

Package ‘scanMiRApp’

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Description A shiny interface to the scanMiR package. The application enables the scanning of transcripts and custom sequences for miRNA binding sites, the visualization of KdModels and binding results, as well as browsing predicted repression data. In addition contains the IndexedFst class for fast indexed reading of large GenomicRanges or data.frames, and some utilities for facilitating scans and identifying enriched miRNA-target pairs.

Depends R (>= 4.0), scanMiR

License GPL-3

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| | |
|--------------------|---------------------------|
| enrichedMirTxPairs | <i>enrichedMirTxPairs</i> |
|--------------------|---------------------------|

Description

Identifies pairs of miRNA and target transcripts that have an unexpectedly high number of sites.

Usage

```
enrichedMirTxPairs(m, minSites = 5, max.binom.p = 0.001)
```

Arguments

| | |
|--------------------------|---|
| <code>m</code> | A GRanges of matches, as produced by <code>findSeedMatches</code> . This will be filtered down to only 8mer and 7mer sites. |
| <code>minSites</code> | The minimum number of sites for a given miRNA-target pair to be considered. |
| <code>max.binom.p</code> | The maximum binomial p-value of miRNA-target pairs. |

Value

A data.frame of top combinations, including number of sites and the log-transformed binomial p-value.

Examples

```
# we create a dummy scan (see `runFullScan`)
library(scanMiR)
seqs <- getRandomSeq(n=10)
mirs <- c("TTGTATAA", "AGCATTAA")
m <- findSeedMatches(seqs, mirs, verbose=FALSE)
# we look for enriched pairs
res <- enrichedMirTxPairs(m, minSites=1, max.binom.p=1)
res
```

| | |
|----------|-----------------------------------|
| fakeTxDb | <i>Example 'fake' TxDb object</i> |
|----------|-----------------------------------|

Description

A fake transcript database used for examples.

Value

a named character vector of length 1.

getTranscriptSequence *getTranscriptSequence*

Description

Utility wrapper to extracts the sequence of a given transcript (UTR or CDS+UTR).

Usage

```
getTranscriptSequence(
  tx = NULL,
  annotation,
  annoFilter = NULL,
  extract = c("UTRonly", "withORF", "exons"),
  ...
)
```

Arguments

| | |
|------------|--|
| tx | The ensembl ID of the transcript(s) |
| annotation | A ScanMiRAnno object. |
| annoFilter | An optional 'AnnotationFilter' or 'AnnotationFilterList' to further filter the set of transcripts to be extracted |
| extract | Which parts of the transcripts to extract. For 'UTRonly' (default) only the 3' UTR regions are extracted, 'withORF' additionally extracts the coding regions, and 'exons' extracts all exons |
| ... | Passed to AnnotationHub |

Value

A [DNAStrngSet](#).

Examples

```
anno <- ScanMiRAnno("fake")
seq <- getTranscriptSequence( tx="ENSTFAKE0000056456", annotation=anno )
```

| | |
|------------------|-------------------|
| IndexedFst-class | <i>IndexedFst</i> |
|------------------|-------------------|

Description

Objects of the IndexedFst class enable fast named random access to FST files. This is particularly appropriate for large data.frames which often need to be accessed according to the (e.g. factor) value of a particular column.

Usage

```
## S4 method for signature 'IndexedFst'  
show(object)  
  
## S4 method for signature 'IndexedFst'  
summary(object)  
  
## S4 method for signature 'IndexedFst'  
names(x)  
  
## S4 method for signature 'IndexedFst'  
length(x)  
  
## S4 method for signature 'IndexedFst'  
lengths(x)  
  
## S4 method for signature 'IndexedFst'  
nrow(x)  
  
## S4 method for signature 'IndexedFst'  
ncol(x)  
  
## S4 method for signature 'IndexedFst'  
colnames(x)  
  
## S4 method for signature 'IndexedFst,ANY,ANY'  
x[[i, j = NULL, ...]]  
  
## S4 method for signature 'IndexedFst,ANY,ANY,ANY'  
x[i, j = NULL, ..., drop = TRUE]  
  
## S4 method for signature 'IndexedFst'  
x$name  
  
## S4 method for signature 'IndexedFst'  
head(x, n = 6L, ...)  
  
## S4 method for signature 'IndexedFst'  
as.data.frame(x, name)
```

Arguments

| | |
|---------|--|
| object | an IndexedFst object |
| x | an IndexedFst object |
| i | the desired index (either numeric or name) |
| j, drop | ignored |
| ... | ignored |
| name | the indexed name to fetch |
| n | the desired number of rows |

Value

Depends on the method

Author(s)

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See Also

[saveIndexedFst](#), [loadIndexedFst](#)

Examples

```
# we first create and save an indexed FST file
tmp <- tempdir()
f <- system.file(tmp, "test")
d <- data.frame( category=sample(LETTERS[1:4], 10000, replace=TRUE),
                 var2=sample(LETTERS, 10000, replace=TRUE),
                 var3=runif(10000) )
format(object.size(d),units="Kb")
saveIndexedFst(d, "category", f)
rm(d)
# we then load the index, and can use category names for random access:
d <- loadIndexedFst(f)
format(object.size(d),units="Kb")
nrow(d)
names(d)
head(d$A)
```

loadIndexedFst

Saving and loading IndexedFst

Description

Functions to save or load and indexed [fst](#) file

Saves a data.frame (or GRanges object) into an indexed FST file.

Usage

```
loadIndexedFst(file, nthreads = 1)

saveIndexedFst(
  d,
  index.by,
  file.prefix,
  nthreads = 1,
  index.properties = NULL,
  add.info = list(),
  ...
)
```

Arguments

| | |
|------------------|--|
| file | Path to the fst file, it's index (.idx), or their prefix. |
| nthreads | Number of threads to use for reading (default 1). This does not affect the loading of the index itself, but will affect all downstream reading operations performed on the object. If NULL, will use 'fst::threads_fst()'. |
| d | A data.frame or GRanges object |
| index.by | A column of 'd' by which it should be indexed. |
| file.prefix | Path and prefix of the output files. |
| index.properties | An optional data.frame of properties, with the levels of 'index.by' as row names. |
| add.info | An optional list of additional information to save. |
| ... | Passed to 'write.fst' |

Value

'loadIndexedFst' returns an object of class [IndexedFst-class](#), and 'saveIndexedFst' returns nothing.

See Also

[IndexedFst-class](#)
[IndexedFst-class](#)

Examples

```
# we first create and save an indexed FST file
tmp <- tempdir()
f <- system.file(tmp, "test")
d <- data.frame( category=sample(LETTERS[1:4], 10000, replace=TRUE),
                var2=sample(LETTERS, 10000, replace=TRUE),
                var3=runif(10000) )
saveIndexedFst(d, "category", f)
# we then load the index, and can use category names for random access:
d <- loadIndexedFst(f)
```

| | |
|----------------|-----------------------|
| plotSitesOnUTR | <i>plotSitesOnUTR</i> |
|----------------|-----------------------|

Description

Wrapper function with minimal arguments to plot scanMiR-Binding sites on 3'UTRs of specified transcripts. The red dashed line indicates the background threshold is indicated, the lightblue dashed line shows the average 8mer dissociation rate of the given miRNA

Usage

```
plotSitesOnUTR(
  tx,
  annotation,
  miRNA = NULL,
  label_6mers = FALSE,
  label_notes = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

| | |
|-------------|---|
| tx | An ensembl TranscriptID |
| annotation | A ScanMiRAnno object. |
| miRNA | A miRNA name in the mirbase format (eg. "hsa-miR-485-5p"), a 'KdModel', or a miRNA sequence or target seed. |
| label_6mers | Logical whether to label 6mer sites in the plot |
| label_notes | Logical whether to label special sites in the plot (as TDMD or Slicing) |
| verbose | Logical; whether to print updates on the processing |
| ... | Any further arguments passed to findSeedMatches |

Value

Returns a ggplot.

Examples

```
anno <- ScanMiRAnno("fake")
plotSitesOnUTR( tx="ENSTFAKE0000056456", annotation=anno,
  miRNA="hsa-miR-155-5p" )
```

| | |
|-------------|--------------------|
| runFullScan | <i>runFullScan</i> |
|-------------|--------------------|

Description

Runs a full miRNA scan on all protein-coding transcripts (or UTRs) of an annotation.

Usage

```
runFullScan(
  annotation,
  mods = NULL,
  annoFilter = NULL,
  extract = c("UTRonly", "withORF", "exons"),
  onlyCanonical = TRUE,
  shadow = 15,
  cores = 1,
  maxLogKd = c(-1, -1.5),
  save.path = NULL,
  ...
)
```

Arguments

| | |
|---------------|--|
| annotation | A ScanMiRAnno object |
| mods | An optional 'KdModelList' (defaults to the one in 'annotation') |
| annoFilter | An optional 'AnnotationFilter' or 'AnnotationFilterList' to filter the set of transcripts to be extracted |
| extract | Which parts of the transcripts to extract. For 'UTRonly' (default) only the 3' UTR regions are extracted, 'withORF' additionally extracts the coding regions, and 'exons' extracts all exons |
| onlyCanonical | passed to findSeedMatches |
| shadow | The size of the ribosomal shadow at the UTR starts |
| cores | The number of threads to use. Alternatively accepts a BiocParallelParam-class , as for instance produced by MulticoreParam . |
| maxLogKd | The maximum log _{kd} of sites to report |
| save.path | Optional, the path to which to save the results |
| ... | Arguments passed to findSeedMatches |

Value

A 'GRanges' object

Examples

```
anno <- ScanMiRAnno("fake")
m <- runFullScan( annotation=anno )
m
```

ScanMiRAnno-class *ScanMiRAnno*

Description

ScanMiRAnno

Usage

```
ScanMiRAnno(
  species = NULL,
  genome = NULL,
  ensdb = NULL,
  models = NULL,
  scan = NULL,
  aggregated = NULL,
  version = NULL,
  addDBs = list(),
  ...
)
```

Arguments

| | |
|------------|--|
| species | The species/build acronym for automatic construction; if omitted, 'genome' and 'ensdb' should be given. Current possible values are: GRCh38, GRCm38, GRCm39, Rnor_6. |
| genome | A BSgenome-class , or a TwoBitFile |
| ensdb | An EnsDb-class (or a TxDb-class) object |
| models | An optional KdModelList |
| scan | An optional full scan (IndexedFst or GRanges) |
| aggregated | An optional per-transcript aggregation (IndexedFst or data.frame) |
| version | optional ensembl version |
| addDBs | A named list of additional tx-miRNA databases, each of which should be a data.frame with the columns 'transcript', 'miRNA', and 'score'. |
| ... | Arguments passed to 'AnnotationHub' |

Value

A 'ScanMiRAnno' object

Examples

```
anno <- ScanMiRAnno(species="fake")
anno
```

ScanMiRAnno-methods *Methods for the [ScanMiRAnno](#) class*

Description

Methods for the [ScanMiRAnno](#) class

Usage

```
## S4 method for signature 'ScanMiRAnno'  
summary(object)
```

```
## S4 method for signature 'ScanMiRAnno'  
show(object)
```

Arguments

object An object of class [ScanMiRAnno](#)

Value

Depends on the method.

See Also

[ScanMiRAnno](#)

scanMiRApp *scanMiRApp A wrapper for launching the scanMiRApp shiny app*

Description

scanMiRApp A wrapper for launching the scanMiRApp shiny app

Usage

```
scanMiRApp(annotations = NULL, ...)
```

Arguments

annotations A named list of [ScanMiRAnno](#) objects. If omitted, will use the base ones.

... Passed to [scanMiRserver](#)

Value

A shiny app

Examples

```
if(interactive()){
  anno <- ScanMiRAnno("fake")
  scanMiRApp(list(fakeAnno=anno))
}
```

| | |
|---------------|----------------------|
| scanMiRserver | <i>scanMiRserver</i> |
|---------------|----------------------|

Description

Server function for the scanMiR shiny app. Most users are expected to use [scanMiRApp](#) instead.

Usage

```
scanMiRserver(
  annotations = list(),
  modlists = NULL,
  gc.time = Inf,
  maxCacheSize = 10 * 10^6,
  BP = SerialParam()
)
```

Arguments

| | |
|--------------|---|
| annotations | A named list of ScanMiRAnno object. |
| modlists | A named list of 'KdModelList' objects. If omitted, will fetch it from the annotation objects. |
| gc.time | The number of microseconds after which a garbage collect should be performed. |
| maxCacheSize | Maximum cache size in bytes. |
| BP | BPPARAM for multithreading |

Value

A shiny server function

Examples

```
# we'd normally fetch a real annotation:
# anno <- ScanMiRAnno("Rnor_6")
# here we'll use a fake one:
anno <- ScanMiRAnno("fake")
srv <- scanMiRserver(list(fake=anno))
```

`scanMiRui`*scanMiRui*

Description

UI for the scanMiR app.

Usage

```
scanMiRui()
```

Value

A shiny ui

Examples

```
ui <- scanMiRui()
```

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