Value

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

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

```r
transcripts(txdb, columns=c("tx_id", "tx_name", "gene_id"))
```
that is:

- **tx_id**: The internal transcript ID. This ID is unique within the scope of the `TxDb` object. It is not an official or public ID (like an Ensembl or FlyBase ID) or an Accession number, so it cannot be used to lookup the transcript in public data bases or in other `TxDb` objects. Furthermore, this ID could change when re-running the code that was used to make the `TxDb` object.

- **tx_name**: An official/public transcript name or ID that can be used to lookup the transcript in public data bases or in other `TxDb` objects. This column is not guaranteed to contain unique values and it can contain NAs.

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

The other columns are quantitative:

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

**Author(s)**

Hervé Pagès

**See Also**

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

**Examples**

```r
library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)

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

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

head(dm3_txlens)

# When cds_len is 0 (non-coding transcript), utr5_len and utr3_len
# must also be 0:
non_coding <- dm3_txlens[dm3_txlens$cds_len == 0, ]
stopifnot(all(non_coding[6:8] == 0))
```
transcriptLocs2refLocs

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

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

transcriptLocs2refLocs

Converting transcript-based locations into reference-based locations

Description

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

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

Usage

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

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

Arguments

tlocs A list of integer vectors of the same length as exonStarts and exonEnds. Each element in tlocs must contain transcript-based locations.
exonStarts, exonEnds The starts and ends of the exons, respectively. Each argument can be a list of integer vectors, an IntegerList object, or a character vector where each element is a comma-separated list of integers. In addition, the lists represented by exonStarts and exonEnds must have the same shape i.e. have the same lengths and have elements of the same lengths. The length of exonStarts and exonEnds is the number of transcripts.
strand A character vector of the same length as exonStarts and exonEnds specifying the strand ("+" or "+") from which the transcript is coming.
decreasing.rank.on.minus.strand TRUE or FALSE. Describes the order of exons in transcripts located on the minus strand: are they ordered by increasing (default) or decreasing rank?
error.if.out.of.bounds TRUE or FALSE. Controls how out of bound tlocs are handled: an error is thrown (default) or NA is returned.

Value

For transcriptLocs2refLocs: A list of integer vectors of the same shape as tlocs.
For transcriptWidths: An integer vector with one element per transcript.
transcriptLocs2refLocs

Author(s)
Hervé Pagès

See Also
- `extractTranscriptSeqs` for extracting transcript (or CDS) sequences from chromosomes.
- `coverageByTranscript` for computing coverage by transcript (or CDS) of a set of ranges.

Examples

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

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

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

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

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

Extract genomic features from an object

Description

Generic functions to extract genomic features from an object. This page documents the methods for \texttt{TxDb} objects only.

Usage

\begin{verbatim}
transcripts(x, ...)  # S4 method for signature 'TxDb'
transcripts(x, columns=c("tx_id", "tx_name"), filter=NULL, vals=NULL)

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

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

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

# S4 method for signature 'TxDb'
promoters(x, upstream=2000, downstream=200, ...)
\end{verbatim}
transcripts

Arguments

x   A TxDb object.

... For the transcripts, exons, cds, and genes generic functions: arguments to be passed to methods.

For the promoters method for TxDb objects: arguments to be passed to the internal call to transcripts.

columns Columns to include in the output. Must be NULL or a character vector as given by the columns method. With the following restrictions:

- "TXCHROM" and "TXSTRAND" are not allowed for transcripts.
- "EXONCHROM" and "EXONSTRAND" are not allowed for exons.
- "CDSCHROM" and "CDSSTRAND" 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.

filter 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".

vals Defunct. Please use the filter argument instead.

single.strand.genes.only TRUE or FALSE. If TRUE (the default), then genes that have exons located on both strands of the same chromosome or on two different chromosomes are dropped. In that case, the genes are returned in a GRanges object. Otherwise, all genes are returned in a GRangesList object with the columns specified thru the columns argument set as top level metadata columns. (Please keep in mind that the top level metadata columns of a GRangesList object are not displayed by the show method.)

upstream For promoters: An integer(1) value indicating the number of bases upstream from the transcription start site. For additional details see ?promoters,GRanges-method.

downstream For promoters: An integer(1) value indicating the number of bases downstream from the transcription start site. For additional details see ?promoters,GRanges-method.

Details

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

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

Value

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

Author(s)

M. Carlson, P. Aboyoun and H. Pagès
transcripts

See Also

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

Examples

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

## transcripts()

transcripts(txdb)

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

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

## exons()

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

## genes()

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

## Because we've returned single strand genes only, the "tx_chrom"
## and "exon_chrom" metadata columns are guaranteed to match
## transcriptsBy

TranscriptsBy is a function in the R programming language that is used to extract and group genomic features of a given type based on another type of genomic feature. This page documents the methods for TxDb objects only.

### Description

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

### Usage

```r
transcriptsBy(x, by=c("gene", "exon", "cds"), ...)  
```

### Examples

```r
all_genes <- genes(txdb, columns=cols, single.strand.genes.only=FALSE)  
multiple_strand_genes <- all_genes[elementNROWS(all_genes) >= 2]  
```

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

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

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

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

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

### Arguments

- **x**  
  A `TxDb` 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 NaNs). 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` or `cdsBy` with `by = "tx"`, the returned exons or CDS are ordered by ascending rank for each transcript, that is, by their position in the transcript. In all other cases, the ranges will be ordered by chromosome, strand, start, and end values.

### Value

A `GRangesList` object.

### Author(s)

M. Carlson, P. Aboyoun and H. Pagès
transcriptsByOverlaps

See Also

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

Examples

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

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

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

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

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

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

Description

Generic functions to extract genomic features for specified genomic locations. This page documents the methods for TxDb objects only.
transcriptsByOverlaps

Usage

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

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

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

Arguments

x
    A TxDb 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 `TxDb` object.
- `select-methods` for how to use the simple "select" interface to extract information from a `TxDb` object.
- `id2name` for mapping `TxDb` internal ids to external names for a given feature type.
- The `TxDb` class.

Examples

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

Description

The `TxDb` class is a container for storing transcript annotations.

See `?FeatureDb` for a more generic container for storing genomic locations of an arbitrary type of genomic features.

See `?makeTxDbFromUCSC` and `?makeTxDbFromBiomart` for convenient ways to make `TxDb` objects from UCSC or BioMart online resources.

See `?makeTxDbFromGFF` for making a `TxDb` object from annotations available as a GFF3 or GTF file.

Methods

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

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

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

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

`seqinfo(x), seqinfo(x) <- value`: Get or set the information about the underlying sequences.

Note that, for now, the setter only supports replacement of the sequence names, i.e., except for their sequence names (accessed with `seqnames(value)` and `seqnames(seqinfo(x))`, respectively), `Seqinfo` objects `value` (supplied) and `seqinfo(x)` (current) must be identical.

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

`isActiveSeq(x) <- value`: Allows the user to change which sequences will be actively accessed by the accessor methods by altering the contents of this named logical vector.
seqlevelsStyle(x), seqlevelsStyle(x) <- value: Get or set the seqname style for x. See the seqlevelsStyle generic getter and setter in the GenomeInfoDb package for more information.

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

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

Examples

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

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

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

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