

Package ‘EpiTxDb’

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Type Package

Title Storing and accessing epitranscriptomic information using the AnnotationDbi interface

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Description EpiTxDb facilitates the storage of epitranscriptomic information. More specifically, it can keep track of modification identity, position, the enzyme for introducing it on the RNA, a specifier which determines the position on the RNA to be modified and the literature references each modification is associated with.

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LazyData false

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Depends R (>= 4.0), AnnotationDbi, Modstrings

Imports methods, utils, httr, xml2, curl, GenomicFeatures, GenomicRanges, GenomeInfoDb, BiocGenerics, BiocFileCache, S4Vectors, IRanges, RSQLite, DBI, Biostrings, tRNAdbImport

Suggests BiocStyle, knitr, rmarkdown, testthat, httpptest, AnnotationHub, ensemblDb, ggplot2, EpiTxDb.Hs.hg38, BSgenome.Hsapiens.UCSC.hg38, BSgenome.Scerevisiae.UCSC.sacCer3, TxDb.Hsapiens.UCSC.hg38.knownGene

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BugReports <https://github.com/FelixErnst/EpiTxDb/issues>

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R topics documented:

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| EpiTxDb-package | <i>EpiTxDb - Storing and accessing epitranscriptomic information using the AnnotationDbi interface</i> |
|-----------------|--|

Description

title

Author(s)

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References

Jia-Jia Xuan, Wen-Ju Sun, Ke-Ren Zhou, Shun Liu, Peng-Hui Lin, Ling-Ling Zheng, Liang-Hu Qu, Jian-Hua Yang (2017): "RMBase v2.0: Deciphering the Map of RNA Modifications from Epitranscriptome Sequencing Data." *Nucleic Acids Research*, Volume 46, Issue D1, 4 January 2018, Pages D327–D334. doi: 10.1093/nar/gkx934

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EpiTxDb-class

EpiTxDb objects

Description

The EpiTxDb class is a [AnnotationDb](#) type container for storing Epitranscriptomic information.

The information are typically stored on a per transcript and not as genomic coordinates, but the EpiTxDb class is agnostic to this. In case of genomic coordinates transcriptsBy will return modifications per chromosome.

Usage

```
## S4 method for signature 'EpiTxDb'  
organism(object)
```

```
## S4 method for signature 'EpiTxDb'  
seqinfo(x)
```

```
## S4 method for signature 'EpiTxDb'  
seqlevels(x)
```

```
## S4 method for signature 'EpiTxDb'  
as.list(x)
```

Arguments

x, object a EpiTxDb object

Value

For

- organism() and seqlevels() a character vector
- seqinfo() a [Seqinfo](#) object
- as.list() a list

See Also

- [makeEpiTxDbFromGRanges](#) for creating a EpiTxDb object from a [GRanges](#) object and its metadata columns
- [makeEpiTxDbFromRMBase](#) for creating a EpiTxDb object from RMBase online resources
- [makeEpiTxDbFromtRNadb](#) for creating a EpiTxDb object from tRNadb online resources
- [makeEpiTxDb](#) for creating a EpiTxDb object from data.frames
- [modifications](#), [modificationsBy](#) for getting epitranscriptomic modification locations
- [select](#) for using the default interface of [AnnotationDb](#) objects.
- [shiftGenomicToTranscript](#) and [shiftTranscriptToGenomic](#) for transferring genomic to transcript coordinates and back again.

Examples

```
etdb_file <- system.file("extdata", "EpiTxDb.Hs.hg38.snoRNadb.sqlite",
                        package="EpiTxDb")
etdb <- loadDb(etdb_file)
etdb

# general methods
seqinfo(etdb) #
seqlevels(etdb) # easy access to all transcript names
```

EpiTxDb-data

EpiTxDb internal data

Description

EpiTxDb internal data

Usage

```
data(rmbase_data)
```

Format

```
data.frame
```

makeEpiTxDb

Creating a EpiTxDb from user supplied annotations as data.frames

Description

makeEpiTxDb is a low-level constructor for creating a [EpiTxDb](#) object from user supplied annotations.

This functions typically will not be used by regular users.

Usage

```
makeEpiTxDb(
  modifications,
  reactions = NULL,
  specifiers = NULL,
  references = NULL,
  metadata = NULL,
  reassign.ids = FALSE
)
```

Arguments

modifications A `data.frame` containing the following columns:

- `mod_id`: a unique integer value per modification.
- `mod_type`: the modification type as a character or factor value. Must be a value from `shortName(ModRNAStrng())`.
- `mod_name`: a character or factor name for the specific modification
- `mod_start`: the start position for the modification as integer value. Usually `mod_start = mod_end`
- `mod_end`: the end position for the modification as integer value. Usually `mod_start = mod_end`
- `mod_strand`: the strand information for the modification as a character or factor.
- `sn_id`: a integer value per unique sequence
- `sn_name`: a character or factor as sequence name, e.g a chromosome or a transcript identifier like `chr1`.

The first six are mandatory, whereas one of the last two has to be set. `sn_id` will be generated from `sn_name`, if `sn_id` is not set.

reactions An optional `data.frame` containing the following columns:

- `mod_id`: a integer value per modification and the link to the modification `data.frame`.
- `rx_genename`: a character or factor referencing a genename for the enzyme incorporating the modification.

- rx_rank: a integer for sorting enzyme reactions, if multiple enzymes are involved in the modification's incorporation/maintenance.
- rx_ensembl: a character or factor with an ensembl identifier for the gene name of the enzyme.
- rx_ensembltrans: a character or factor with an ensembl identifier for the transcript being translated into the enzyme.
- rx_entrezid: a character or factor with an entrezid for the gene name of the enzyme.

(default: reactions = NULL)

specifiers An optional data.frame containing the following columns:

- mod_id: a integer value per modification and the link to the modification data.frame.
- spec_type: a character or factor referencing a type of specifier, e.g. snoRNA. Not checked for validity.
- spec_gene name: a character or factor referencing a gene name for the specifier directing an enzyme to the specific location for the modification to be incorporated.
- spec_ensembl: a character or factor with an ensembl identifier for the gene name of the specifier.
- spec_ensembltrans: a character or factor with an ensembl identifier for the transcript being translated into the specifier.
- spec_entrezid: a character or factor with an entrezid for the gene name of the specifier.

(default: specifiers = NULL)

references An optional data.frame containing the following columns:

- mod_id: a integer value per modification and the link to the modification data.frame.
- ref_type: a character or factor with a reference type, e.g. PMID. Is not checked for validity.
- ref: a character or factor with a reference value, e.g. a specific pubmed id or an journal article. Is not checked for validity.

(default: references = NULL)

metadata An optional data.frame containing the following columns:

- name: a character value used as name
- value: a character value

This dataframe will be returned by metadata() (default: metadata = NULL)

reassign.ids TRUE or FALSE Controls how internal mod_ids should be assigned. If reassign.ids is FALSE (the default) 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 modifications first by chromosome, then by strand, then by start, and finally by end.

Value

a EpiTxDb object.

See Also

- [makeEpiTxDbFromGRanges](#) for creating a EpiTxDb object from a [GRanges](#) object and its metadata columns
- [makeEpiTxDbFromRMBase](#) for creating a EpiTxDb object from RMBase online resources
- [makeEpiTxDbFromtRNadb](#) for creating a EpiTxDb object from tRNadb online resources
- [shortName](#) and [ModRNAString](#) for information on ModRNAString objects.

Examples

```

mod <- data.frame("mod_id" = 1L,
                 "mod_type" = "m1A",
                 "mod_name" = "m1A_1",
                 "mod_start" = 1L,
                 "mod_end" = 1L,
                 "mod_strand" = "+",
                 "sn_id" = 1L,
                 "sn_name" = "test")
rx <- data.frame(mod_id = 1L,
                 rx_genename = "test",
                 rx_rank = 1L,
                 rx_ensembl = "test",
                 rx_ensembltrans = "test",
                 rx_entrezid = "test")
spec <- data.frame(mod_id = 1L,
                  spec_type = "test",
                  spec_genename = "test",
                  spec_ensembl = "test",
                  spec_ensembltrans = "test",
                  spec_entrezid = "test")
ref <- data.frame(mod_id = 1L,
                 ref_type = "test",
                 ref = "test")
etdb <- makeEpiTxDb(mod,rx,spec,ref)

```

makeEpiTxDbFromGRanges

Create a EpiTxDb object from a GRanges object

Description

makeEpiTxDbFromGRanges extracts informations from a [GRanges](#) object. The following metadata columns can be used:

- mod_id, mod_type, mod_name and tx_ensembl. The first three are mandatory, whereas tx_ensembl is optional.
- rx_genename, rx_rank, rx_ensembl, rx_ensembltrans and rx_entrezid
- spec_type, spec_genename, spec_ensembl, spec_ensembltrans and spec_entrezid
- ref_type and ref

... and passed on the [makeEpiTxDb](#).

Usage

```
makeEpiTxDbFromGRanges(gr, metadata = NULL, reassign.ids = FALSE)
```

Arguments

`gr` A [GRanges](#) object, which contains at least the mandatory columns.

`metadata` A 2-column `data.frame` containing meta information to be included in the `EpiTxDb` object. This `data.frame` is just passed to `makeEpiTxDb`. See `makeEpiTxDb` for more information about the format of metadata. (default: `metadata = NULL`)

`reassign.ids` = FALSE

Value

a `EpiTxDb` object.

Examples

```
library(GenomicRanges)
gr <- GRanges(seqnames = "test",
              ranges = IRanges::IRanges(1,1),
              strand = "+",
              DataFrame(mod_id = 1L,
                       mod_type = "Am",
                       mod_name = "Am_1"))
etdb <- makeEpiTxDbFromGRanges(gr)
```

`makeEpiTxDbFromRMBase` *Create a `EpiTxDb` object from `RMBase` v2.0 online resources*

Description

`makeEpiTxDbFromRMBase` will make use of the `RMBase` v2.0 online resources.

Usage

```
EPITXDB_RMBASE_URL

downloadRMBaseFiles(organism, genome, modtype)

makeEpiTxDbFromRMBase(
  organism,
  genome,
  modtype,
  tx = NULL,
  sequences = NULL,
  metadata = NULL,
  reassign.ids = FALSE)
```

```

)

getRMBaseDataAsGRanges(files)

makeEpiTxDbFromRMBaseFiles(
  files,
  tx = NULL,
  sequences = NULL,
  metadata = NULL,
  reassign.ids = FALSE
)

listAvailableOrganismsFromRMBase()

listAvailableGenomesFromRMBase(organism)

listAvailableModFromRMBase(organism, genome)

```

Arguments

| | |
|------------------------|---|
| organism | A character value, which must match an organism descriptor on the RMBase download website. |
| genome | A character value, which must match a genome descriptor on the RMBase download website. |
| modtype | A character value, which must match one or more modification descriptors on the RMBase download website. |
| tx | A GRangesList object which will be used to shift the genomic coordinates to transcript coordinates. This is optional, but highly recommended. (default: tx = NULL). |
| sequences | A named DNAStringSet or RNAStringSet , which will be used to check whether the defined modifications are compatible with the original base. This uses removeIncompatibleModifications function from the Modstrings package. |
| metadata, reassign.ids | See makeEpiTxDb |
| files | From organism, genome and modtype the available files will be downloaded using the BiocFileCache interface and passed on to makeEpiTxDbFromRMBaseFiles . However, individual files can be provided as well. |

Format

An object of class character of length 1.

Value

a [EpiTxDb](#) object.

makeEpiTxDbFromtRNAdb *Create a EpiTxDb object from tRNAdb resources*

Description

makeEpiTxDbFromtRNAdb will make use of the tRNAdb online resources and extract the modification information from the RNA database.

If a named [DNAStrngSet](#) is provided as sequences, the result from the tRNAdb will be matched against the sequences. Valid matches will be used as transcript identifiers and returned after a check of modification compatibility with the provided sequence. By this process multiple copies of transcripts can be associated with a single modification.

makeEpiTxDbFromtRNAdb uses the functions provided by the [tRNAdbImport](#) package. `import.tRNAdb` will be used with `database = "RNA"` and the three different values for `origin`.

Usage

```
gettRNAdbDataAsGRanges(  
  organism,  
  sequences = NULL,  
  dbURL = tRNAdbImport::TRNA_DB_URL  
)  
  
makeEpiTxDbFromtRNAdb(  
  organism,  
  sequences = NULL,  
  metadata = NULL,  
  dbURL = tRNAdbImport::TRNA_DB_URL  
)  
  
listAvailableOrganismsFromtRNAdb()
```

Arguments

| | |
|-----------|--|
| organism | A character value for an organism available on the tRNAdb website. |
| sequences | A named DNAStrngSet or RNAStrngSet , which will be used to associate a tRNAdb result with a specific transcript. |
| dbURL | The URL to the tRNA db website. |
| metadata | See makeEpiTxDb |

Value

a EpiTxDb object.

References

Juehling F, Moerl M, Hartmann RK, Sprinzl M, Stadler PF, Puetz J. 2009. "tRNADB 2009: compilation of tRNA sequences and tRNA genes." *Nucleic Acids Research*, Volume 37 (suppl_1): D159–162. doi:10.1093/nar/gkn772.

Examples

```
## Not run:
# getting just the annotation data
etdb <- makeEpiTxDbFromtRNADB("Saccharomyces cerevisiae")

# For associating the result with transcripts, provide an additional
# named DNASTringSet object. Matching will be done against each sequence
# allowing 5 mismatches and indels. The final result will be checked for
# validity regarding the identity of the modifications
etdb <- makeEpiTxDbFromtRNADB("Saccharomyces cerevisiae",
                             some_transcript_sequences)

## End(Not run)
```

modifications

Getting modification data from a EpiTxDb-object

Description

`modifications` and `modificationsBy` are functions to extract modification annotation from a [EpiTxDb](#) object.

`modifiedSeqsByTranscript` returns a [ModRNAStringSet](#) from a [EpiTxDb](#) object and compatible [RNAStringSet](#) object. This used the [combineIntoModstrings\(\)](#) function from the [Modstrings](#) package.

Usage

```
modifications(
  x,
  columns = c("mod_id", "mod_type", "mod_name"),
  filter = NULL,
  use.names = FALSE,
  ...
)

modificationsBy(
  x,
  by = c("seqnames", "mod_type", "reaction", "specifier", "specifier_type"),
  ...
)
```

```

modifiedSeqsByTranscript(x, sequences, ...)

## S4 method for signature 'EpiTxDb'
modifications(
  x,
  columns = c("mod_id", "mod_type", "mod_name"),
  filter = NULL,
  use.names = FALSE
)

## S4 method for signature 'EpiTxDb'
modificationsBy(
  x,
  by = c("seqnames", "modtype", "reaction", "specifier", "specifiertype")
)

## S4 method for signature 'EpiTxDb,DNAStringSet'
modifiedSeqsByTranscript(x, sequences)

```

Arguments

| | |
|-----------|--|
| x | a EpiTxDb |
| columns | Columns to include in the result. If the vector is named, those names are used for the corresponding column in the element metadata of the returned object. (default: columns = c("mod_id", "mod_type", "mod_name")) |
| filter | Either NULL or a named list of vectors to be used to restrict the output. Valid names for this list are: "mod_id", "mod_type", "mod_name", "sn_id", "sn_name", "rx_genename", "rx_ensembl", "rx_ensembltrans", "rx_entrezid", "spec_genename", "spec_type", "spec_ensembl", "spec_ensembltrans", "spec_entrezid", "ref_type" and "ref". (default: filter = NULL) |
| use.names | TRUE or FALSE. If TRUE, the modification names are set as the names of the returned object. (default: use.names = FALSE) |
| ... | Not used. |
| by | By which information type should the result be split into? A character value from one of the following values: <ul style="list-style-type: none"> • seqnames • mod_type • reaction • specifier • specifier_type |
| sequences | A RNAStringSet , which can be used as input for combineIntoModstrings() . See ?combineIntoModstrings for additional details. |

Value

a [GRanges](#) object for modifications and a [GRangesList](#) for modificationsBy.

Examples

```
etdb_file <- system.file("extdata", "EpiTxDb.Hs.hg38.snoRNADB.sqlite",
                        package="EpiTxDb")
etdb <- loadDb(etdb_file)
etdb
```

positionSequence *Generate integer sequences from position information of Ranges*

Description

positionSequence generates sequences of integer values along the range information of x. This can be used for navigating specific positions on a range information.

Usage

```
positionSequence(x, order = FALSE, decreasing = FALSE)

## S4 method for signature 'Ranges'
positionSequence(x, order = FALSE, decreasing = FALSE)

## S4 method for signature 'RangesList'
positionSequence(x, order = FALSE, decreasing = FALSE)

## S4 method for signature 'Ranges'
as.integer(x)
```

Arguments

| | |
|------------|--|
| x | a Ranges object, like a GRanges or IRanges , or a RangesList object, like a GRangesList or IRangesList |
| order | TRUE or FALSE: Should the position be ordered? (default: order = FALSE) |
| decreasing | TRUE or FALSE: If order = TRUE Should the position be ordered in a decreasing order? (default: order = FALSE) |

Value

a integer vector if x is a [GRanges](#) object and a IntegerList if x is a [GRangesList](#)

Examples

```
library(GenomicRanges)
# Returns an integer vector
gr <- GRanges("chr1:1-5:+")
positionSequence(gr)
gr2 <- GRanges("chr1:1-5:-")
positionSequence(gr)
```

```
# returns an IntegerList
gr1 <- GRangesList("1" = gr,"2" = gr,"3" = gr2) # must be named
positionSequence(gr1)
```

rescale

Rescaling Ranges object

Description

rescale() rescales IRanges, GRanges, IRangesList and GRangesList by using minima and maxima derived from to and from.

Usage

```
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'IRanges'
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'IRangesList'
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'GRanges'
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'GRangesList'
rescale(x, to = 1L, from = 1L)
```

Arguments

| | |
|----------|---|
| x | a IRanges, GRanges, IRangesList and GRangesList object |
| to, from | an IRanges object, a character vector coercible to IRanges or a integer vector parallel to x or with length = 1L. |

Value

an object of the same type and dimensions as x

Author(s)

H. Pagès, F. Ernst

See Also

[IRanges](#) for details on character vectors coercible to IRanges.

Examples

```
x <- IRanges("5-10")
# widen the ranges
rescale(x, 100, 10)
# widen and shift
rescale(x, "31-60", "5-14")
```

select

Using the "select" interface on EpiTxDb objects

Description

As expected for a `AnnotationDb` object, the general accessors `select`, `keys`, `columns` and `keytypes` can be used to get information from a [EpiTxDb](#) object.

Usage

```
## S4 method for signature 'EpiTxDb'
select(x, keys, columns, keytype, ...)

## S4 method for signature 'EpiTxDb'
columns(x)

## S4 method for signature 'EpiTxDb'
keys(x, keytype, ...)

## S4 method for signature 'EpiTxDb'
keytypes(x)
```

Arguments

`x` a [EpiTxDb](#) object
`keys`, `columns`, `keytype`, ...

See [AnnotationDb](#) for more comprehensive description of the methods `select`, `keys`, `columns` and `keytypes` and their arguments.

Value

a `data.frame` object for `select()` and a character vector for `keytypes()`, `keys()` and `columns()`.

Examples

```
etdb_file <- system.file("extdata", "EpiTxDb.Hs.hg38.snoRNADB.sqlite",
                        package="EpiTxDb")
etdb <- loadDb(etdb_file)
etdb
```

`shiftTranscriptToGenomic`*Shift GRanges coordinates based on another GRanges object*

Description

`shiftGenomicToTranscript` shifts positions of a [GRanges](#) object based on coordinates of another [GRanges](#) object. The most common application is to shift genomic coordinates to transcript coordinates, which is reflected in the name. `shiftTranscriptToGenomic` implements the reverse operation.

Matches are determined by [findOverlaps](#) for `shiftGenomicToTranscript` and by [findMatches](#) for `shiftTranscriptToGenomic` using the seqnames of the subject and the names of tx.

Usage

```
shiftTranscriptToGenomic(subject, tx)

shiftGenomicToTranscript(subject, tx)

## S4 method for signature 'GRanges,GRangesList'
shiftTranscriptToGenomic(subject, tx)

## S4 method for signature 'GRangesList,GRangesList'
shiftTranscriptToGenomic(subject, tx)

## S4 method for signature 'GRanges,GRangesList'
shiftGenomicToTranscript(subject, tx)

## S4 method for signature 'GRangesList,GRangesList'
shiftGenomicToTranscript(subject, tx)
```

Arguments

`subject` a [GRanges](#) or [GRangesList](#) object
`tx` a named [GRangesList](#) object.

Value

a [GRanges](#) or [GRangesList](#) object depending on the type of subject

Examples

```
library(GenomicRanges)
# Construct some example data
subject1 <- GRanges("chr1", IRanges(3, 6),
                    strand = "+")
subject2 <- GRanges("chr1", IRanges(c(17,23), width=3),
```

```
strand = c("+","-"))
subject3 <- GRanges("chr2", IRanges(c(51, 54), c(53, 59)),
strand = "-")
subject <- GRangesList(a=subject1, b=subject2, c=subject3)
tx1 <- GRanges("chr1", IRanges(1, 40),
strand="+")
tx2 <- GRanges("chr1", IRanges(10, 30),
strand="+")
tx3 <- GRanges("chr2", IRanges(50, 60),
strand="-")
tx <- GRangesList(a=tx1, b=tx2, c=tx3)

# shift to transcript coordinates. Since the third subject does not have
# a match in tx it is dropped with a warning
shifted_gr1 <- shiftGenomicToTranscript(subject,tx)

# ... and back
shifted_gr12 <- shiftTranscriptToGenomic(shifted_gr1,tx)

# comparison of ranges work. However the seqlevels differ
ranges(shifted_gr12) == ranges(subject[list(1,c(1,1),c(1,2))])
```

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