

# Package ‘scanMiRApp’

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**Title** scanMiR shiny application

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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)

**License** GPL-3

**VignetteBuilder** knitr

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**biocViews** miRNA, SequenceMatching, GUI

**Config/testthat/edition** 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 <a href="#">findSeedMatches</a> . 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
```

---

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 <a href="#">ScanMiRAnno</a> 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 <a href="#">AnnotationHub</a>  |

**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)

Pierre-Luc Germain, <pierre-luc.germain@hest.ethz.ch>

### 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

|                               |  |
|-------------------------------|--|
| <code>file</code>             | Path to the <code>fst</code> file, it's index ( <code>.idx</code> ), or their prefix.  |
| <code>nthreads</code>         | 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 <code>NULL</code> , will use <code>'fst::threads_fst()'</code> . |
| <code>d</code>                | A <code>data.frame</code> or <code>GRanges</code> object   |
| <code>index.by</code>         | A column of <code>'d'</code> by which it should be indexed.  |
| <code>file.prefix</code>      | Path and prefix of the output files.   |
| <code>index.properties</code> | An optional <code>data.frame</code> of properties, with the levels of <code>'index.by'</code> as row names.  |
| <code>add.info</code>         | An optional list of additional information to save.  |
| <code>...</code>              | Passed to <code>'write.fst'</code>   |

### 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      plotSitesOnUTR
```

---

**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 <a href="#">ScanMiRAnno</a> 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 <a href="#">findSeedMatches</a>   |

**Value**

Returns a ggplot.

**Examples**

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

---

runFullScan

*runFullScan*


---

**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 <a href="#">ScanMiRAnno</a> 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 <a href="#">findSeedMatches</a>  |
| shadow        | The size of the ribosomal shadow at the UTR starts   |
| cores         | The number of threads to use. Alternatively accepts a <a href="#">BiocParallelParam-class</a> , as for instance produced by <a href="#">MulticoreParam</a> .                                 |
| maxLogKd      | The maximum log <sub>k</sub> d of sites to report  |
| save.path     | Optional, the path to which to save the results  |
| ...           | Arguments passed to <a href="#">findSeedMatches</a>  |



**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, Rnor_6. |
| genome     | A <a href="#">BSgenome-class</a> , or a <a href="#">TwoBitFile</a>   |
| ensdb      | An <a href="#">EnsDb-class</a> (or a <a href="#">TxDb-class</a> ) object   |
| models     | An optional <a href="#">KdModelList</a>  |
| scan       | An optional full scan ( <a href="#">IndexedFst</a> or <a href="#">GRanges</a> )  |
| aggregated | An optional per-transcript aggregation ( <a href="#">IndexedFst</a> or <a href="#">data.frame</a> )  |
| version    | optional ensembl version   |
| addDBs     | A named list of additional tx-miRNA databases, each of which should be a <a href="#">data.frame</a> with the columns ‘transcript’, ‘miRNA’, and ‘score’.     |
| ...        | Arguments passed to ‘ <a href="#">AnnotationHub</a> ’  |

**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 | <i>scanMiRApp</i> 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 <a href="#">ScanMiRAnno</a> objects. If omitted, will use the base ones. |
| ...         | Passed to <a href="#">scanMiRserver</a>  |

**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,  
  maxCacheSize = 10 * 10^6,  
  BP = SerialParam()  
)
```

**Arguments**

|              |   |
|--------------|---|
| annotations  | A named list of <code>ScanMiRAnno</code> object.  |
| modlists     | A named list of ‘KdModelList’ objects. If omitted, will fetch it from the annotation objects. |
| 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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